



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 131140

TO: James Schultz
Location: REM/2D18/2C18
Art Unit: 1635
Monday, August 30, 2004

Case Serial Number: 09/925139

From: David Schreiber
Location: Biotech-Chem Library
Remsen E01A61
Phone: 272-2526

david.schreiber@uspto.gov

Search Notes

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 09:17:56 ; Search time 1 Seconds
(without alignments)
3.307 Million cell updates/sec

Title: US-09-925-139-3

Perfect score: 139

Sequence: 1 ggatggggctgttagcagaa.....ctatcctaaaggccactgg 139

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 718 seqs, 11895 residues

Total number of hits satisfying chosen parameters: 1436

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 739 summaries

Database : rge3.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	15.1	21	1	BD102270
C 2	17.2	12.4	22	1	ACCESION: E25734
C 3	16.8	12.1	21	1	ACCESION: BD101979
C 4	16.8	12.1	21	1	ACCESION: BD101979
C 5	16.4	11.8	20	1	ACCESION: BD131270
C 6	16.2	11.7	22	1	ACCESION: AR381288
C 7	15.2	10.9	20	1	ACCESION: AR129513
C 8	15.2	10.9	23	1	ACCESION: AR142933
C 9	14.4	10.4	20	1	ACCESION: AR293741
C 10	14.4	10.4	20	1	ACCESION: AR488425
C 11	14.4	10.4	20	1	ACCESION: AR171443
C 12	14.2	10.2	20	1	ACCESION: AR011791
C 13	14.2	10.2	20	1	ACCESION: AR025499
C 14	14.2	10.2	20	1	ACCESION: E08471
C 15	14.2	10.2	20	1	ACCESION: E08471
C 16	14.2	10.2	20	1	ACCESION: E26707
C 17	14.2	10.2	20	1	ACCESION: AR211960
C 18	14.2	10.2	20	1	ACCESION: AR281496
C 19	14.2	10.2	20	1	ACCESION: BD185884
C 20	14	10.1	20	1	ACCESION: AR777492
C 21	13.8	9.9	18	1	ACCESION: A06347
C 22	13.8	9.9	20	1	ACCESION: BD074024
C 23	13.8	9.9	20	1	ACCESION: AR241103
C 24	13.8	9.9	20	1	ACCESION: AR281777
C 25	13.8	9.9	20	1	ACCESION: AR250715
C 26	13.8	9.9	20	1	ACCESION: AR253315
C 27	13.8	9.9	20	1	ACCESION: AR283518
C 28	13.8	9.9	20	1	ACCESION: BD006136
C 29	13.6	9.8	20	1	ACCESION: BD179019
C 30	13.6	9.8	20	1	ACCESION: A98445
C 31	13.6	9.8	20	1	ACCESION: AR050289
C 32	13.6	9.8	20	1	ACCESION: AR100579
C 33	13.6	9.8	20	1	ACCESION: AR100585
C 34	13.6	9.8	20	1	ACCESION: AR158965
C 35	13.6	9.8	20	1	ACCESION: AR158965
C 36	13.6	9.8	20	1	ACCESION: AR158965
C 37	13.6	9.8	20	1	ACCESION: AR158965
C 38	13.6	9.8	20	1	ACCESION: AR158965
C 39	13.6	9.8	20	1	ACCESION: AR158965
C 40	13.6	9.8	20	1	ACCESION: AR158965
C 41	13.6	9.8	20	1	ACCESION: AR158965
C 42	13.6	9.8	20	1	ACCESION: AR158965
C 43	13.4	9.6	18	1	ACCESION: AR352825
C 44	13.4	9.6	18	1	ACCESION: AR352825
C 45	13.4	9.6	18	1	ACCESION: AR352825
C 46	13.4	9.6	18	1	ACCESION: AR352825
C 47	13.4	9.6	19	1	ACCESION: BD088226
C 48	13.4	9.6	19	1	ACCESION: BD088234
C 49	13.4	9.6	19	1	ACCESION: AB069135
C 50	13.4	9.6	19	1	ACCESION: AB069137
C 51	13.4	9.6	20	1	ACCESION: AR163797
C 52	13.4	9.6	20	1	ACCESION: AR233647
C 53	13.2	9.5	18	1	ACCESION: A63088
C 54	13.2	9.5	18	1	ACCESION: AR018185
C 55	13.2	9.5	18	1	ACCESION: AR106914
C 56	13.2	9.5	18	1	ACCESION: AR173918
C 57	13.2	9.5	18	1	ACCESION: AR268665
C 58	13.2	9.5	18	1	ACCESION: BD089837
C 59	13.2	9.5	18	1	ACCESION: AB068204
C 60	13.2	9.5	19	1	ACCESION: AR011803
C 61	13.2	9.5	19	1	ACCESION: AR361501
C 62	13.2	9.5	20	1	ACCESION: A70767
C 63	13.2	9.5	20	1	ACCESION: A79251
C 64	13.2	9.5	20	1	ACCESION: AR163916
C 65	13.2	9.5	20	1	ACCESION: E08376
C 66	13.2	9.5	20	1	ACCESION: AR220154
C 67	13.2	9.5	20	1	ACCESION: AR315612
C 68	13.2	9.5	20	1	ACCESION: AX180379
C 69	13.2	9.5	20	1	ACCESION: AX268920
C 70	13.2	9.5	20	1	ACCESION: AX287952
C 71	13.2	9.5	20	1	ACCESION: BD003481
C 72	13.2	9.5	20	1	ACCESION: BD011678
C 73	13.2	9.5	20	1	ACCESION: BD011679
C 74	13.2	9.5	20	1	ACCESION: BD011680
C 75	12.8	9.2	16	1	ACCESION: AX710950
C 76	12.8	9.2	16	1	ACCESION: BD001091
C 77	12.8	9.2	16	1	ACCESION: BD001520
C 78	12.8	9.2	17	1	ACCESION: AR011799
C 79	12.8	9.2	17	1	ACCESION: AR192421
C 80	12.8	9.2	17	1	ACCESION: AR326290
C 81	12.8	9.2	17	1	ACCESION: AX421994
C 82	12.8	9.2	17	1	ACCESION: AX422971
C 83	12.8	9.2	17	1	ACCESION: AX673768
C 84	12.8	9.2	17	1	ACCESION: AX724290
C 85	12.8	9.2	17	1	ACCESION: AX753715
C 86	12.8	9.2	17	1	ACCESION: AX753716
C 87	12.8	9.2	17	1	ACCESION: AX805118
C 88	12.8	9.2	17	1	ACCESION: BD104946
C 89	12.8	9.2	18	1	ACCESION: AR011802
C 90	12.8	9.2	18	1	ACCESION: AR051200
C 91	12.8	9.2	18	1	ACCESION: AR106948
C 92	12.8	9.2	18	1	ACCESION: AR106981
C 93	12.8	9.2	19	1	ACCESION: AX129110
C 94	12.8	9.2	19	1	ACCESION: L77467
C 95	12.6	9.1	19	1	ACCESION: AR053162
C 96	12.6	9.1	19	1	ACCESION: E08539
C 97	12.6	9.1	19	1	ACCESION: E11147
C 98	12.6	9.1	19	1	ACCESION: AR296543
C 99	12.6	9.1	19	1	ACCESION: AX130657
C 100	12.6	9.1	19	1	ACCESION: AX131856
C 101	12.4	8.9	15	1	ACCESION: A28990
C 102	12.4	8.9	15	1	ACCESION: AR030911
C 103	12.4	8.9	15	1	ACCESION: I28303
C 104	12.4	8.9	16	1	ACCESION: AR127505
C 105	12.4	8.9	16	1	ACCESION: I50742
C 106	12.4	8.9	16	1	ACCESION: AR328506

ACCESION: E26692
ACCESION: I31522
ACCESION: AR298667
ACCESION: AR316120
ACCESION: AR316177
ACCESION: AR370267
ACCESION: AX115823
ACCESION: BD144090
ACCESION: AX723714
ACCESION: AX352825
ACCESION: AX352825
ACCESION: AX362670
ACCESION: AB069639
ACCESION: AX129291
ACCESION: BD088226
ACCESION: BD088234
ACCESION: AB069135
ACCESION: AB069137
ACCESION: AR163797
ACCESION: AR233647
ACCESION: A63088
ACCESION: AR018185
ACCESION: AR106914
ACCESION: AR173918
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ACCESION: AX180379
ACCESION: AX268920
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ACCESION: BD003481
ACCESION: BD011678
ACCESION: BD011679
ACCESION: BD011680
ACCESION: AX710950
ACCESION: BD001091
ACCESION: BD001520
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ACCESION: AR192421
ACCESION: AR326290
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ACCESION: AX422971
ACCESION: AX673768
ACCESION: AX724290
ACCESION: AX753715
ACCESION: AX753716
ACCESION: AX805118
ACCESION: BD104946
ACCESION: AR011802
ACCESION: AR051200
ACCESION: AR106948
ACCESION: AR106981
ACCESION: AX129110
ACCESION: L77467
ACCESION: AR053162
ACCESION: E08539
ACCESION: E11147
ACCESION: AR296543
ACCESION: AX130657
ACCESION: AX131856
ACCESION: A28990
ACCESION: AR030911
ACCESION: I28303
ACCESION: AR127505
ACCESION: I50742
ACCESION: AR328506

107	12.4	8.9	16	1	AX039862	ACCESSION:AX039862	180	12	8.6	17	1	AX723858	ACCESSION:AX723858
C 108	12.4	8.9	16	1	AX135793	ACCESSION:AX135793	181	12	8.6	18	1	AR169593	ACCESSION:AR169593
C 109	12.4	8.9	17	1	BD255127	ACCESSION:BD255127	C 182	12	8.6	18	1	BD235157	ACCESSION:BD235157
C 110	12.4	8.9	17	1	BD255128	ACCESSION:BD255128	C 183	12	8.6	18	1	BD235175	ACCESSION:BD235175
C 111	12.4	8.9	17	1	AR327591	ACCESSION:AR327591	C 184	12	8.6	18	1	BD235176	ACCESSION:BD235176
C 112	12.4	8.9	17	1	AX266079	ACCESSION:AX266079	C 185	12	8.6	18	1	E33346	ACCESSION:E33346
C 113	12.4	8.9	17	1	AX266080	ACCESSION:AX266080	186	12	8.6	18	1	AX599639	ACCESSION:AX599639
C 114	12.4	8.9	17	1	AX727607	ACCESSION:AX727607	187	11.8	8.5	15	1	A64217	ACCESSION:A64217
C 115	12.4	8.9	17	1	AX753717	ACCESSION:AX753717	C 188	11.8	8.5	15	1	AR011805	ACCESSION:AR011805
C 116	12.4	8.9	17	1	AX753718	ACCESSION:AX753718	C 189	11.8	8.5	15	1	AR102516	ACCESSION:AR102516
C 117	12.4	8.9	17	1	AX757161	ACCESSION:AX757161	C 190	11.8	8.5	15	1	I27821	ACCESSION:I27821
C 118	12.4	8.9	18	1	AR018181	ACCESSION:AR018181	C 191	11.8	8.5	15	1	I36660	ACCESSION:I36660
C 119	12.4	8.9	18	1	AR018183	ACCESSION:AR018183	C 192	11.8	8.5	15	1	I83457	ACCESSION:I83457
C 120	12.4	8.9	18	1	AR018184	ACCESSION:AR018184	C 193	11.8	8.5	15	1	I83461	ACCESSION:I83461
C 121	12.4	8.9	18	1	AR187552	ACCESSION:AR187552	C 194	11.8	8.5	15	1	AR213614	ACCESSION:AR213614
C 122	12.4	8.9	18	1	AR299488	ACCESSION:AR299488	C 195	11.8	8.5	15	1	AR262819	ACCESSION:AR262819
C 123	12.4	8.9	18	1	AR324066	ACCESSION:AR324066	C 196	11.8	8.5	15	1	BD057672	ACCESSION:BD057672
C 124	12.4	8.9	18	1	AR326245	ACCESSION:AR326245	C 197	11.8	8.5	15	1	BD081502	ACCESSION:BD081502
C 125	12.4	8.9	18	1	AR365708	ACCESSION:AR365708	C 198	11.8	8.5	15	1	BD090530	ACCESSION:BD090530
C 126	12.4	8.9	18	1	AX786023	ACCESSION:AX786023	C 199	11.8	8.5	15	1	BD090534	ACCESSION:BD090534
C 127	12.4	8.9	18	1	BD206162	ACCESSION:BD206162	C 200	11.8	8.5	16	1	AR011801	ACCESSION:AR011801
C 128	12.4	8.9	19	1	AR074596	ACCESSION:AR074596	C 201	11.8	8.5	16	1	BD233058	ACCESSION:BD233058
C 129	12.4	8.9	19	1	AR083935	ACCESSION:AR083935	C 202	11.8	8.5	16	1	ACCESSION:AX007612	ACCESSION:AX007612
C 130	12.4	8.9	19	1	I23815	ACCESSION:I23815	C 203	11.8	8.5	16	1	BD234600	ACCESSION:BD234600
C 131	12.4	8.9	19	1	I29969	ACCESSION:I29969	C 204	11.8	8.5	17	1	BD254104	ACCESSION:BD254104
C 132	12.4	8.9	19	1	AR299173	ACCESSION:AR299173	C 205	11.8	8.5	17	1	AR186388	ACCESSION:AR186388
C 133	12.4	8.9	19	1	AX033909	ACCESSION:AX033909	C 206	11.8	8.5	17	1	AR186389	ACCESSION:AR186389
C 134	12.2	8.8	17	1	AR046916	ACCESSION:AR046916	C 207	11.8	8.5	17	1	AR230196	ACCESSION:AR230196
C 135	12.2	8.8	17	1	BD254187	ACCESSION:BD254187	C 208	11.8	8.5	17	1	AR286032	ACCESSION:AR286032
C 136	12.2	8.8	17	1	I53968	ACCESSION:I53968	C 209	11.8	8.5	17	1	AR286132	ACCESSION:AR286132
C 137	12.2	8.8	17	1	AR365741	ACCESSION:AR365741	C 210	11.8	8.5	17	1	AR286133	ACCESSION:AR286133
C 138	12.2	8.8	17	1	AX215134	ACCESSION:AX215134	C 211	11.8	8.5	17	1	AR286141	ACCESSION:AR286141
C 139	12.2	8.8	17	1	AX499445	ACCESSION:AX499445	C 212	11.8	8.5	17	1	AR286177	ACCESSION:AR286177
C 140	12.2	8.8	17	1	AX532097	ACCESSION:AX532097	C 213	11.8	8.5	17	1	AR323019	ACCESSION:AR323019
C 141	12.2	8.8	17	1	AX532099	ACCESSION:AX532099	C 214	11.8	8.5	17	1	AR323020	ACCESSION:AR323020
C 142	12.2	8.8	17	1	AX532103	ACCESSION:AX532103	C 215	11.8	8.5	17	1	AR398022	ACCESSION:AR398022
C 143	12.2	8.8	17	1	AX532253	ACCESSION:AX532253	C 216	11.8	8.5	17	1	AR398122	ACCESSION:AR398122
C 144	12.2	8.8	17	1	AX532254	ACCESSION:AX532254	C 217	11.8	8.5	17	1	AR398123	ACCESSION:AR398123
C 145	12.2	8.8	17	1	AX687667	ACCESSION:AX687667	C 218	11.8	8.5	17	1	AR398131	ACCESSION:AR398131
C 146	12.2	8.8	17	1	AX687850	ACCESSION:AX687850	C 219	11.8	8.5	17	1	AR398167	ACCESSION:AR398167
C 147	12.2	8.8	17	1	AX726673	ACCESSION:AX726673	C 220	11.8	8.5	17	1	AR401998	ACCESSION:AR401998
C 148	12.2	8.8	17	1	AX728392	ACCESSION:AX728392	C 221	11.8	8.5	17	1	AX039622	ACCESSION:AX039622
C 149	12.2	8.8	17	1	AX734168	ACCESSION:AX734168	C 222	11.8	8.5	17	1	AX039652	ACCESSION:AX039652
C 150	12.2	8.8	17	1	AX762563	ACCESSION:AX762563	C 223	11.8	8.5	17	1	AX263012	ACCESSION:AX263012
C 151	12.2	8.8	18	1	AR106981	ACCESSION:AR106981	C 224	11.8	8.5	17	1	AX263013	ACCESSION:AX263013
C 152	12.2	8.8	18	1	A56884	ACCESSION:A56884	C 225	11.8	8.5	17	1	AX263016	ACCESSION:AX263016
C 153	12.2	8.8	18	1	A56885	ACCESSION:A56885	C 226	11.8	8.5	17	1	AX263017	ACCESSION:AX263017
C 154	12.2	8.8	18	1	AR092022	ACCESSION:AR092022	C 227	11.8	8.5	17	1	AX266567	ACCESSION:AX266567
C 155	12.2	8.8	18	1	AR112157	ACCESSION:AR112157	C 228	11.8	8.5	17	1	AX266568	ACCESSION:AX266568
C 156	12.2	8.8	18	1	AR118335	ACCESSION:AR118335	C 229	11.8	8.5	17	1	AX422716	ACCESSION:AX422716
C 157	12.2	8.8	18	1	AR118346	ACCESSION:AR118346	C 230	11.8	8.5	17	1	AX498904	ACCESSION:AX498904
C 158	12.2	8.8	18	1	AR137364	ACCESSION:AR137364	C 231	11.8	8.5	17	1	AX498905	ACCESSION:AX498905
C 159	12.2	8.8	18	1	AR149199	ACCESSION:AR149199	C 232	11.8	8.5	17	1	AX498906	ACCESSION:AX498906
C 160	12.2	8.8	18	1	AR160845	ACCESSION:AR160845	C 233	11.8	8.5	17	1	AX499446	ACCESSION:AX499446
C 161	12.2	8.8	18	1	BD231347	ACCESSION:BD231347	C 234	11.8	8.5	17	1	AX499447	ACCESSION:AX499447
C 162	12.2	8.8	18	1	E10022	ACCESSION:E10022	C 235	11.8	8.5	17	1	AX532098	ACCESSION:AX532098
C 163	12.2	8.8	18	1	I14568	ACCESSION:I14568	C 236	11.8	8.5	17	1	AX532251	ACCESSION:AX532251
C 164	12.2	8.8	18	1	I88615	ACCESSION:I88615	C 237	11.8	8.5	17	1	AX532252	ACCESSION:AX532252
C 165	12.2	8.8	18	1	AR350406	ACCESSION:AR350406	C 238	11.8	8.5	17	1	AX672921	ACCESSION:AX672921
C 166	12.2	8.8	18	1	AR409159	ACCESSION:AR409159	C 239	11.8	8.5	17	1	AX687558	ACCESSION:AX687558
C 167	12.2	8.8	18	1	AX037486	ACCESSION:AX037486	C 240	11.8	8.5	17	1	AX687559	ACCESSION:AX687559
C 168	12.2	8.8	18	1	AX244626	ACCESSION:AX244626	C 241	11.8	8.5	17	1	AX687560	ACCESSION:AX687560
C 169	12.2	8.8	18	1	AX795173	ACCESSION:AX795173	C 242	11.8	8.5	17	1	AX687848	ACCESSION:AX687848
C 170	12.2	8.8	18	1	BD075238	ACCESSION:BD075238	C 243	11.8	8.5	17	1	AX687849	ACCESSION:AX687849
C 171	12.2	8.8	21	1	BD102270	ACCESSION:BD102270	C 244	11.8	8.5	17	1	AX723249	ACCESSION:AX723249
C 172	12	8.6	16	1	AR264860	ACCESSION:AR264860	C 245	11.8	8.5	17	1	AX723448	ACCESSION:AX723448
C 173	12	8.6	17	1	BD254997	ACCESSION:BD254997	C 246	11.8	8.5	17	1	AX725456	ACCESSION:AX725456
C 174	12	8.6	17	1	AX531436	ACCESSION:AX531436	C 247	11.8	8.5	17	1	AX727005	ACCESSION:AX727005
C 175	12	8.6	17	1	AX531437	ACCESSION:AX531437	C 248	11.8	8.5	17	1	AX730367	ACCESSION:AX730367
C 176	12	8.6	17	1	AX531438	ACCESSION:AX531438	C 249	11.8	8.5	17	1	AX732114	ACCESSION:AX732114
C 177	12	8.6	17	1	AX531439	ACCESSION:AX531439	C 250	11.8	8.5	17	1	AX734174	ACCESSION:AX734174
C 178	12	8.6	17	1	AX531440	ACCESSION:AX531440	C 251	11.8	8.5	17	1	AX734182	ACCESSION:AX734182
C 179	12	8.6	17	1	AX531441	ACCESSION:AX531441	C 252	11.8	8.5	17	1	AX736515	ACCESSION:AX736515

[illegible]

545	11	7.9	15	1	AR180150	ACCESSION:AR180150	618	10.4	7.5	14	1	BD197859	ACCESSION:BD197859
546	11	7.9	15	1	AR180787	ACCESSION:AR180787	c 619	10.4	7.5	15	1	A07567	ACCESSION:A07567
c 547	11	7.9	15	1	AX028347	ACCESSION:AX028347	620	10.4	7.5	15	1	A07569	ACCESSION:A07569
548	11	7.9	16	1	AR008042	ACCESSION:AR008042	c 621	10.4	7.5	15	1	AR033573	ACCESSION:AR033573
549	11	7.9	16	1	AR029494	ACCESSION:AR029494	c 622	10.4	7.5	15	1	AR113395	ACCESSION:AR113395
550	11	7.9	16	1	AR110507	ACCESSION:AR110507	623	10.4	7.5	15	1	AR132845	ACCESSION:AR132845
551	11	7.9	16	1	AR137060	ACCESSION:AR137060	c 624	10.4	7.5	15	1	AR143397	ACCESSION:AR143397
552	11	7.9	16	1	I26587	ACCESSION:I26587	625	10.4	7.5	15	1	E05479	ACCESSION:E05479
c 553	11	7.9	16	1	AX349231	ACCESSION:AX349231	c 626	10.4	7.5	15	1	I15197	ACCESSION:I15197
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ALIGNMENTS

BD102270/c 21 bp DNA linear PAT 27-AUG-2002
LOCUS Method of detecting risk factor for onset of arteriosclerosis.
DEFINITION
ACCESSION BD102270
VERSION BD102270.1 GI:22647844
KEYWORDS WO 0171032-A/33.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
Nagano,M., Ito,M., Sageshashi,Y., Hattori,H., Egashira,T.,
Yamashita,S. and Matsuzawa,Y.
Method of detecting risk factor for onset of arteriosclerosis
Patent: WO 0171032-A 33 27-SEP-2001;
BML INC, MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGEHASHI, HIROAKI HATTORI,
TORU EGASHIRA, SHIZUYA YAMASHITA, YUJI MATSUZAWA
OS Homo sapiens (human)

RESULT 1
BD102270/c
LOCUS 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Method of detecting risk factor for onset of arteriosclerosis.
ACCESSION BD102270
VERSION BD102270.1 GI:22647844
KEYWORDS WO 0171032-A/33.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
Nagano,M., Ito,M., Sageshashi,Y., Hattori,H., Egashira,T.,
Yamashita,S. and Matsuzawa,Y.
Method of detecting risk factor for onset of arteriosclerosis
Patent: WO 0171032-A 33 27-SEP-2001;
BML INC, MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGEHASHI, HIROAKI HATTORI,
TORU EGASHIRA, SHIZUYA YAMASHITA, YUJI MATSUZAWA
OS Homo sapiens (human)

PN WO 0171032-A/33
PD 27-SEP-2001
PF 23-MAR-2001 WO 2001JP002327
PR 24-MAR-2000 JP 00P 084264
PI MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGEHASHI, HIROAKI HATTORI, TORU
EGASHIRA,
PI SHIZUYA YAMASHITA, YUJI MATSUZAWA
PC C1201/68, C12N15/12
CC Method of detecting risk factor for onset of arteriosclerosis
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E25734
LOCUS 22 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for assaying HBV gene by real time detection PCR method and
primer and probe to be used therein.
ACCESSION E25734
VERSION E25734.1 GI:13024922
KEYWORDS JP 1999103897-A/8.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 22)
AUTHORS Aki.A., Naotake,K., Kazuo,T. and Ryuji,K.
TITLE Method for assaying HBV gene by real time detection PCR method and
primer and probe to be used therein
JOURNAL Patent: JP 1999103897-A 8 20-APR-1999;
COMMENT SRL INC
OS Unidentified
PN JP 1999103897-A/8
PD 20-APR-1999
PR 30-SEP-1997 JP 1997282612
PI AKI ABE, NAOTAKE KAJIYAMA, KAZUO TAKEMURA, RYUJI KAWAGUCHI PC
C1201/70, C12N15/09, G01N33/566, G01N33/576, G01N33/58, PC
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BD101979
LOCUS Novel G protein coupled receptor and its DNA. 21 bp DNA linear PAT 27-AUG-2002
DEFINITION
ACCESSION BD101979
VERSION BD101979.1 GI:22647553
KEYWORDS WO 0177325-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Miwa,M., Matsui,H. and Shintani,Y.
TITLE Novel G protein coupled receptor and its DNA
JOURNAL Patent: WO 0177325-A 4 18-OCT-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,MASANORI MIWA,HIDEKI MATSUI,YASUSHI SHINTANI
COMMENT
OS Artificial Sequence
PN WO 0177325-A/4
PD 18-OCT-2001
PF 12-APR-2001 WO 2001JP003143
PI MASANORI MIWA,HIDEKI MATSUI,YASUSHI SHINTANI
PC C12N15/12,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12Q1/68,A61K45/00,A61P25/00,A61P29/00,A61P35/00,A61P11/06, PC
A61P9/00,
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BD131270
LOCUS Novel G protein-coupled receptor protein and its DNA. 21 bp DNA linear PAT 18-SEP-2002
DEFINITION
ACCESSION BD131270
VERSION BD131270.1 GI:23226215
KEYWORDS JP 200200281-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Miwa,M., Matsui,H. and Shintani,Y.
TITLE Novel G protein-coupled receptor protein and its DNA
JOURNAL Patent: JP 200200281-A 4 08-JAN-2002;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT
OS Artificial Sequence
PN JP 200200281-A/4
PD 08-JAN-2002
PF 12-APR-2001 JP 2001114136
PI MASANORI MIWA,HIDEKI MATSUI,YASUSHI SHINTANI
PC C12N15/09,A61K45/00,A61P3/10,A61P9/00,A61P25/00,A61P29/00, PC
A61P35/00,
PC C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC
C12P21/02,
PC C12Q1/02 C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566//
PC C12P21/08,
PC C12N15/00,C12N5/00
CC Primer

BD101979
LOCUS Novel G protein coupled receptor and its DNA. 21 bp DNA linear PAT 27-AUG-2002
DEFINITION
ACCESSION BD101979
VERSION BD101979.1 GI:22647553
KEYWORDS WO 0177325-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Miwa,M., Matsui,H. and Shintani,Y.
TITLE Novel G protein coupled receptor and its DNA
JOURNAL Patent: WO 0177325-A 4 18-OCT-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,MASANORI MIWA,HIDEKI MATSUI,YASUSHI SHINTANI
COMMENT
OS Artificial Sequence
PN WO 0177325-A/4
PD 18-OCT-2001
PF 12-APR-2001 WO 2001JP003143
PI MASANORI MIWA,HIDEKI MATSUI,YASUSHI SHINTANI
PC C12N15/12,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12Q1/68,A61K45/00,A61P25/00,A61P29/00,A61P35/00,A61P11/06, PC
A61P9/00,
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DEFINITION
ACCESSION AR129513
VERSION AR129513.1 GI:14117410
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Bell,G.I., Yamagata,K., Oda,N., Kaisaki,P.J., Furuta,H.,
Horikawa,Y. and Menzel,S.
TITLE Mutations in the diabetes susceptibility genes hepatocyte nuclear
factor (HNF) 1 alpha (alpha.), HNF1.beta. and HNF4.alpha
JOURNAL Patent: US 6187533-A 102 13-FEB-2001;
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LOCUS Sequence 19 from patent US 6607915. 20 bp DNA linear PAT 18-DEC-2003
DEFINITION
ACCESSION AR381288
VERSION AR381288.1 GI:40089107
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Wancewicz,E.
TITLE Antisense inhibition of E2A-Pbx1 expression
JOURNAL Patent: US 6607915-A 19 19-AUG-2003;
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Bell,G.I., Yamagata,K., Oda,N., Kaisaki,P.J., Furuta,H.,
Horikawa,Y. and Menzel,S.
TITLE Mutations in the diabetes susceptibility genes hepatocyte nuclear
factor (HNF) 1 alpha (alpha.), HNF1.beta. and HNF4.alpha
JOURNAL Patent: US 6187533-A 102 13-FEB-2001;
FEATURES
source Location/Qualifiers
1..22 /organism="unknown"
/mol_type="unassigned DNA"
Query Match 11.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1658 ACCAGGCTCACAGCTGGAACC 1678
|||||

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Db      2 ACCAGACTCAGCGCTGAACC 22

RESULT 7
AX323427
LOCUS      20 bp      DNA      linear      PAT 07-JAN-2002
DEFINITION Sequence 19 from Patent WO0192578.
ACCESSION AX323427
VERSION    AX323427.1 GI:18094190
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS    Roninson, I.B., Dokmanovic, M. and Chang, B.D.
TITLE      Reagents and methods for identifying and modulating expression of
            genes regulated by retinoids
JOURNAL    Patent: WO 0192578-A 19 06-DEC-2001;
            Board of Trustees of the University of Illinois (US)
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="Antisense primer for beta IG-H3"

Query Match      10.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 55;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1653 CAAGCACCAGGCTCACAGCT 1672
      |||||
Db 1 CATGCACAAGGCTCACATCT 20

RESULT 8
ARI142933
LOCUS      23 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 19 from patent US 6204025.
ACCESSION  ARI142933
VERSION     ARI142933.1 GI:15104219
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS     Liu, Q.
TITLE       Efficient linking of nucleic acid segments
JOURNAL     Patent: US 6204025-A 19 20-MAR-2001;
            Location/Qualifiers
FEATURES     source
            1..23
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      10.9%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1713 AGGAGTACGGAGATGGAGAT 1732
      |||||
Db 4 AGGAGGAGGGAGATGGACAT 23

RESULT 9
AX293741/c
LOCUS      20 bp      DNA      linear      PAT 21-NOV-2001
DEFINITION Sequence 5503 from Patent WO0179548.
ACCESSION  AX293741
VERSION     AX293741.1 GI:17055424
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct

artificial sequences.
1
REFERENCE 1
AUTHORS     Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE       Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
JOURNAL     Patent: WO 0179548-A 5503 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES     Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Hypothetical Probe Sequence"

Query Match      10.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1728 GAGATTGGCTCCCAAC 1743
      |||||
Db 18 GAGATTGGCTCGCAAC 3

RESULT 10
AX488425
LOCUS      20 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 5725 from Patent WO02053728.
ACCESSION  AX488425
VERSION     AX488425.1 GI:22322505
KEYWORDS    .
SOURCE      Candida albicans
ORGANISM    Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1
AUTHORS     Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.
TITLE       Gene disruption methodologies for drug target discovery
JOURNAL     Patent: WO 02053728-A 5725 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES     Location/Qualifiers
            source
            1..20
            /organism="Candida albicans"
            /mol_type="unassigned DNA"
            /db_xref="taxon:5476"

Query Match      10.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1737 TCCCAACTCTCCCTA 1752
      |||||
Db 1 TCCCAACTCTCCCAA 16

RESULT 11
BD171443/c
LOCUS      20 bp      DNA      linear      PAT 18-FEB-2003
DEFINITION Nucleic acid molecule derived from actinomycetes plasmid.
ACCESSION  BD171443
VERSION     BD171443.1 GI:28412733
KEYWORDS    JP 2002233380-A/2.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
            1 (bases 1 to 23)
REFERENCE 1
AUTHORS     Kawai, T., Onji, Y., Hiraki, J., Inoue, S., Takagi, H. and Nakamori, S.
TITLE       Nucleic acid molecule derived from actinomycetes plasmid
JOURNAL     Patent: JP 2002233380-A 2 20-AUG-2002;
            CHISSO CORP
COMMENT     OS Artificial Sequence
            PN JP 2002233330-A/2
            PD 20-AUG-2002
            PF 08-FEB-2001 JP 2001031958

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Key	Location/Qualifiers
FT	1. .20
FT	/organism='Artificial Sequence'.

ORGANISM	unidentified unclassified.
REFERENCE	1 (bases 1 to 20)
AUTHORS	Uchida, T. and Shikata, T.
TITLE	POLYPEPTIDE DERIVED FROM HEPATITIS B VIRUS AND GENE CODING THE SAME
JOURNAL	Patent: JP 1994321991-A 7 22-NOV-1994;

Query Match
10.2%; Score 14.2; DB 1; Length 20;

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/mol_type="unassigned DNA"
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JRES	Location
source	1. .20

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/organism="unknown"  
/mol_type="unassigned DNA"
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Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTACAGCTG 1673
Db 19 AACACCCGGCTCAGATG 1

RESULT 16
LOCUS AR211960/c
DEFINITION Sequence 16 from patent US 6399378.
ACCESSION AR211960
VERSION AR211960.1 GI:21515420
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASIFIED.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ward,D.T. and Watt,A.T.
TITLE Antisense modulation of RECOL2 expression
JOURNAL Patent: US 6399378-A 16 04-JUN-2002;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGACCTGGAACCTT 1680
Db 20 GGCTCAGACCTGTAATCCT 2

RESULT 17
LOCUS AR281496
DEFINITION Sequence 109 from patent US 6518411.
ACCESSION AR281496
VERSION AR281496.1 GI:29717183
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASIFIED.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murray,J.C. and Semina,E.
TITLE RGS compositions and therapeutic and diagnostic uses therefor
JOURNAL Patent: US 6518411-A 109 11-FEB-2003;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="mrna"

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1733 TGGCTCCCACTCTCCCT 1751
Db 2 TGTCTCCCAATTCCTCACT 20

RESULT 18
LOCUS BD185884/c
DEFINITION A stabilization method and a preservation method for a reagent for
ACCESSION BD185884
VERSION BD185884.1 GI:31878084

Query Match      10.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 99;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCTCCAGCGT 1697
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KEYWORDS
SOURCE WO 02101042-A/80.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Sagawa,H., Uemori,T., Mukai,H., Yamamoto,J., Tomono,J., Kobayashi,E., Enoki,T., Asada,K. and Kato,I.
TITLE A stabilization method and a preservation method for a reagent for nucleic acid amplification or detection reaction
JOURNAL Patent: WO 02101042-A 80 19-DEC-2002;
COMMENT TAKARA BIO INC, EIROAKI SAGAWA, TAKASHI UEMORI, HIROYUKI MUKAI, JUNKO YAMAMOTO, JUN TOMONO, EIJI KOBAYASHI, TATSUJI ENOKI, KIYOZO ASADA, IKUNOSHIN KATO
OS Artificial Sequence
PN WO 02101042-A/80
PD 19-DEC-2002
PF 12-JUN-2002 WO 2002JP005832
PR 12-JUN-2001 JP 01P 177737.20-AUG-2001 JP 01P 249689 PI
HIROAKI SAGAWA, TAKASHI UEMORI, HIROYUKI MUKAI, JUNKO YAMAMOTO, PI JUN TOMONO,
PI EIJI KOBAYASHI, TATSUJI ENOKI, KIYOZO ASADA, IKUNOSHIN KATO PC
C12N15/09,C12Q1/68
CC Designed oligonucleotide probe as HBV-probe2 to detect a DNA fragment
CC amplifying a portion of X-protein-encoding sequence from CC Hepatitis B virus.
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.

FEATURES
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        Location/Qualifiers
            1..20
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                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 CTCCCAACTCTCCCTATC 1754
Db 19 CCCCCAACTCTCCCTAGTC 1

RESULT 19
LOCUS AX777492
DEFINITION Sequence 40 from Patent WO03029458.
ACCESSION AX777492
VERSION AX777492.1 GI:32694510
KEYWORDS
SOURCE
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Breitling,F., Moldenhauer,G., Poustka,A. and Kuehlwein,T.
TITLE Method for producing protein libraries and for selecting proteins from said libraries
JOURNAL Patent: WO 03029458-A 40 10-APR-2003;
DEUTSCHES Krebsforschungszentrum Stiftung des Oeffentlichen Rechts (DE)
FEATURES
    source
        Location/Qualifiers
            1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Primer vH3-11"

Query Match      10.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 99;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCTCCAGCGT 1697
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FEATURES	source	Location/Qualifiers
Db	1 CTGCCCTCTCTCCAGCGT 19	1..18 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"
RESULT 20		
LOCUS	A06347	20 bp RNA linear PAT 22-JUL-1993
DEFINITION	oligonucleotide d.	
ACCESSION	A06347	
VERSION	A06347.1	GI:412830
KEYWORDS	synthetic construct	
SOURCE	synthetic construct	
ORGANISM	artificial sequences.	
REFERENCE	1 (bases 1 to 20)	
AUTHORS	Hilder,V.A., Gatehouse,A.M.R., Gatehouse,J.A. and Boulter,D.	
TITLE	DNA molecules useful in plant protection	
JOURNAL	Patent: EP 0272144-A 7 22-JUN-1988;	
FEATURES	AGRICULTURAL GENETICS COMPANY LIMITED	
source	Location/Qualifiers	
	1..20	
	/organism="synthetic construct"	
	/mol_type="unassigned RNA"	
	/db_xref="taxon:32630"	
Query Match	10.1%; Score 14; DB 1; Length 20;	
Best Local Similarity	61.1%; Pred. No. 1e+02;	
Matches	1; Conservative 6; Mismatches 1; Indels 0; Gaps 0;	
Qy	1637 GGCTGTAGCAGAGGCA 1654	
Db	20 GGYTTRTARCAARTCR 3	
RESULT 21		
LOCUS	BD074024	18 bp DNA linear PAT 27-AUG-2002
DEFINITION	Human glial cell-line derived neurotrophic factor promoter, vector containing the promoter, and method for screening a compound by the promoter.	
ACCESSION	BD074024	
VERSION	BD074024.1	GI:22619627
KEYWORDS	JP 2001512679-A/6.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 19)	
AUTHORS	Albert,B.P., Mels,J.R., Lee,W.O. and Nei,B.A.	
TITLE	Human glial cell-line derived neurotrophic factor promoter, vector containing the promoter, and method for screening a compound by the promoter	
JOURNAL	Patent: JP 2001512679-A 6 28-AUG-2001;	
COMMENT	F HOFFMANN LA ROCHE AG	
	OS Unidentified	
	PN JP 2001512679-A/6	
	PD 28-AUG-2001	
	PF 23-JUL-1998 JP 2000506328	
	PR 05-AUG-1997 US 60/054812 14-APR-1998 US 60/081751 PI	
	HECKER PRESTON ALBERT,JOHNSON RADOLF MELS,WALTER OM LEE,BERTY	
	PI ADRIAN NEIL	
	PC C12N15/09,A61K45/00,A61P25/28,C12N5/10,C12Q1/68,G01N33/15, PC	
	G01N33/50,	
	PC C12N15/00,C12N5/00	
	CC Strandedness: Single;	
	CC Topology: Linear;	
	CC Human glial cell-line derived neurotrophic factor promoter,	
	CC vector	
	CC containing the promoter, and method for screening a compound	
	CC by the	
	CC promoter	
	FF Key	
	FT source	
	1..18	
	/organism="Unidentified".	
FEATURES	Location/Qualifiers	
	1..18	
	/organism="unidentified"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:32644"	
Query Match	9.9%; Score 13.8; DB 1; Length 18;	
Best Local Similarity	88.2%; Pred. No. 92;	
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1655 AGCACCAGGCTCAGC 1671	
Db	2 AGCACCAGGCTCAGC 18	
RESULT 22		
LOCUS	AR241103/c	20 bp DNA linear PAT 20-DEC-2002
DEFINITION	Sequence 74 from patent US 6468796.	
ACCESSION	AR241103	
VERSION	AR241103.1	GI:27286320
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 20)	
AUTHORS	Watt,A.T.	
TITLE	Antisense modulation of bifunctional apoptosis regulator expression	
JOURNAL	Patent: US 6468796-A 74 22-OCT-2002;	
FEATURES	Location/Qualifiers	
source	1..20	
	/organism="unknown"	
	/mol_type="genomic DNA"	
Query Match	9.9%; Score 13.8; DB 1; Length 20;	
Best Local Similarity	88.2%; Pred. No. 1.1e+02;	
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1662 GGCTCACAGCTGAACC 1678	
Db	17 GGCTCACACCTGGATCC 1	
RESULT 23		
LOCUS	AR281777	20 bp DNA linear PAT 10-APR-2003
DEFINITION	Sequence 4 from patent US 6521225.	
ACCESSION	AR281777	
VERSION	AR281777.1	GI:29717571
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 20)	
AUTHORS	Srivastava,A., Ponnazhagan,S., Chloemer,R.H., Wang,X.-S., Yoder,M.C., Zhou,S.-Z., Escobedo,J. and Dwarki,V.	
TITLE	AAV vectors	
JOURNAL	Patent: US 6521225-A 4 18-FEB-2003;	
FEATURES	Location/Qualifiers	
source	1..20	
	/organism="unknown"	
	/mol_type="genomic DNA"	
Query Match	9.9%; Score 13.8; DB 1; Length 20;	
Best Local Similarity	88.2%; Pred. No. 1.1e+02;	
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1681 GGTTCTCTCTCCAGCGT 1697	
Db	2 GGTTCTCTCTCCAGCAT 18	
RESULT 24		

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AX250715
LOCUS AX250715 20 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 7 from Patent WO0168670.
ACCESSION AX250715
VERSION AX250715.1 GI:15984453
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL
FEATURES
Source
misc_feature
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Oligonucleotide utilise pour l'analyse des biots,
marque au P32"
Query Match 9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGTGGG 1675
Db 1 CCAGGCTCCAGCTGGA 17

RESULT 25
AX253315/c
LOCUS AX253315 20 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 21 from Patent WO0170993.
ACCESSION AX253315
VERSION AX253315.1 GI:16073855
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Winther,M.D., Smith,H.L., Allen,S.J., Ponton,A. and de Antueno R.J.
TITLE Polynucleotides that control delta-6-desaturase genes and methods
for identifying compounds for modulating delta-6-desaturase
JOURNAL Patent: WO 0170993-A 21 27-SEP-2001;
Scotia Holdings plc (GB)
FEATURES
Source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
Query Match 9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1685 TCTCTCCAGCGTGGTG 1701
Db 19 TCTTCTCCAGCGTAGTG 3

RESULT 26
AX283518/c
LOCUS AX283518 20 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 1 from Patent WO0178754.
ACCESSION AX283518
VERSION AX283518.1 GI:17044265
KEYWORDS

AX250715
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chancellor,M.B., Huard,J., Capelli,C.C. and Qu,Z.
TITLE Soft tissue and bone augmentation and bulking utilizing
muscle-derived progenitor cells, compositions and treatments
thereof
JOURNAL Patent: WO 0178754-A 1 25-OCT-2001;
University of Pittsburgh (US)
FEATURES
Source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="CD34 UP OLIGONUCLEOTIDE SEQUENCE"
Query Match 5.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 TTGTAGCAGAGGCAAG 1656
Db 20 TGGTAGCAGAGTCAAG 4

RESULT 27
BD006136
LOCUS BD006136 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Methods and compositions for liver specific delivery of therapeutic
molecules using recombinant AAV vectors.
ACCESSION BD006136
VERSION BD006136.1 GI:18634507
KEYWORDS JP 2001500376-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Srivastava,A., Ponnazhagan,S., Chloemer,R.H., Wang,X.S.,
Yoder,M.C., Zhou,S.Z., Escobedo,J. and Dwaraki,V.
TITLE Methods and compositions for liver specific delivery of therapeutic
molecules using recombinant AAV vectors
JOURNAL Patent: JP 2001500376-A 4 16-JAN-2001;
CHIRON CORP, INDIANA UNIVERSITY
COMMENT OS Homo sapiens (human)
PN JP 2001500376-A/4
PD 16-JAN-2001
PF 02-SEP-1997 JP 1998512823
PR 06-SEP-1996 US 60/025616 11-SEP-1996 US 60/025649 PI
ARON SRIVASTAVA,SELVARANGAN PONNAZHAGAN,ROBERT H CHLOEMER,PI XU
SHAN WANG,
PI MERVIN C YODER,SHANG ZHEN ZHOU,JAIME ESCOBEDO,VARAVANI DWARKI
PC A01N43/04,A51K31/70,C12N15/63
CC
FH Key Location/Qualifiers
FT source
FT Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTCTCTCCTCCAGCGT 1697
Db 2 GGTCTCTCCTCCAGCAT 18

```

RESULT 28
BD179019/c
LOCUS BD179019 20 bp DNA linear PAT 16-APR-2003
DEFINITION A method of secreting and producing proteins.
ACCESSION BD179019
VERSION BD179019.1 GI:30016287
KEYWORDS WO 02081694-A/45.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kikuchi.Y., Date,M., Umezawa.Y., Yokoyama.K., Heima,H. and Matsui,H.
TITLE A method of secreting and producing proteins
JOURNAL Patent: WO 02081694-A 45 17-OCT-2002;
AJINOMOTO CO INC, YOSHIMI KIKUCHI, MASAYO DATE, YUKIKO UMEZAWA, KEIICHI YOKOYAMA, HARUO HEIMA, HIROSHI MATSUI
COMMENT OS Artificial Sequence
PN WO 02081694-A/45
PD 17-OCT-2002
PF 27-MAR-2002 WO 2002JP002978
PR 30-MAR-2001 JP 01P 098808
PI YOSHIMI KIKUCHI, MASAYO DATE, YUKIKO UMEZAWA, KEIICHI YOKOYAMA, HARUO HEIMA, HIROSHI MATSUI
PC .C12N15/09.C12N1/21.C12P21/02.C07K19/00.C07K7/06.C07K7/08 CC
Description of Artificial Sequence: PCR primer FH Key
Location/Qualifiers
FT source 1..20
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 9.8%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1725 ATGGAGATTGGCTCCCA 1741
Db 19 ATGGAGATAGCTCCCA 3
RESULT 29
A98445/c
LOCUS A98445 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 29 from Patent WO9912948.
ACCESSION A98445
VERSION A98445.1 GI:6781546
KEYWORDS unidentified
SOURCE unclassified.
ORGANISM
REFERENCE 1
AUTHORS Landt,O.
TITLE Protein-coated polyribonucleic acids, method for the production thereof, and use of the same
JOURNAL Patent: WO 9912948-A 29 18-MAR-1999;
LANDT OLPERT (DE)
FEATURES
source Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1631 CGATGGGCTTGTACAGAA 1650
||| ||||| | |||||

Db 20 GGACAGGGCTTATGGCAGAA 1
RESULT 30
AR050289
LOCUS AR050289 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5827661.
ACCESSION AR050289
VERSION AR050289.1 GI:5973014
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Blais,B.W.
TITLE Enhancing detection polymerase chain reaction assays by RNA transcription and immunodetection of RNA:DNA hybrids
JOURNAL Patent: US 5827661-A 2 27-OCT-1998;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1684 GTCCTCTCCAGCGGTGGGA 1703
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Db 1 GTATCTCCAGATGATCGA 20
RESULT 31
AR100579
LOCUS AR100579 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 95 from patent US 6080588.
ACCESSION AR100579
VERSION AR100579.1 GI:12811027
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Klick,G.D.
TITLE Therapeutic methods for benzodiazepine derivatives
JOURNAL Patent: US 6080588-A 95 27-JUN-2000;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1692 CAGCGTGTGCAACTGGGT 1711
||| ||||| | |||||
Db 1 CACTGTGTGGACGTTCGGT 20
RESULT 32
AR100585
LOCUS AR100585 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 103 from patent US 6080588.
ACCESSION AR100585
VERSION AR100585.1 GI:12811033
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Klick,G.D.
TITLE Therapeutic methods for benzodiazepine derivatives

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JOURNAL Patent: US 6080588-A 103 27-JUN-2000;
FEATURES
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    Location/Qualifiers
      1..20
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1692 CAGCGTGGTGAAGTTGGGT 1711
  |||||
  1 CACTGTGGTGGACGTTGGT 20
  |||||

RESULT 33
AR158965/C
LOCUS AR158965 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 587 from patent US 6251588.
ACCESSION AR158965
VERSION AR158965.1 GI:16221399
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 587 26-JUN-2001;
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1701 GGAAGTTGGTTAGGAGTAC 1720
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  20 GGAAGTTCAATTAGGAATAC 1
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RESULT 34
E26692
LOCUS E26692 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Improved method for measuring cytokine gene expression.
ACCESSION E26692
VERSION E26692.1 GI:13026279
KEYWORDS JP 1999155600-A/42.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Michio,S., Takeshi,H., Masato,H. and Hideyuki,I.
TITLE Improved method for measuring cytokine gene expression
JOURNAL Patent: JP 1999155600-A 42 15-JUN-1999;
COMMENT SHISEIDO CO LTD
OS Unidentified
PN JP 1999155600-A/42
PD 15-JUN-1999
PF 28-NOV-1997 JP 1997328171
PR
PI MICHIO SHIBATA, TAKESHI HARIYA, MASATO HATAO, HIDEYUKI ICHIKAWA
PC C12Q1/68,C07K14/52,C07K14/54,C07K14/55,C07K14/56,C07K14/57, PC
PC C12N15/09,
CC G01N33/50//C12Q1/68,C12R1:91
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT Key
FT source
  1..20
  /organism='Unidentified'.

JOURNAL Patent: US 6080588-A 103 27-JUN-2000;
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="unidentified"
      /mol_type="genomic DNA"
      /db_xref="taxon:32644"

Query Match
  5.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGCTCCC 1740
  |||||
  1 GAAGATGGTATCGGCTTCC 20
  |||||

RESULT 35
I31522
LOCUS I31522 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 434 from patent US 5582979.
ACCESSION I31522
VERSION I31522.1 GI:1822313
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 434 10-DEC-1996;
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1713 AGGAGTACGGAGATGGAGAT 1732
  |||||
  1 AGGAGTTAGGAGCTGGAGT 20
  |||||

RESULT 36
AR298667/C
LOCUS AR298667 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 10402 from patent US 6537751.
ACCESSION AR298667
VERSION AR298667.1 GI:31685951
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 10402 25-MAR-2003;
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
  9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1746 CTCCTATCTCTAAAGCCCCA 1765
  |||||
  20 CTCCTATCTCTACTTCCCA 1
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RESULT 37
AR316120/c
LOCUS AR316120 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6657 from patent US 6559294.
ACCESSION AR316120
VERSION AR316120.1 GI:31709546
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 20)
Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,I.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6657 06-MAY-2003;
FEATURES
LOCATION/Qualifiers
source 1..20
/mol_type="genomic DNA"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1633 ATGGGCTTGTAGCAGAGG 1652
|||||
Db 20 ATGGTGTAGTATCAGCAGG 1

RESULT 38
AR316177/c
LOCUS AR316177 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6714 from patent US 6559294.
ACCESSION AR316177
VERSION AR316177.1 GI:31709603
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 20)
Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,I.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6714 06-MAY-2003;
FEATURES
LOCATION/Qualifiers
source 1..20
/mol_type="genomic DNA"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1633 ATGGGCTTGTAGCAGAGG 1652
|||||
Db 20 ATGGTGTAGTATCAGCAGG 1

RESULT 39
AR370267
LOCUS AR370267 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 88 from patent US 6300132.
ACCESSION AR370267
VERSION AR370267.1 GI:34606773
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 20)
Monia,B.P. and Cowsett,L.M.
TITLE Antisense inhibition of telomeric repeat binding factor 2
JOURNAL Patent: US 6300132-A 88 09-OCT-2001;

FEATURES
source 1..20
/mol_type="genomic DNA"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1720 CGGAGATGGAGATGGCTCC 1739
|||||
Db 20 CGGATAGGGAGACTGGCTGC 1

RESULT 40
AR315823/c
LOCUS AR315823 20 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 946 from Patent WO0129262.
ACCESSION AR315823
VERSION AR315823.1 GI:14032765
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS 1 Picoult-Newburg,L. and Pohl,M.
Genotyping reagents, kits and methods of use thereof
TITLE Patent: WO 0129262-A 946 26-APR-2001;
JOURNAL Orchid Biosciences, Inc. (US)
FEATURES
LOCATION/Qualifiers
source 1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1737 TCCCAACTCTCCCTATCCT 1756
|||||
Db 20 TCCCAACTCTCCCTATCCT 1

RESULT 41
BD144090
LOCUS BD144090 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid of uncoupling protein-1, -2 or -3
and reagent therefor, and method for screening diet drug.
ACCESSION BD144090
VERSION BD144090.1 GI:27849848
KEYWORDS JP 2002125680-A/14.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS 1 (bases 1 to 20)
Hariya,T., Shibata,M., Soma,T. and Ichikawa,H.
TITLE Method for assaying nucleic acid of uncoupling protein-1, -2 or -3
and reagent therefor, and method for screening diet drug
JOURNAL Patent: JP 2002125680-A 14 08-MAY-2002;
SHISEIDO CO LTD
COMMENT OS Artificial Sequence
PN JP 2002125680-A/14
PD 08-MAY-2002
PF 24-OCT-2000 JP 2000324581
PI TAKESHI HARIYA, MICHIO SHIBATA, TSUTOMU SOMA, HIDEYUKI ICHIKAWA
PC C12N15/09,A61K45/00,A61P3/04,C12Q1/68,G01N33/53,G01N33/566//
PC C12N9/02,
PC C12N15/00
CC Reverse primer for amplification of gene for glyceroldehyde-3-
CC phosphate
CC dehydrogenase
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FH Key      Location/Qualifiers
FT source   1..20
FT          /organism='Artificial Sequence'.

FEATURES             source
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                Location/Qualifiers
                1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match      9.6%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATGGCTCC 1740
Db 1 GAAGATGGTGGGGCTTC 20

RESULT 42
AX723714
LOCUS AX723714 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1401 from Patent WO03025176.
ACCESSION AX723714
VERSION AX723714.1 GI:30503057
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
        reversion, apoptosis and/or virus resistance and their use as
        medicines
JOURNAL Patent: WO 03025176-A 1401 27-MAR-2003;
        Molecular Engines Laboratories (FR)
FEATURES             source
    source       1..17
                Location/Qualifiers
                1..17
                /organism="Mus musculus"
                /mol_type="unassigned DNA"
                /db_xref="taxon:10090"

Query Match      9.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 GCTCCCAACTCTCC 1749
Db 1 GATCCCAACTCTCC 15

RESULT 43
AX352825
LOCUS AX352825 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 31 from Patent EP1174518.
ACCESSION AX352825
VERSION AX352825.1 GI:18617907
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Loukachov,V.V., van Gemen,B. and Goudsmit,J.
TITLE Collection of binding molecules
JOURNAL Patent: EP 1174518-A 31 23-JAN-2002;
        Amsterdam Support Diagnostics B.V. (NL)
FEATURES             source
    source       1..18
                Location/Qualifiers
                1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="position 41"

FH Key      Location/Qualifiers
FT source   1..20
FT          /organism='Artificial Sequence'.

FEATURES             source
    source       1..20
                Location/Qualifiers
                1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match      9.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1717 GTACGAGATGGAGA 1731
Db 1 GTACGAGATGGAGA 15

RESULT 44
AX362670
LOCUS AX362670 18 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 31 from Patent WO0208463.
ACCESSION AX362670
VERSION AX362670.1 GI:18694810
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Loukachov,V.V., Goudsmit,J. and van Gemen,B.
TITLE Collection of binding molecules
JOURNAL Patent: WO 0208463-A 31 31-JAN-2002;
        Amsterdam Support Diagnostics B.V. (NL)
FEATURES             source
    source       1..18
                Location/Qualifiers
                1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="position 41"

Query Match      9.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1717 GTACGAGATGGAGA 1731
Db 1 GTACGAGATGGAGA 15

RESULT 45
AB069639/c
LOCUS AB069639/c 18 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-A007F44
        at 1p36
ACCESSION AB069639
VERSION AB069639.1 GI:15130443
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
        Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
        Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
        and Soeda,E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
        chromosome 1p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 13)
AUTHORS Horii,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
        Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
        Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
        Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             source
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                Location/Qualifiers
                1..18
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

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misc_feature 1. .18
/notes=reverse primer for human STS sts-A007F44 at 1p36
sts-A007F44 obtained from clones B22K3, B24C10, B30J5,
B358I24, B242E21, Human BAC library RPCI-11"

Query Match          9.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1654 AAGCACCAGGCTCAC 1668
|||||
Db 17 AAGCACCGAGCTCTC 3

RESULT 46
AX129291/c
LOCUS AX129291 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 509 from Patent WO0130362.
ACCESSION AX129291
VERSION AX129291.1 GI:14135596
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 509 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source 1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cdk4 ribozyme binding site"

Query Match          9.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCCTCC 1749
|||||
Db 16 GCTCCGACTCCTCC 2

RESULT 47
BD088226/c
LOCUS BD088226 19 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088226
VERSION BD088226.1 GI:22633836
KEYWORDS JP 2001321190-A/470.
SOURCE Synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 470 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECs
OS Artificial Sequence
PN JP 2001321190-A/470
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key

QY 1735 GCTCCCACTCCTCC 1749
|||||
Db 16 GCTCCGACTCCTCC 2

RESULT 47
BD088226/c
LOCUS BD088226 19 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088226
VERSION BD088226.1 GI:22633836
KEYWORDS JP 2001321190-A/470.
SOURCE Synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 470 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECs
OS Artificial Sequence
PN JP 2001321190-A/470
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key

FT source 1. .19
/organism='Artificial Sequence'.
FEATURES
source 1. .19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match          9.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCAAGCA 1658
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Db 18 AGCAGAAGGCATGCA 4

RESULT 48
BD088234/c
LOCUS BD088234 19 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088234
VERSION BD088234.1 GI:22633844
KEYWORDS JP 2001321190-A/478.
SOURCE Synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 478 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECs
OS Artificial Sequence
PN JP 2001321190-A/478
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key

FT source 1. .19
/organism='Artificial Sequence'.
FEATURES
source 1. .19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match          9.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCAAGCA 1658
|||||
Db 18 AGCAGAAGGCATGCA 4

RESULT 49
AB069135/c
LOCUS AB069135 19 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-stSG8994
at 1p36.
ACCESSION AB069135
VERSION AB069135.1 GI:15129939
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
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Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Mochizashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E.

A BAC-based STS-content map spanning a 35-Mb region of human

chromosome 1p35-p36
Genomics 74 (1), 55-70 (2001)

21269192
PUBMED
11374902

REFERENCE
2 (bases 1 to 19)

AUTHORS
Horii,A.

TITLE
Direct Submission

Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)

FEATURES
Location/Qualifiers

1..19
source

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

misc_feature

1..19

/note="reverse primer for human STS sts-stSG9994 at 1p36
sts-stSG9994 obtained from clones B369B23, B18717,
B305A18, B372M12, B225E8, B45E6, B258116, B194113, Human
BAC library RFCI-11"

Query Match 9.6%; Score 13.4; DB 1; Length 19;

Best Local Similarity 93.3%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAAGGCAAGCA 1658

Db 18 AGCAGAAGGCAATGCA 4
|||||

RESULT 50

AB069137/c

LOCUS

AB069137
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-stSG9994
at 1p36.

ACCESSION AB069137

VERSION AB069137.1 GI:15129941

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS

Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Mochizashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E.

A BAC-based STS-content map spanning a 35-Mb region of human

chromosome 1p35-p36
Genomics 74 (1), 55-70 (2001)

21269192
PUBMED
11374902

REFERENCE
2 (bases 1 to 19)

AUTHORS
Horii,A.

TITLE
Direct Submission

Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)

FEATURES
Location/Qualifiers

1..19
source

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

misc_feature

1..19

/note="reverse primer for human STS sts-stSG9994 at 1p36
sts-stSG9994 obtained from clones B369B23, B18717,
B305A18, B372M12, B225E8, B45E6, B258116, B194113, Human
BAC library RFCI-11"

Query Match 9.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAAGGCAAGCA 1658

Db 18 AGCAGAAGGCAATGCA 4
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RESULT 51

AR163797

LOCUS

AR163797
DEFINITION Sequence 84 from patent US 6271029.

ACCESSION AR163797

VERSION AR163797.1 GI:16234547

KEYWORDS

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 23)

AUTHORS Bennett,C.Frank. and Cowser,L.M.

TITLE Antisense inhibition of cytohesin-2 expression

JOURNAL Patent: US 6271029-A 84 07-AUG-2001;

FEATURES Location/Qualifiers

1..20
source

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 9.6%; Score 13.4; DB 1; Length 20;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1685 TCTCTCCAGGTG 1699

Db 5 TCTCTCTCCAGGTG 19
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RESULT 52

AR233647/c

LOCUS

AR233647
DEFINITION Sequence 9 from patent US 6458536.

ACCESSION AR233647

VERSION AR233647.1 GI:27276271

KEYWORDS

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 20)

AUTHORS Gatti,R.A.

TITLE Modified SSCP method using sequential electrophoresis of multiple

nucleic acid segments

JOURNAL Patent: US 6458536-A 9 01-OCT-2002;

FEATURES Location/Qualifiers

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source

/organism="unknown"

/mol_type="genomic DNA"

Query Match 9.6%; Score 13.4; DB 1; Length 20;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1742 ACTCTCCCTCTCCT 1756

Db 15 ACTCTCCCTCTCCT 1
|||||

RESULT 53

AG3088/c

LOCUS

AG3088
DEFINITION Sequence 15 from Patent WO9720197.

ACCESSION AG3088

VERSION AG3088.1 GI:3716952

[illegible][illegible]

artificial sequences.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Soeda,E.
 TITLE A method of arraying genome clone
 JOURNAL Patent: JP 2001321190-A 2081 20-NOV-2001;
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
 GENOTECHS
 COMMENT OS Artificial Sequence
 PN JP 2001321190-A/2081
 PD 20-NOV-2001
 PF 12-MAR-2001 JP 2001068285
 PI EIICHI SOEDA
 PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
 C12N15/00,
 PC C12N15/00
 CC Description of Artificial Sequence:Synthetic DNA FH Key
 FT source
 FT 1. .18
 /organism='Artificial Sequence'.
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 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 9.5%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1720 CGGAGATGGAGATTGGCT 1737
 Db 18 CTGAGATGGAGTTTCGCT 1

RESULT 59
 AB068204/c
 LOCUS Synthetic construct DNA, forward primer for human STS sts-DIS2666
 at lp36.
 DEFINITION AB068204
 ACCESSION AB068204.1 GI:15129008
 VERSION
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
 Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
 Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
 and Soeda,E.
 TITLE A BAC-based STS-content map spanning a 35-Mb region of human
 chromosome 1p35-p36
 JOURNAL Genomics 74 (1), 55-70 (2001)
 MEDLINE 21269192
 PUBMED 11374902
 REFERENCE 2 (bases 1 to 18)
 AUTHORS Horii,A.
 TITLE Direct Submission
 JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
 Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-Ku, Sendai,
 Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
 Tel:81-22-717-8042, Fax:81-22-717-8047)
 FEATURES
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 1. .18
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

misc_feature
 1. .18
 /note="forward primer for human STS sts-DIS2666 at lp36
 sts-DIS2666 obtained from clones B279H/6, B332B8,
 B156C13, B370L6, B310A20, B359J17, B45N15, B63P6, Human
 BAC library RPCI-11"

Query Match 9.5%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1720 CGGAGATGGAGATTGGCT 1737
 Db 18 CTGAGATGGAGTTTCGCT 1

RESULT 60
 AR011803/c
 LOCUS AR011803
 DEFINITION Sequence 16 from patent US 5763172.
 ACCESSION AR011803
 VERSION AR011803.1 GI:3969793
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Magda,D., Sessler,J.L., Wright,M., Miller,R.A. and Dow,W.C.
 TITLE Method of phosphate ester hydrolysis
 JOURNAL Patent: US 5763172-A 16 09-JUN-1998;
 FEATURES
 Location/Qualifiers
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 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 9.5%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCGAGCTCACAGCT 1672
 Db 18 AACACCGGCTCACAGAT 1

RESULT 61
 AR361501
 LOCUS AR361501
 DEFINITION Sequence 27 from patent US 6599728.
 ACCESSION AR361501
 VERSION AR361501.1 GI:33769349
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Morin,G.B., Funk,W.D. and Piatyszek,M.A.
 TITLE Second mammalian tankyrase
 JOURNAL Patent: US 6599728-A 27 29-JUL-2003;
 FEATURES
 Location/Qualifiers
 1. .19
 source
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 9.5%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1715 GAGTACGAGATGGAGAT 1732
 Db 1 GAGCACAGATGGAGGT 18

RESULT 62
 A70767/c
 LOCUS A70767
 DEFINITION Sequence 88 from Patent WO9813490.
 ACCESSION A70767
 VERSION A70767.1 GI:4774770
 KEYWORDS
 SOURCE unidentified

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ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS Ophoff,R.A., Terwindt,G.M., Ferrari,M.D. and Frants,R.R.
TITLE A gene related to migraine in man
JOURNAL Patent: WO 9813490-A 88 02-APR-1998;
OPHOFF ROEL ANDRE (NL)
FEATURES
source
1..20
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 9.5%; Score 13.2; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1689 CTCACGGGTGGTGAAGT 1706
Db 20 CACCAGGGTGGCGGAAGT 3

RESULT 63
LOCUS A79251 20 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 88 from Patent EP0834561.
ACCESSION A79251
VERSION A79251.1 GI:6092296
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS A GENE RELATED TO MIGRAINE IN MAN
TITLE A GENE RELATED TO MIGRAINE IN MAN
JOURNAL Patent: EP 0834561-A 88 08-APR-1998;
UNIV LEIDEN (NL)
FEATURES
source
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Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 9.5%; Score 13.2; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1689 CTCACGGGTGGTGAAGT 1706
Db 20 CACCAGGGTGGCGGAAGT 3

RESULT 64
LOCUS AR163916 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 114 from patent US 6271030.
ACCESSION AR163916
VERSION AR163916.1 GI:16234741
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 114 07-AUG-2001;
FEATURES
source
1..20
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 9.5%; Score 13.2; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1689 CTCACGGGTGGTGAAGT 1706
Db 20 CACCAGGGTGGCGGAAGT 3

RESULT 65
LOCUS E08376 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for enterovirus complementary to the downstream gene coding
partially Vp4 and Vp2 proteins.
ACCESSION E08376
VERSION E08376.1 GI:2176493
KEYWORDS JP 1994311900-A/2.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS Marisawa,T., Ishiko,H., Sakae,K., Ishihara,Y., Takeda,N.,
Miyamura,K. and Inoue,S.
TITLE DETECTION OF ENTEROVIRUS AND DISCRIMINATION OF THE SAME
JOURNAL Patent: JP 1994311900-A 2 08-NOV-1994;
MITSUBISHI YUKA B C L.KK, INOUE SAKAE
COMMENT OS None
OC Artificial sequences.
PN JP 1994311900-A/2
PD 08-NOV-1994
PF 28-APR-1993 JP 1993102254
PI NARISAWA TADASHI, ISHIKO HIROAKI, SAKAE KENJI, PI ISHIHARA
YUICHI,
PI TAKEDA NAOKAZU, MIYAMURA KIKUKO, INOUE SAKAE
PC C12Q1/70//C12N15/41;
CC strandedness: Single;
CC topology: Linear;
FH Key
FH Location/Qualifiers
FT
1..20
Location/Qualifiers
/organism='Artificial sequences'.
1..20
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 9.5%; Score 13.2; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1696 GTGGTGAAGTTGGTTA 1713
Db 3 GTGGTGAAGTTGCCTGA 20

RESULT 66
LOCUS AR220154/c 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 19 from patent US 6423543.
ACCESSION AR220154
VERSION AR220154.1 GI:23324597
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS Marcotte,P.A. and Cowseert,L.M.
TITLE Antisense modulation of hepsin expression
JOURNAL Patent: US 6423543-A 19 23-JUL-2002;
FEATURES
source
1..20
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
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Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAACCTG 1681
    ||||| ||||| |||||
Db 19 CTCAC TGGGGGACCTG 2

RESULT 67
AR315612
LOCUS AR315612 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6149 from patent US 6559294.
ACCESSION AR315612
VERSION AR315612
KEYWORDS AR315612.1 GI:31709038
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B., and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6149 06-MAY-2003;
FEATURES Location/Qualifiers
    source 1..20
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1744 TCCTCCTATCTCTAAGG 1761
    ||||| ||||| |||||
Db 3 TCCTCTCTACCTAAGG 20

RESULT 68
AX180379
LOCUS AX180379 20 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 16 from Patent WO0146260.
ACCESSION AX180379
VERSION AX180379.1 GI:15132316
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Starling, G.C. and Finger, J.
TITLE Novel immunoglobulin superfamily members apex-1, apex-2 and apex-3
JOURNAL and uses thereof
PATENT: WO 0146260-A 16 28-JUN-2001;
Bristol-Myers Squibb Co. (US)
FEATURES Location/Qualifiers
    source 1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="JNF14 PRIMER"

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCACAGCTGGACCC 1679
    ||||| ||||| |||||
Db 2 GGCTCACAGCTGTAATCC 19

RESULT 69
AX268920/c
LOCUS AX268920 20 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 16 from Patent WO0179481.
ACCESSION AX268920
VERSION AX268920.1 GI:16541939
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Mcconlogue, L.C., Games, K.D., Yednock, T.A., Hua, T., Messersmith, E.
and Bard, F.
TITLE Screening markers and methods for neurodegenerative disorders
JOURNAL Patent: WO 0175165-A 1 11-OCT-2001;
Elan Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
    source 1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="forward primer MoGapdh251F"

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1723 AGATGGAGATTGGCTCCC 1740
    ||||| ||||| |||||
Db 19 AGATGGTGGTGGCTTCC 2

RESULT 70
AX287952
LOCUS AX287952 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 338 from Patent WO0179481.
ACCESSION AX287952
VERSION AX287952.1 GI:17049698
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ladner, R.C., Cohen, E.H., Nastri, H.G., Rookey, K.L. and Hoet, R.
TITLE Novel methods of constructing libraries of genetic packages that
collectively display the members of a diverse family of peptides,
polypeptides or proteins
JOURNAL Patent: WO 0179481-A 338 25-OCT-2001;
Dyax Corp. (US)
FEATURES Location/Qualifiers
    source 1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic oligonucleotide"

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGGCTC 1738
    ||||| ||||| |||||
Db 3 GAAGATGGAGACTGGGTC 20

RESULT 71
BD003481/c
LOCUS BD003481 20 bp DNA linear PAT 31-JAN-2002
DEFINITION A gene related to migraine in man.
ACCESSION BD003481
VERSION BD003481.1 GI:18631442
KEYWORDS JP 2001500743-A/50.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

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REFERENCE 1 (bases 1 to 20)
AUTHORS Prantz,R.R.I.E., Ferrari,M.D., Teruvinto,H.M. and Opuhofu,R.A.
TITLE A gene related to migraine in man
JOURNAL Patent: JP 2001500743-A 50 23-JAN-2001;
COMMENT RYUKUS UNIVERSITY/TAT TO RAIDEN
OS Homo sapiens (human)
PN JP 2001500743-A/50
PD 23-JAN-2001
PF 26-SEP-1997 JP 1998515527
PI RENE ROBERT ISAAC ERIK FRANTZ MICHEL DOMINIQUE FERRARI, PI
HISERA MARRY TERUVINTO, RURU ANDRE OPUHOFU
PC C12N15/09,A01K67/027,C07K14/435,C07K16/18,C12N1/15,C12N1/19,
C12N1/21,
PC C12N5/10,C12Q1/02,C12Q1/68,C12N15/00,C12N5/00 CC
FH Key Location/Qualifiers
FT primer bind (1)..(20).

FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1689 CTCACGGCTGCTGGAAGT 1706
| | | | | | | | | | | | | | | | | |
Db 20 CACCAGGCTGCGGGAAGT 3

RESULT 72
BD011678
LOCUS 20 bp DNA linear PAT 02-AUG-2002
DEFINITION Method for detecting Pseudomonas bacteria.
ACCESSION BD011678
VERSION BD011678.1 GI:22091867
KEYWORDS JP 2001190279-A/4.
SOURCE synthetic construct
ORGANISM artificial construct
1 (bases 1 to 20)
Sawai,H. and Nakamura,T.
Method for detecting Pseudomonas bacteria
Patent: JP 2001190279-A 4 17-JUL-2001;
MITSUBISHI HEAVY IND LTD
OS Artificial sequence
PN JP 2001190279-A/4
PD 17-JUL-2001
PF 13-JAN-2000 JP 2000004160
PI HIDEKI SAWAI,TSUYOSHI NAKAMURA
PC C12N15/09,C12Q1/04,C12Q1/68//((C12N15/09,C12R1:40),(C12Q1/04,
C12R1:40),
PC C12N15/00,(C12N15/00,C12R1:40)
CC primer
FH Key Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1657 CACACGGCTACAGCTGG 1674
| | | | | | | | | | | | | | | | | |
Db 2 CACCAGTTTCAGTCTGG 19

RESULT 73
BD011678
LOCUS 20 bp DNA linear PAT 02-AUG-2002
DEFINITION Method for detecting Pseudomonas bacteria.
ACCESSION BD011678
VERSION BD011678.1 GI:22091867
KEYWORDS JP 2001190279-A/6.
SOURCE synthetic construct
ORGANISM artificial construct
1 (bases 1 to 20)
Sawai,H. and Nakamura,T.
Method for detecting Pseudomonas bacteria
Patent: JP 2001190279-A 6 17-JUL-2001;
MITSUBISHI HEAVY IND LTD
OS Artificial sequence
PN JP 2001190279-A/6
PD 17-JUL-2001
PF 13-JAN-2000 JP 2000004160
PI HIDEKI SAWAI,TSUYOSHI NAKAMURA
PC C12N15/09,C12Q1/04,C12Q1/68//((C12N15/09,C12R1:40),(C12Q1/04,
C12R1:40),
PC C12N15/00,(C12N15/00,C12R1:40)
CC primer
FH Key Location/Qualifiers
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source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1657 CACACGGCTACAGCTGG 1674
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Db 2 CACCAGTTTCAGTCTGG 19

RESULT 73

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BD011679
LOCUS 20 bp DNA linear PAT 02-AUG-2002
DEFINITION Method for detecting Pseudomonas bacteria.
ACCESSION BD011679
VERSION BD011679.1 GI:22091868
KEYWORDS JP 2001190279-A/5.
SOURCE synthetic construct
ORGANISM artificial construct
1 (bases 1 to 20)
Sawai,H. and Nakamura,T.
Method for detecting Pseudomonas bacteria
Patent: JP 2001190279-A 5 17-JUL-2001;
MITSUBISHI HEAVY IND LTD
OS Artificial sequence
PN JP 2001190279-A/5
PD 17-JUL-2001
PF 13-JAN-2000 JP 2000004160
PI HIDEKI SAWAI,TSUYOSHI NAKAMURA
PC C12N15/09,C12Q1/04,C12Q1/68//((C12N15/09,C12R1:40),(C12Q1/04,
C12R1:40),
PC C12N15/00,(C12N15/00,C12R1:40)
CC primer
FH Key Location/Qualifiers
FEATURES
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1657 CACCAGCTCACAGCTGG 1674
| | | | | | | | | | | | | | | | | |
Db 2 CACCAGTTTCAGTCTGG 19

RESULT 74
BD011680
LOCUS 20 bp DNA linear PAT 02-AUG-2002
DEFINITION Method for detecting Pseudomonas bacteria.
ACCESSION BD011680
VERSION BD011680.1 GI:22091869
KEYWORDS JP 2001190279-A/6.
SOURCE synthetic construct
ORGANISM artificial construct
1 (bases 1 to 20)
Sawai,H. and Nakamura,T.
Method for detecting Pseudomonas bacteria
Patent: JP 2001190279-A 6 17-JUL-2001;
MITSUBISHI HEAVY IND LTD
OS Artificial sequence
PN JP 2001190279-A/6
PD 17-JUL-2001
PF 13-JAN-2000 JP 2000004160
PI HIDEKI SAWAI,TSUYOSHI NAKAMURA
PC C12N15/09,C12Q1/04,C12Q1/68//((C12N15/09,C12R1:40),(C12Q1/04,
C12R1:40),
PC C12N15/00,(C12N15/00,C12R1:40)
CC primer
FH Key Location/Qualifiers
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1657 CACCAGGCTCACAGCTGG 1674
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Db 2 CACCAGTTCACTGCTGG 19

RESULT 75
AX710950
LOCUS AX710950 16 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 250 from Patent EP1288296.
ACCESSION AX710950
VERSION AX710950.1 GI:29787331
KEYWORDS
SOURCE Human herpesvirus 5
ORGANISM Human herpesvirus 5
REFERENCE
AUTHORS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
          Betaherpesvirinae; Cytomegalovirus.
1 Draper,K.G., Mcswiggen,J.A., Holecsek,J.J., Dudycz,L.W.,
  Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 250 03-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
1 .16
Location/Qualifiers
/organism="Human herpesvirus 5"
/mol_type="unassigned RNA"
/db_xref="taxon:10359"

Query Match 9.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1679 CTGGTGTCCTCCACG 1694
      ||||| ||||| ||||| |||||
Db 1 CTGGTGTCACCCCCAG 16

RESULT 77
BD001520
LOCUS BD001520 16 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001520
VERSION BD001520.1 GI:18626079
KEYWORDS JP 2000342286-A/251.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G., Dadykzt,L.W., Macswigen,J.A., Maysejak,D.G.,
          Holecsek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 251 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2000342286-A/251
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SRP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER,LEC W DADYKZT,JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
PC A61K39/135,
PC A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
PC A61P1/16,
PC A61P31/14,A51P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
(C12N15/09,C1231:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
C12R1:93)
CC Key Location/Qualifiers
FH source 1. .16
FT /organism="Artificial Sequence".
FT Location/Qualifiers

FEATURES
source
1 .16
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 9.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1679 CTGGTGTCCTCCACG 1694
      ||||| ||||| ||||| |||||
Db 1 CTGGTGTCACCCCCAG 16

RESULT 77
BD001520
LOCUS BD001520 16 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001520
VERSION BD001520.1 GI:18626079
KEYWORDS JP 2000342286-A/251.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G., Dadykzt,L.W., Macswigen,J.A., Maysejak,D.G.,
          Holecsek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 251 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2000342286-A/251
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SRP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER,LEC W DADYKZT,JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
PC A61K39/135,
PC A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
PC A61P1/16,
PC A61P31/14,A51P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
(C12N15/09,C1231:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
C12R1:93)
CC Key Location/Qualifiers
FH source 1. .16
FT /organism="Artificial Sequence".
FT Location/Qualifiers

FEATURES
source
1 .16
Location/Qualifiers
/organism="Artificial Sequence".
FT Location/Qualifiers

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source 1. .16
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 9.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1679 CTGGTGCTCTCCAG 1694
||||| |||||
Db 1 CTGGTGTCACCCCGAG 16

RESULT 78
AR011799/c
LOCUS AR011799 17 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 12 from patent US 5763172.
ACCESSION AR011799
VERSION AR011799.1 GI:3969789
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Magda,D., Sessler,J.L., Wright,M., Miller,R.A. and Dow,W.C.
TITLE Method of phosphate ester hydrolysis
JOURNAL Patent: US 5763172-A 12 09-JUN-1998;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670
||||| |||||
Db 16 AACACCGGCTCAG 1

RESULT 79
AR192421/c
LOCUS AR192421 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7909 from patent US 6346398.
ACCESSION AR192421
VERSION AR192421.1 GI:20238386
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7909 12-FEB-2002;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGCCAGCCCA 1661
||||| |||||
Db 17 CAGAAGCCAGCCCA 2

RESULT 80
AR326290/c
LOCUS AR326290 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3692 from patent US 6566127.
ACCESSION AR326290
VERSION AR326290.1 GI:33712098
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3692 20-MAY-2003;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGCCAGCCCA 1661
||||| |||||
Db 17 CAGAAGCCAGCCCA 2

RESULT 81
AX421994/c
LOCUS AX421994 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 330 from Patent WO0188124.
ACCESSION AX421994
VERSION AX421994.1 GI:21525376
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 330 22-NOV-2001;
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCTCC 1689
||||| |||||
Db 17 GAACCTGGAGTCTCC 2

RESULT 82
AX422971/c
LOCUS AX422971 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1307 from Patent WO0188124.
ACCESSION AX422971
VERSION AX422971.1 GI:21526353
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
```

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TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 1307 22-NOV-2001; GLAXO GROUP LIMITED (GB)
FEATURES   RIBOZYME PHARMACEUTICALS, INC. (US) ;
source     Location/Qualifiers
          1..17
            /organism="Homo sapiens"
            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

Query Match      9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1674 GAACCTCGTGTCTCC 1689
Db 16 GAACCTCGAGTCTCC 1

RESULT 83
LOCUS      AX673768             17 bp      DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 2213 from Patent WO03004526.
ACCESSION  AX673768
VERSION     AX673768.1  GI:29332116
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
JOURNAL    Patent: WO 03004526-A 2213 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
source     1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1693 ACCGTGTGGAGTTG 1708
Db 2 ATCGTGTGGAGTTG 17

RESULT 84
LOCUS      AX724290/c           17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 1977 from Patent WO03025176.
ACCESSION  AX724290
VERSION     AX724290.1  GI:30503633
KEYWORDS    Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL    Patent: WO 03025176-A 1977 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
source     1..17
            /organism="Mus musculus"
            /mol_type="unassigned DNA"

TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 1307 22-NOV-2001; GLAXO GROUP LIMITED (GB)
FEATURES   RIBOZYME PHARMACEUTICALS, INC. (US) ;
source     Location/Qualifiers
          1..17
            /organism="Homo sapiens"
            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

Query Match      9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGAGAT 1732
Db 17 GTAGGGAGGTGGAGAT 2

RESULT 85
LOCUS      AX753715             17 bp      DNA      linear      PAT 23-JUN-2003
DEFINITION Sequence 62 from Patent WO03037931.
ACCESSION  AX753715
VERSION     AX753715.1  GI:32166412
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Shannon,M. and Paan,T.
TITLE      Human angiomotin-like protein 1
JOURNAL    Patent: WO 03037331-A 62 08-MAY-2003;
            Amersham Biosciences SV Corp. (US)
FEATURES    Location/Qualifiers
source     1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1716 AGTACGGAGATGGAGA 1731
Db 2 AATACGGTGTGGAGA 17

RESULT 86
LOCUS      AX753716             17 bp      DNA      linear      PAT 23-JUN-2003
DEFINITION Sequence 63 from Patent WO03037931.
ACCESSION  AX753716
VERSION     AX753716.1  GI:32166413
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Shannon,M. and Paan,T.
TITLE      Human angiomotin-like protein 1
JOURNAL    Patent: WO 03037331-A 63 08-MAY-2003;
            Amersham Biosciences SV Corp. (US)
FEATURES    Location/Qualifiers
source     1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1716 AGTACGGAGATGGAGA 1731
Db 1 AATACGGTGTGGAGA 16
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RESULT 87
AX805118
LOCUS AX805118 17 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 1286 from Patent WO03060160.
ACCESSION AX805118
VERSION AX805118.1 GI:38522259
SOURCE Oreochromis niloticus (Nile tilapia)
ORGANISM Oreochromis niloticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Labroidae; Cichlidae; Oreochromis.
REFERENCE 1
AUTHORS Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,P.
TITLE Verification of food origin based on nucleic acid pattern
recognition
JOURNAL Patent: WO 03060160-A 1286 24-JUL-2003;
GenomAR ASA (NO)
FEATURES
source 1..17
/mol_type="unassigned DNA"
/db_xref="taxon:8128"
Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1677 CCTGGTGTCTCCTCC 1692
||||| |||||
Db 1 CCTGGTGTCTCCTCC 16

RESULT 88
BD104946/c
LOCUS BD104946 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104946
VERSION BD104946.1 GI:22650520
KEYWORDS WO 0192572-A/1050.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko,H.; Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 1050 06-DEC-2001;
NISSHINO INDUSTRIES INC. SYSTEM RESEARCH INC. HIDEYOSHI INOKO, TAEKO
KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/1050
PD 06-DEC-2001
PE 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP ODP 164798
PI HIDEYOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
MATSUMURA,
PI SHOGO MORIYA,MICHIO NISHIDA
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
CC Description of Artificial Sequence:capture
FH key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
source 1..17
/mol_type="synthetic construct"
/db_xref="taxon:32630"
Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 GGCTCCAACTCTCTCC 1749
||||| |||||
Db 16 GGCTCTCAACTGCTCC 1

RESULT 89
AR011802/c
LOCUS AR011802 18 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 15 from patent US 5763172.
ACCESSION AR011802
VERSION AR011802.1 GI:3969792
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Magda,D., Sessler,J.L., Wright,M., Miller,R.A. and Dow,W.C.
TITLE Method of phosphate ester hydrolysis
JOURNAL Patent: US 5763172-A 15 09-JUN-1998;
FEATURES
source 1..18
/mol_type="unassigned DNA"
Query Match 9.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670
||||| |||||
Db 17 AACCCGGCTCAG 2

RESULT 90
AR051200
LOCUS AR051200 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5830656.
ACCESSION AR051200
VERSION AR051200.1 GI:5974564
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Milo,G.E. Jr., Casto,B.C., Li,D., Chen,J., Shuler,C.F.,
Ribovich,M.L., Noyes,I., Sun,X.Li. and Theil,K.S.
TITLE Detecting the expression of the catrl gene in squamous cell
carcinoma
JOURNAL Patent: US 5830656-A 7 03-NOV-1998;
FEATURES
source 1..18
/mol_type="unassigned DNA"
Query Match 9.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1691 CCAGCGTGGTGAAGT 1706
||||| |||||
Db 2 CCAGTGTGGTGAAT 17

RESULT 91
AR106948
LOCUS AR106948 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 109 from patent US 6107092.
ACCESSION AR106948
VERSION AR106948.1 GI:12821478
KEYWORDS Unknown.
SOURCE Unknown.

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Best Local Similarity 70.5%; Area: NO; 1.000027
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1657 CACCAAGCTCACAGTGGGA 1675
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Db 1 CACCAAGCTCCTGATGGA 19

RESULT 96
E08539
LOCUS 19 bp DNA linear PAT 29-SEP-1997
DEFINITION PCR primer to detect Aspergillus sp. and Penicillium sp. rDNA.
ACCESSION E08539
VERSION E08539.1 GI:2176654
KEYWORDS JP 1994339400-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Makimura,K., Murayama,S. and Yamaguchi,H.
TITLE PRIMER FOR PATHOGENIC MOULD GENE AMPLIFICATION
JOURNAL Patent: JP 1994339400-A 2 13-DEC-1994;
YAMAGUCHI HIDEYO
COMMENT OS None
OC Artificial sequences.
PN JP 1994339400-A/2
PD 13-DEC-1994
PF 01-JUN-1993 JP 1993130778
PI MAKIMURA KOUICHI, MURAYAMA SOUMEI, YAMAGUCHI HIDEYO PC
C12Q1/68, C12N15/11, (C12Q1/68, C12R1:66), (C12Q1/68, C12R1:80); CC
strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..19
FT Location/Qualifiers
FT /organism='Artificial sequences'.
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/db_xref='taxon:32644'
Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1646 CAGAAGCGACGACCCAGGC 1664
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Db 1 CAGAAGGAAAGTCCAGCC 19

RESULT 98
AR296543/c
LOCUS 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 8278 from patent US 6537751.
ACCESSION AR296543
VERSION AR296543.1 GI:31683827
KEYWORDS Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 8278 25-MAR-2003;
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/mol_type='genomic DNA'
Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1694 GCGTGTGGAGTGGGTT 1712
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Db 19 GAGTTGTGGATGTTGGGT 1

RESULT 99
AX130657
LOCUS 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1875 from Patent WO0130362.
ACCESSION AX130657
VERSION AX130657.1 GI:14136962
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 1875 03-MAY-2001;
IMMUSOL, INC. (US)

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(C12Q1/68,
PC C12R1:725), (C12Q1/68, C12R1:645), (C12Q1/68, C12R1:68); CC
strandedness: Both;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Artificial sequences' FT
misc_feature 1..19
FT /note='Synthetic DNA having complementary FT
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source
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Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1646 CAGAAGCGACGACCCAGGC 1664
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Db 1 CAGAAGGAAAGTCCAGCC 19

RESULT 98
AR296543/c
LOCUS 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 8278 from patent US 6537751.
ACCESSION AR296543
VERSION AR296543.1 GI:31683827
KEYWORDS Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 8278 25-MAR-2003;
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Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1694 GCGTGTGGAGTGGGTT 1712
||||| ||||| |||||
Db 19 GAGTTGTGGATGTTGGGT 1

RESULT 99
AX130657
LOCUS 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1875 from Patent WO0130362.
ACCESSION AX130657
VERSION AX130657.1 GI:14136962
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 1875 03-MAY-2001;
IMMUSOL, INC. (US)

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        /db_xref="taxon:9606"
        /note="Cyclin D1 ribozyme binding site"

Query Match
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  Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1739 CCAACTCTCTCCATCCTTA 1757
Db 1 CCAACAACCTCTCTGCTTA 19

RESULT 100
AX131856
LOCUS AX131856 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3074 from Patent WO0130362.
ACCESSION AX131856
VERSION AX131856.1 GI:14138161
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Robbins, J.M. and Tritz, R.
  Ribozyme therapy for the treatment of proliferative skin and eye
  diseases
JOURNAL Patent: WO 0130362-A 3074 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
      /note="Cyclin A1 ribozyme binding site"

Query Match
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  Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1698 GGTGGAAGTTGGTTAGGA 1716
Db 1 GGTGAGGTTGGGAGAA 19

RESULT 101
A28990
LOCUS A28990 15 bp DNA linear PAT 30-JUN-1995
DEFINITION Oligo 9 from patent EP0522880.
ACCESSION A28990
VERSION A28990.1 GI:1248843
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
  1 (bases 1 to 15)
  Holton, T.A., Cornish, E.C., Kovacic, F., Tanaka, Y. and Lester, D.R.
  Genetic sequences encoding flavonoid pathway enzymes and uses
  therefor
JOURNAL Patent: EP 0522880-A 9 13-JAN-1993;
INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"

Query Match
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FEATURES
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Query Match
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  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1683 TGTCTCTCTCCAGCG 1696
Db 2 TGTCTCTCTCCAGTG 15

RESULT 102
AR030911
LOCUS AR030911 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5861487.
ACCESSION AR030911
VERSION AR030911.1 GI:5344125
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 15)
  Holton, T.A., Cornish, E.C., Kovacic, F., Tanaka, Y. and
  Lester, D.Ruth.
  Genetic sequences encoding flavonoid pathway enzymes and uses
  therefor
JOURNAL Patent: US 5861437-A 11 19-JAN-1999;
  Location/Qualifiers
  1..15
    /organism="unassigned DNA"

Query Match
  Best Local Similarity 8.9%; Score 12.4; DB 1; Length 15;
  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1683 TGTCTCTCTCCAGCG 1696
Db 2 TGTCTCTCTCCAGTG 15

RESULT 103
I28303
LOCUS I28303 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 11 from patent US 5569832.
ACCESSION I28303
VERSION I28303.1 GI:1813079
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 15)
  Holton, T.A., Cornish, E.C., Kovacic, F., Tanaka, Y. and Lester, D.R.
  Genetic sequences encoding flavonoid pathway enzymes and uses
  therefor
JOURNAL Patent: US 5569832-A 11 29-OCT-1996;
  Location/Qualifiers
  1..15
    /organism="unassigned DNA"

Query Match
  Best Local Similarity 8.9%; Score 12.4; DB 1; Length 15;
  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1683 TGTCTCTCTCCAGCG 1696
Db 2 TGTCTCTCTCCAGTG 15

RESULT 104
AR127505/c
LOCUS AR127505/c 16 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 20 from patent US 6180766.
ACCESSION AR127505
VERSION AR127505.1 GI:14114100
KEYWORDS
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SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Schinazi,R.F., Fulcrand-El Kattan,G. and Lesnikowski,Z.Jan.
TITLE      Nucleosides and oligonucleotides containing boron clusters
JOURNAL    Patent: US 6180766-A 20 30-JAN-2001;
FEATURES   Location/Qualifiers
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            /mol_type="unassigned DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 CCTCGGTGTCCT 1690
Db 16 CCTCGGTGTCAT 3

RESULT 105
LOCUS      I50742      16 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 24 from patent US 5643724.
ACCESSION  I50742
VERSION    I50742.1 GI:2472445
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS    Fildes,N.Jane. and Reynolds,R.Lynne.
TITLE      Methods and reagents for Glycophorin A typing
JOURNAL    Patent: US 5643724-A 24 01-JUL-1997;
FEATURES   Location/Qualifiers
            source
            1..16
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Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GGTGGAAGTTGGGT 1711
Db 16 GGTGGAAGCTGGGT 3

RESULT 106
LOCUS      AR328506/c
DEFINITION Sequence 5908 from patent US 6566127.
ACCESSION  AR328506
VERSION    AR328506.1 GI:33714314
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 5908 20-MAY-2003;
FEATURES   Location/Qualifiers
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            1..16
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            /mol_type="unassigned RNA"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Schinazi,R.F., Fulcrand-El Kattan,G. and Lesnikowski,Z.Jan.
TITLE      Nucleosides and oligonucleotides containing boron clusters
JOURNAL    Patent: US 6180766-A 20 30-JAN-2001;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 CCTCGGTGTCCT 1690
Db 16 CCTCGGTGTCAT 3

RESULT 107
LOCUS      AX039862      16 bp      DNA      linear      PAT 18-NOV-2000
DEFINITION Sequence 251 from Patent WO0063441.
ACCESSION  AX039862
VERSION    AX039862.1 GI:11229891
KEYWORDS   .
SOURCE     Synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    Herrstadt,C. and Davis,R.E.
TITLE      Single nucleotide polymorphisms in mitochondrial genes that segregate with Alzheimer's disease
JOURNAL    Patent: WO 0063441-A 251 26-OCT-2000;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="PCR primer"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1709 GGTAGGAGTACGG 1722
Db 3 GGTAGGCGTACGG 16

RESULT 108
LOCUS      AX135793      16 bp      DNA      linear      PAT 29-MAY-2001
DEFINITION Sequence 20 from Patent EP1113020.
ACCESSION  AX135793
VERSION    AX135793.1 GI:14272029
KEYWORDS   .
SOURCE     Human immunodeficiency virus 1 (HIV-1)
            Human immunodeficiency virus 1
            Viruses; Retrovirdae; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE  1
AUTHORS    Lesnikowski,Z.J., Kattan,G.F. and Schinazi,R.F.
TITLE      Nucleosides and oligonucleotides containing boron clusters
JOURNAL    Patent: EP 1113020-A 20 04-JUL-2001;
            EMORY UNIVERSITY (US)
FEATURES   Location/Qualifiers
            source
            1..16
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            /db_xref="taxon:11676"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 CCTCGGTGTCCT 1690
Db 16 CCTCGGTGTCAT 3

RESULT 109
LOCUS      BD255127/c
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD255127

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VERSION      BD255127.1  GI:33064897
KEYWORDS     JP 2002541795-A/2920.
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS     Blatt L., Zwick M., Pavco P. and Mcswiggen J.
TITLE       Regulation of repressor genes using nucleic acid molecules
JOURNAL     Patent: JP 2002541795-A 2920 10-DEC-2002;
COMMENT     RIBOZYME PHARMACEUTICALS INC
OS          Eukaryote
PN          JP 2002541795-A/2920
PD          10-DEC-2002
PF          11-APR-2000 JP 2000611654
PR          12-APR-1999 US 60/129390
PI          LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC          C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC          (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC          A61K37/02,
PC          (C12N5/00, C12R1:91)
CC          Regulation of repressor genes using nucleic acid molecules FH
Key source  1. .17
Location/Qualifiers
FT          source
FEATURES
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Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          1696 GTGGTGAAGTTGG 1709
Db          16 GAGGTGAAGTTGG 3
RESULT 110
LOCUS      BD255128
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255128
VERSION   BD255128.1  GI:33064898
KEYWORDS  JP 2002541795-A/2921.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Blatt L., Zwick M., Pavco P. and Mcswiggen J.
TITLE     Regulation of repressor genes using nucleic acid molecules
JOURNAL   Patent: JP 2002541795-A 2921 10-DEC-2002;
COMMENT   RIBOZYME PHARMACEUTICALS INC
OS        Eukaryote
PN        JP 2002541795-A/2921
PD        10-DEC-2002
PF        11-APR-2000 JP 2000611654
PR        12-APR-1999 US 60/129390
PI        LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC          C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC          (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC          A61K37/02, C12R1:91)
PC          (C12N5/00, C12R1:91)
CC          Regulation of repressor genes using nucleic acid molecules FH
Key source  1. .17
Location/Qualifiers
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Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          1696 GTGGTGAAGTTGG 1709
Db          16 GAGGTGAAGTTGG 3
RESULT 110
LOCUS      BD255128
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255128
VERSION   BD255128.1  GI:33064898
KEYWORDS  JP 2002541795-A/2921.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Blatt L., Zwick M., Pavco P. and Mcswiggen J.
TITLE     Regulation of repressor genes using nucleic acid molecules
JOURNAL   Patent: JP 2002541795-A 2921 10-DEC-2002;
COMMENT   RIBOZYME PHARMACEUTICALS INC
OS        Eukaryote
PN        JP 2002541795-A/2921
PD        10-DEC-2002
PF        11-APR-2000 JP 2000611654
PR        12-APR-1999 US 60/129390
PI        LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC          C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC          (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC          A61K37/02, C12R1:91)
PC          (C12N5/00, C12R1:91)
CC          Regulation of repressor genes using nucleic acid molecules FH
Key source  1. .17
Location/Qualifiers
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FEATURES
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Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          1696 GTGGTGAAGTTGG 1709
Db          16 GAGGTGAAGTTGG 3
RESULT 111
LOCUS      AR327591
DEFINITION Sequence 4993 from patent US 6566127.
ACCESSION AR327591
VERSION   AR327591.1  GI:33713399
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco P., McSwiggen J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
          Patent: US 6566127-A 4993 20-MAY-2003;
JOURNAL   Patent: US 6566127-A 4993 20-MAY-2003;
FEATURES
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Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          1663 GCTCACAGCTGAA 1676
Db          15 GCCACAGCTGAA 2
RESULT 112
LOCUS      AX266079
DEFINITION Sequence 3470 from Patent WO0173002.
ACCESSION AX266079
VERSION   AX266079.1  GI:16514878
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Kmiec, E.B., Gamper, H.B. and Rice, M.C.
TITLE     Targeted chromosomal genomic alterations with modified single
          stranded oligonucleotides
          Patent: WO 0173002-A 3470 04-OCT-2001;
JOURNAL   UNIVERSITY OF DELAWARE (US)
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Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          1663 GCTCACAGCTGAA 1676
Db          15 GCCACAGCTGAA 2
RESULT 112
LOCUS      AX266079
DEFINITION Sequence 3470 from Patent WO0173002.
ACCESSION AX266079
VERSION   AX266079.1  GI:16514878
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Kmiec, E.B., Gamper, H.B. and Rice, M.C.
TITLE     Targeted chromosomal genomic alterations with modified single
          stranded oligonucleotides
          Patent: WO 0173002-A 3470 04-OCT-2001;
JOURNAL   UNIVERSITY OF DELAWARE (US)
FEATURES
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            /mol_type='unassigned DNA'
            /db_xref='taxon:9606'
Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          1663 GCTCACAGCTGAA 1676
Db          15 GCCACAGCTGAA 2

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Qy 1686 CTCCTCCAGCTGG 1699
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Db 14 CTCCTCCAGCTGG 1

RESULT 113
AX266080
LOCUS AX266080 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3471 from Patent WO0173002.
ACCESSION AX266080
VERSION AX266080.1 GI:16514879
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Kniec,E.B., Ganper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL Patent: WO 0173002-A 3471 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCTGG 1699
|||||
Db 4 CTCCTCCAGCTGG 17

RESULT 114
AX727607/C
LOCUS AX727607 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5294 from Patent WO03025176.
ACCESSION AX727607
VERSION AX727607.1 GI:30506950
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
JOURNAL reversion, apoptosis and/or virus resistance and their use as
Patent: WO 03025176-A 5294 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1725 ATGGAGATTGCTC 1738
|||||
Db 14 ATGGAGATTGATC 1

RESULT 115
AX753717

LOCUS AX753717 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 64 from Patent WO03037931.
ACCESSION AX753717
VERSION AX753717.1 GI:32166414
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiominotin-like protein 1
JOURNAL Patent: WO 03037931-A 64 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1718 TACGGAGATGGAGA 1731
|||||
Db 2 TACGGTGTGGAGA 15

RESULT 116
AX753718
LOCUS AX753718 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 65 from Patent WO03037931.
ACCESSION AX753718
VERSION AX753718.1 GI:32166415
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiominotin-like protein 1
JOURNAL Patent: WO 03037931-A 65 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1718 TACGGAGATGGAGA 1731
|||||
Db 1 TACGGTGTGGAGA 14

RESULT 117
AX757161
LOCUS AX757161 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 482 from Patent WO03040369.
ACCESSION AX757161
VERSION AX757161.1 GI:32251777
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.

TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 482 15-MAY-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCT 1687
Db 1 GATCCCTGGTGCT 14

RESULT 118
AR018181/c
LOCUS AR018181 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 8 from patent US 5780611.
ACCESSION AR018181
VERSION AR018181.1 GI:3973784
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.
TITLE Oligomers which inhibit expression of collagen genes
JOURNAL Patent: US 5780611-A 8 14-JUL-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
Db 17 CTCCTCCCTTTCCT 4

RESULT 119
AR018183/c
LOCUS AR018183 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 10 from patent US 5780611.
ACCESSION AR018183
VERSION AR018183.1 GI:3973786
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.
TITLE Oligomers which inhibit expression of collagen genes
JOURNAL Patent: US 5780611-A 10 14-JUL-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
Db 17 CTCCTCCCTTTCCT 4

RESULT 120
AR018184/c
LOCUS AR018184 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 11 from patent US 5780611.
ACCESSION AR018184
VERSION AR018184.1 GI:3973787
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.
TITLE Oligomers which inhibit expression of collagen genes
JOURNAL Patent: US 5780611-A 11 14-JUL-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
Db 17 CTCCTCCCTTTCCT 4

RESULT 121
AR187552/c
LOCUS AR187552 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 3040 from patent US 6346398.
ACCESSION AR187552
VERSION AR187552.1 GI:23233517
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 3040 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGAA 1676
Db 16 GCCCACAGCTGAA 3

RESULT 122
AR299488
LOCUS AR299488 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 11223 from patent US 6537751.
ACCESSION AR299488
VERSION AR299488.1 GI:3.686772
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density

Db 17 CTCCTCCCTTTCCT 4

RESULT 120
AR018184/c
LOCUS AR018184 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 11 from patent US 5780611.
ACCESSION AR018184
VERSION AR018184.1 GI:3973787
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.
TITLE Oligomers which inhibit expression of collagen genes
JOURNAL Patent: US 5780611-A 11 14-JUL-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
Db 17 CTCCTCCCTTTCCT 4

RESULT 121
AR187552/c
LOCUS AR187552 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 3040 from patent US 6346398.
ACCESSION AR187552
VERSION AR187552.1 GI:23233517
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 3040 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGAA 1676
Db 16 GCCCACAGCTGAA 3

RESULT 122
AR299488
LOCUS AR299488 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 11223 from patent US 6537751.
ACCESSION AR299488
VERSION AR299488.1 GI:3.686772
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density

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disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 11223 25-MAR-2003;
FEATURES
    source
        Location/Qualifiers
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1722 GAGATGGAGATTGG 1735
Db 5 GAGATGGAGATTAGG 18

RESULT 123
AR324066/c
LOCUS AR324066 18 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1468 from patent US 6566127.
ACCESSION AR324066
VERSION AR324066.1 GI:33709874
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
    1 (bases 1 to 18)
    Unclassified.
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1468 20-MAY-2003;
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1663 GCTCACAGCTGGAA 1676
Db 16 GCCACACAGCTGGAA 3

RESULT 124
AR362645
LOCUS AR362645 18 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 15 from patent US 5179198.
ACCESSION AR362645
VERSION AR362645.1 GI:34422997
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
    1 (bases 1 to 18)
    Unclassified.
AUTHORS Okada,H., Okada,N., Nagami,Y., Takahashi,K., Takizawa,H. and
Kondo,J.
TITLE Glycoprotein and gene coding therefor
JOURNAL Patent: US 5179198-A 15 12-JAN-1993;
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1702 GAAGTTGGTTAGG 1715
Db 5 GCAGTTGGTTAGG 18

disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 11223 25-MAR-2003;
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1702 GAAGTTGGTTAGG 1715
Db 5 GCAGTTGGTTAGG 18

RESULT 125
AR365708
LOCUS AR365708 18 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 11 from patent US 5521296.
ACCESSION AR365708
VERSION AR365708.1 GI:34429630
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
    1 (bases 1 to 18)
    Unclassified.
AUTHORS Okada,H., Okada,N., Nagami,Y., Takahashi,K., Takizawa,H. and
Kondo,J.
TITLE Glycoprotein and gene coding therefor
JOURNAL Patent: US 5521296-A 11 28-MAY-1996;
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1702 GAAGTTGGTTAGG 1715
Db 5 GCAGTTGGTTAGG 18

RESULT 126
AR786023/c
LOCUS AX786023 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 19 from Patent WO03050272.
ACCESSION AX786023
VERSION AX786023.1 GI:32953643
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
    1
    Bandelier,M.A., Denys,P., Denormandie,P., Sapena,R.,
    Lepailleur-Enouf,D. and Youssefian,T.
    Bone development model
    Patent: WO 03050272-A 19 19-JUN-2003;
    Sympathos (FR)
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Amorce PCR sens pour l'amplification specifique du
            gene du collagene de type I alpha 1 (COL1A1)"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1655 AGCACCAGGCTCAC 1668
Db 14 AGCACCAGGTTTAC 1

RESULT 127
BD206162
LOCUS BD206162 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Human antithrombin III and method concerning the same.
ACCESSION BD206162
VERSION BD206162.1 GI:33015932
KEYWORDS JP 2002514579-A/16.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
AUTHORS Bock,S.C., Picard,V. and Zendeherouh,P.
TITLE Human antithrombin III and method concerning the same
JOURNAL Patent: JP 2002514579-A 16 21-MAY-2002;
SUSAN C BOCK,VERONIQUE PICARD,PEDRAM ZENDEHROUH
COMMENT OS Homo sapiens (human)
PN JP 2002514579-A/16
PD 21-MAY-2002
PF 12-MAY-1999 JP 2000547950
PR 12-MAY-1998 US 60/085197,05-MAY-1999 US 09/305.588 P1
SUSAN C BOCK,VERONIQUE PICARD,PEDRAM ZENDEHROUH PC
AG1K38/00,AG1K38/55,AG1P7/02,AG1P43/00,C07K14/47,C07K14/81, PC
C12N15/09,
PC AG1K37/02,AG1K37/64,C12N15/00
CC Human antithrombin III and method concerning the same. FH
Key Location/Qualifiers
FT source 1..18
FT /organism='Homo sapiens (human)'.
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source
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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1640 TTGTAGCAGAGGC 1653
Db 3 TTGTTCAGAGAGGC 16
RESULT 128
AR074596/c
LOCUS AR074596 19 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 13 from patent US 5955265.
ACCESSION AR074596
VERSION AR074596.1 GI:10001349
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Brook,J.David., Housman,D.E., Shaw,D.J., Harley,H.G. and Johnson,K.J.
TITLE DNA sequence encoding the myotonic dystrophy gene and uses thereof
JOURNAL Patent: US 5955265-A 13 21-SEP-1999;
FEATURES
source
1..19
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCACAGCTGGACCC 1679
Db 18 GGCTCAVRCCTGTATCC 1
RESULT 129
AR083935/c
LOCUS AR083935 19 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 13 from patent US 5977333.
ACCESSION AR083935
VERSION AR083935.1 GI:10010706
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Brook,J.David., Housman,D.E., Shaw,D.J., Harley,H.G. and Johnson,K.J.
TITLE DNA sequence encoding the myotonic dystrophy gene and uses thereof
JOURNAL Patent: US 5977333-A 13 02-NOV-1999;
FEATURES
source
1..19
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCACAGCTGGACCC 1679
Db 18 GGCTCAVRCCTGTATCC 1
RESULT 130
AR083935/c
LOCUS AR083935 19 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 1 from patent US 5538869.
ACCESSION AR083935
VERSION AR083935.1 GI:1603685
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Siciliano,M.J. and Liu,P.
TITLE In-situ hybridization probes for identification and banding of specific human chromosomes and regions
JOURNAL Patent: US 5538869-A 1 23-JUL-1996;
FEATURES
source
1..19
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCACAGCTGGACCC 1679
Db 18 GGCTCAVRCCTGTATCC 1
RESULT 131
AR083935/c
LOCUS AR083935 19 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5578493.
ACCESSION AR083935
VERSION AR083935.1 GI:1820760
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Gilliam,T.Conrad. and Tanzi,R.E.
TITLE Wilson's disease gene
JOURNAL Patent: US 5578493-A 1 26-NOV-1996;
FEATURES
source
1..19
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCACAGCTGGACCC 1679
Db 18 GGCTCAVRCCTGTATCC 1

1 (bases 1 to 19)
AUTHORS Brook,J.David., Housman,D.E., Shaw,D.J., Harley,H.G. and Johnson,K.J.
TITLE DNA sequence encoding the myotonic dystrophy gene and uses thereof
JOURNAL Patent: US 5977333-A 13 02-NOV-1999;
FEATURES
source
1..19
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCACAGCTGGACCC 1679
Db 18 GGCTCAVRCCTGTATCC 1
RESULT 130
AR083935/c
LOCUS AR083935 19 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 1 from patent US 5538869.
ACCESSION AR083935
VERSION AR083935.1 GI:1603685
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Siciliano,M.J. and Liu,P.
TITLE In-situ hybridization probes for identification and banding of specific human chromosomes and regions
JOURNAL Patent: US 5538869-A 1 23-JUL-1996;
FEATURES
source
1..19
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCACAGCTGGACCC 1679
Db 18 GGCTCAVRCCTGTATCC 1
RESULT 131
AR083935/c
LOCUS AR083935 19 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5578493.
ACCESSION AR083935
VERSION AR083935.1 GI:1820760
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Gilliam,T.Conrad. and Tanzi,R.E.
TITLE Wilson's disease gene
JOURNAL Patent: US 5578493-A 1 26-NOV-1996;
FEATURES
source
1..19
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCACAGCTGGACCC 1679
Db 18 GGCTCAVRCCTGTATCC 1

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Db      18  GGCTCAVRCCTGTAATCC 1

RESULT 132
LOCUS      AR299173/c
DEFINITION Sequence 10908 from patent US 6537751.
ACCESSION  AR299173
VERSION     AR299173.1  GI:31686457
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1  (bases 1 to 19)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL     Patent: US 6537751-A 10908 25-MAR-2003;
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1631  GGATGGGCTTGTA 1644
Db      19  GGTGGGGCTTGTA 6

RESULT 133
LOCUS      AX033909/c
DEFINITION Sequence 1 from Patent WO9851790.
ACCESSION  AX033909
VERSION     AX033909.1  GI:10280477
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1
AUTHORS     Cancilla,M.R., Choo,K.H. and Du,S.D.
TITLE       A novel nucleic acid molecule
JOURNAL     Patent: WO 9851790-A 1 19-NOV-1998;
            CANCELLA MICHAEL ROBERT (AU) ; CHOO KONG HONG ANDY (AU) ; SART
            DESIRBE DU (AU) ; AMRAD OPERATIONS PTY LTD (AU)
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1662  GGCTCACAGCTGGAAACC 1679
Db      18  GGCTCAVRCCTGTAATCC 1

RESULT 134
LOCUS      AR046916
DEFINITION Sequence 1709 from patent US 5817796.
ACCESSION  AR046916
VERSION     AR046916.1  GI:5968381
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1
AUTHORS     Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL     Patent: US 5817796-A 1709 06-OCT-1998;
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1665  TCACAGCTGGAACCCCTG 1681
Db      1  TCTCAGCTCGAACTCTG 17

RESULT 135
LOCUS      BD254187/c
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD254187
VERSION     BD254187.1  GI:33063957
KEYWORDS    JP 2002541795-A/1980.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1  (bases 1 to 17)
AUTHORS     Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE       Regulation of repressor genes using nucleic acid molecules
JOURNAL     Patent: JP 2002541795-A 1980 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Eukaryote
            PN JP 2002541795-A/1980
            PD 10-DEC-2002
            PF 11-APR-2000 JP 2000611654
            PR 12-APR-1999 US 60/129390
            PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
            C12R1:91),
            PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC A61K37/02,
            PC (C12N5/00,C12R1:91)
            CC Regulation of repressor genes using nucleic acid molecules FH
            Key source
            1..17
            Location/Qualifiers
            FT
            /organism='Eukaryote'.
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1638  GCTTGTCAGCAGGACCA 1654
Db      17  GCTGTAGTAGAGGCCA 1

RESULT 136
LOCUS      I53968
DEFINITION Sequence 1709 from patent US 5646042.
ACCESSION  I53968
VERSION     I53968.1  GI:2475171
KEYWORDS

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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myb targeted ribozymes
JOURNAL     Patent: US 5646042-A 1709 08-JUL-1997;
FEATURES    Location/Qualifiers
            source
            1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1665 TCACAGCTGGAACCTGTG 1681
Db      1 TTTCAGCTCGAAGCTGTG 17

RESULT 137
AX365741
LOCUS      AR365741                17 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION Sequence 6 from patent US 6328971.
ACCESSION  AR365741
VERSION     AR365741.1 GI:34597897
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     van der Bruggen,P. and Boon-Palleur,T.
TITLE       MAGE-1 derived nona peptides, and compositions thereof
JOURNAL     Patent: US 6328971-A 6 11-DEC-2001;
FEATURES    Location/Qualifiers
            source
            1..17
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1653 CAAGCACCAGGCTCACA 1669
Db      1 CAAGCGCCAGGCACAGA 17

RESULT 138
AX215134
LOCUS      AX215134                17 bp      RNA      linear      PAT 07-SEP-2001
DEFINITION Sequence 576 from Patent WO0159103.
ACCESSION  AX215134
VERSION     AX215134.1 GI:15525177
KEYWORDS   synthetic construct
SOURCE     synthetic construct
           artificial sequences.
ORGANISM   1
REFERENCE   1
AUTHORS     Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE       Method and reagent for the modulation and diagnosis of cd20 and
           nogo gene expression
JOURNAL     Patent: WO 0159103-A 576 16-AUG-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
           McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES    Location/Qualifiers
            source
            1..17
              /organism="synthetic construct"
              /mol_type="unassigned RNA"
              /db_xref="taxon:32630"
              /note="Nucleic Acid"

SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myb targeted ribozymes
JOURNAL     Patent: US 5646042-A 1709 08-JUL-1997;
FEATURES    Location/Qualifiers
            source
            1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1704 AGTTGGTTAGAGTAC 1720
Db      1 AGTTGGTTTCAGAAGTAC 17

RESULT 139
AX499445
LOCUS      AX499445                17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 752 from Patent EP1229046.
ACCESSION  AX499445
VERSION     AX499445.1 GI:23381738
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ORGANISM   1
REFERENCE   1
AUTHORS     Zhan,J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 752 07-AUG-2002;
           Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1662 GGCTCACAGTGGACCC 1678
Db      1 GACTCACTGCTGGACCC 17

RESULT 140
AX532097
LOCUS      AX532097                17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 1606 from Patent EP1239051.
ACCESSION  AX532097
VERSION     AX532097.1 GI:25255956
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ORGANISM   1
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 1606 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      3.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1671 CTGGAACCCCTGGTCTCT 1687
Db      1 CCGGAGCCCTGGTCTCT 17

RESULT 141
AX532099

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LOCUS AX532099 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1608 from Patent EP1239051.
ACCESSION AX532099
VERSION AX532099.1 GI:25255985
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1608 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1673 GGACCCCTGGTCTCTCC 1689
|||||
Db 1 GGAGCCCTGGTCTCTAC 17

RESULT 142
AX532103
LOCUS AX532103 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1612 from Patent EP1239051.
ACCESSION AX532103
VERSION AX532103.1 GI:25255993
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1612 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1673 GGACCCCTGGTCTCTCC 1689
|||||
Db 1 GGAGCCCTGGTCTCTAC 17

RESULT 143
AX532253/c
LOCUS AX532253 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1762 from Patent EP1239051.
ACCESSION AX532253
VERSION AX532253.1 GI:25256291
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
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TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1762 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1749 CCTATCCTAAAGGCCCA 1765
|||||
Db 17 CTTGTCTTAAGTCCCA 1

RESULT 144
AX532254/c
LOCUS AX532254 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1763 from Patent EP1239051.
ACCESSION AX532254
VERSION AX532254.1 GI:25256293
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1763 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1748 CCCTATCCTAAAGGCCCC 1764
|||||
Db 17 CTTGTCTTAAGTCCCC 1

RESULT 145
AX687667
LOCUS AX687667 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 399 from Patent EP1281758.
ACCESSION AX687667
VERSION AX687667.1 GI:29410363
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 399 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.8%; Score 12.2; DB 1; Length 17;
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Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1740 CAACCTCCTCCCTATCCT 1756
Db 1 CAGTTCCTCACTATCCT 17

RESULT 146
AX728392/c
LOCUS AX728392 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 582 from Patent EPI281758.
ACCESSION AX728392
VERSION AX687850.1 GI:29410548
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 26 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAACCTCTG 1682
Db 17 CCAGCTGGATGCTGG 1

RESULT 147
AX726673/c
LOCUS AX726673 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4360 from Patent WO03025176.
ACCESSION AX726673
VERSION AX726673.1 GI:30506016
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 4360 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1650 AGGCAAGCACCGCTC 1666
Db 17 AGGCAAGCAACGATC 1

Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1740 CAACCTCCTCCCTATCCT 1756
Db 1 CAGTTCCTCACTATCCT 17

RESULT 148
AX728392/c
LOCUS AX728392 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 26 from Patent WO03025175.
ACCESSION AX728392
VERSION AX728392.1 GI:30507735
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 26 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1641 TGTAGCAGAGGCGACG 1657
Db 17 TGTAGCAGATGCGATC 1

RESULT 149
AX734168
LOCUS AX734168 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5802 from Patent WO03025175.
ACCESSION AX734168
VERSION AX734168.1 GI:30513511
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 5802 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1735 GCTCCCAACTCCTCCT 1751
Db 1 GATCCCAACTGCTCCTT 17

RESULT 150
AX762563/c
LOCUS AX762563 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5884 from Patent WO03040369.
ACCESSION AX762563
VERSION AX762563.1 GI:32257179
KEYWORDS

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL    Patent: WO 03040369-A 5884 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1641 TGTAGCAGAGCGCAGC 1657
      ||||| ||| |||
Db 17 TGTAGCAGATGCGCATC 1

RESULT 151
AR106981/c
LOCUS      AR106981
DEFINITION Sequence 142 from patent US 6107092.
ACCESSION  AR106981
VERSION     AR106981.1 GI:12821511
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Cowser,L.M., Bennett,C.Frank. and O'Malley,B.W.
TITLE      Antisense modulation of SRA expression
JOURNAL    Patent: US 6107092-A 142 22-AUG-2000;
            Location/Qualifiers
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCCAGCTGG 1674
      ||||| ||| ||| |||
Db 17 ACCAGGCTCCAGCAGG 1

RESULT 152
A56874/c
LOCUS      A56874
DEFINITION Sequence 10 from Patent WO9627664.
ACCESSION  A56874
VERSION     A56874.1 GI:3712886
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1
AUTHORS    Morelli,S., Nicolin,A. and Quattrone,A.
TITLE      ANTISENSE TRANSCRIPT EXPRESSED IN B LYMPHOCYTES AND SYNTHETIC
            OLIGONUCLEOTIDES USEFUL TO INHIBIT THE ACTIVITY THEREOF
JOURNAL    Patent: WO 9627664-A 10 12-SEP-1996;
            CONSIGLIO NAZIONALE RICERCA (IT)
COMMENT    Other publication AU 4944396 960923.
FEATURES   Location/Qualifiers
            source
            1..18

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL    Patent: WO 03040369-A 5884 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1641 TGTAGCAGAGCGCAGC 1657
      ||||| ||| |||
Db 17 TGTAGCAGATGCGCATC 1

RESULT 151
AR106981/c
LOCUS      AR106981
DEFINITION Sequence 142 from patent US 6107092.
ACCESSION  AR106981
VERSION     AR106981.1 GI:12821511
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Cowser,L.M., Bennett,C.Frank. and O'Malley,B.W.
TITLE      Antisense modulation of SRA expression
JOURNAL    Patent: US 6107092-A 142 22-AUG-2000;
            Location/Qualifiers
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCCAGCTGG 1674
      ||||| ||| ||| |||
Db 17 ACCAGGCTCCAGCAGG 1

RESULT 152
A56874/c
LOCUS      A56874
DEFINITION Sequence 10 from Patent WO9627664.
ACCESSION  A56874
VERSION     A56874.1 GI:3712886
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1
AUTHORS    Morelli,S., Nicolin,A. and Quattrone,A.
TITLE      ANTISENSE TRANSCRIPT EXPRESSED IN B LYMPHOCYTES AND SYNTHETIC
            OLIGONUCLEOTIDES USEFUL TO INHIBIT THE ACTIVITY THEREOF
JOURNAL    Patent: WO 9627664-A 10 12-SEP-1996;
            CONSIGLIO NAZIONALE RICERCA (IT)
COMMENT    Other publication AU 4944396 960923.
FEATURES   Location/Qualifiers
            source
            1..18

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL    Patent: WO 03040369-A 5884 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1641 TGTAGCAGAGCGCAGC 1657
      ||||| ||| |||
Db 17 TGTAGCAGATGCGCATC 1

RESULT 151
A56885
LOCUS      A56885
DEFINITION Sequence 21 from Patent WO9627664.
ACCESSION  A56885
VERSION     A56885.1 GI:3712897
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1
AUTHORS    Morelli,S., Nicolin,A. and Quattrone,A.
TITLE      ANTISENSE TRANSCRIPT EXPRESSED IN B LYMPHOCYTES AND SYNTHETIC
            OLIGONUCLEOTIDES USEFUL TO INHIBIT THE ACTIVITY THEREOF
JOURNAL    Patent: WO 9627664-A 21 12-SEP-1996;
            CONSIGLIO NAZIONALE RICERCA (IT)
COMMENT    Other publication AU 4944396 960923.
FEATURES   Location/Qualifiers
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            /organism="unidentified"
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            /db_xref="taxon:32644"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1644 AGCAGAAGCGCAGCACC 1660
      ||||| ||| ||| |||
Db 17 AGCAGAAGCCAGCGCATC 1

RESULT 153
A56885
LOCUS      A56885
DEFINITION Sequence 21 from Patent WO9627664.
ACCESSION  A56885
VERSION     A56885.1 GI:3712897
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1
AUTHORS    Morelli,S., Nicolin,A. and Quattrone,A.
TITLE      ANTISENSE TRANSCRIPT EXPRESSED IN B LYMPHOCYTES AND SYNTHETIC
            OLIGONUCLEOTIDES USEFUL TO INHIBIT THE ACTIVITY THEREOF
JOURNAL    Patent: WO 9627664-A 21 12-SEP-1996;
            CONSIGLIO NAZIONALE RICERCA (IT)
COMMENT    Other publication AU 4944396 960923.
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1644 AGCAGAAGCGCAGCACC 1660
      ||||| ||| ||| |||
Db 17 AGCAGAAGCCAGCGCATC 1

RESULT 154
AR092022/c
LOCUS      AR092022
DEFINITION Sequence 46 from patent US 5998141.
ACCESSION  AR092022
VERSION     AR092022.1 GI:10018776
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
            unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Acton,S.Laurene.
TITLE      Intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL    Patent: US 5998141-A 46 07-DEC-1999;
            Location/Qualifiers
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1682 GTGTCTCTCTCCAGCGTG 1698
      ||||| ||| ||| |||
Db 17 GTCTCTCTCTCCCGCTG 1
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RESULT 155
AR112157/c
LOCUS AR112157 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 46 from patent US 6130041.
ACCESSION AR112157
VERSION AR112157.1 GI:14092057
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Acton,S.Laurene.
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 6130041-A 46 10-OCT-2000;
FEATURES
source Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1682 GTGTCCTCTCCAGCGTG 1698
Db 17 GTCTCTCTCCGCGCTG 1
RESULT 156
AR118335/c
LOCUS AR118335 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6140492.
ACCESSION AR118335
VERSION AR118335.1 GI:14099241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Morelli,S., Nicolin,A. and Quattrone,A.
TITLE Antisense transcript expressed in B lymphocytes and synthetic oligonucleotides useful to inhibit the activity thereof
JOURNAL Patent: US 6140492-A 10 31-OCT-2000;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1682 GTGTCCTCTCCAGCGTG 1698
Db 17 GTCTCTCTCCGCGCTG 1
RESULT 157
AR118346
LOCUS AR118346 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6140492.
ACCESSION AR118346
VERSION AR118346.1 GI:14099252
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Morelli,S., Nicolin,A. and Quattrone,A.
TITLE Antisense transcript expressed in B lymphocytes and synthetic oligonucleotides useful to inhibit the activity thereof
JOURNAL Patent: US 6140492-A 21 31-OCT-2000;

FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1644 AGCAGAAGCCAGCAC 1660
Db 2 AGCAGAAGCCAGCATC 18
RESULT 158
AR137364
LOCUS AR137364 18 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 111 from patent US 6197505.
ACCESSION AR137364
VERSION AR137364.1 GI:14478873
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Norberg,L.Torbjorn., Andersson,M.Kristina. and Lindstrom,P.Harry.Rutger.
TITLE Methods for assessing cardiovascular status and compositions for use thereof
JOURNAL Patent: US 6197505-A 111 06-MAR-2001;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1738 CCCACTCTCTCCCTATC 1754
Db 2 CCAACCTCTCTCCCTC 18
RESULT 159
AR149199/c
LOCUS AR149199 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 46 from patent US 6228581.
ACCESSION AR149199
VERSION AR149199.1 GI:15113790
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Acton,S.L. and Ordovas,J.M.
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 6228581-A 46 08-MAY-2001;
FEATURES
source Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1682 GTGTCCTCTCCAGCGTG 1698
Db 17 GTCTCTCTCCGCGCTG 1

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RESULT 160
ARI60845/c
LOCUS      ARI60845      18 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION Sequence 49 from patent US 6255111.
ACCESSION  ARI60845
VERSION     ARI60845.1  GI:16225674
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Bennett, C. Frank, and Cowse, L. M.
TITLE       Antisense modulation of Her-4 expression
JOURNAL     Patent: US 6255111-A 49 03-JUL-2001;
FEATURES    Location/Qualifiers
             1..18
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1723 AGATGGAGATTGGCTCC 1739
Db 18 AGTTGAGATGGCTCC 2

RESULT 161
BD231347
LOCUS      BD231347      18 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Genes for assessing cardiovascular status and compositions for use
ACCESSION  BD231347
VERSION     BD231347.1  GI:33041117
KEYWORDS    JP 2002527079-A/111.
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 18)
AUTHORS     Norberg, L. T., Andersson, M. K., Lindstrom, P. H. R. and Jonsson, L.
TITLE       Genes for assessing cardiovascular status and compositions for use
JOURNAL     Patent: JP 2002527079-A 111 27-AUG-2002;
COMMENT     PAIROSEAKENSINGU AB
OS          Artificial Sequence
PN          JP 2002527079-A/111
PD          27-AUG-2002
PF          13-OCT-1999 JP 2000576056
PR          14-OCT-1998 US 60/104286, 14-OCT-1998 US 60/104302 PI
LEIF TORBJORN NORBERG, MARIA KRISTINA ANDERSSON, PER HARRY PI
RUTGER LINDSTROM,
PI          LENA JONSSON
PC          C1201/68, C12N15/09 // G01N33/53, G01N33/566, C12N15/00 CC Genes
for assessing cardiovascular status
and compositions for
CC          use thereof
FH          Key Location/Qualifiers
FT          1..18
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCCTCCCTATC 1754
Db 2 CCAACTCCTCCCTCTC 18

RESULT 162
E10022
LOCUS      E10022      18 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Antisense phosphorothioate DNA complementary to 2-7th codons of
human amidophosphoribosyltransferase cDNA.
ACCESSION  E10022
VERSION     E10022.1    GI:22026644
KEYWORDS    JP 1995255487-A/1.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 18)
AUTHORS     Itakura, M.
TITLE       DNA AND ITS DERIVATIVE
JOURNAL     Patent: JP 1995255487-A 1 09-OCT-1995;
COMMENT     OTSUKA PHARMACEUTICAL FACTORY INC
OS          None
OC          Artificial sequences.
PN          JP 1995255487-A/1
PD          09-OCT-1995
PF          28-MAR-1994 JP 1994056879
PI          ITAKURA MITSUO
PC          C12N15/09, A61K35/12, C07H21/04 // A61K31/70, A61K48/00, C12N9/10;
CC          strandedness: Single;
CC          topology: Linear;
CC          hypothetical: No;
CC          anti-sense: Yes;
FH          Key Location/Qualifiers
FT          1..18
             /organism="Artificial sequences" FT
             misc_feature 1..18
             /note="phosphorothioate DNA"
             FT
             misc_feature 1..18
             /note="complementary to 2-7th codons of human
             amidophosphoribosyltransferase cDNA".

FEATURES    source
             1..18
             /organism="unidentified"
             /mol_type="genomic DNA"
             /db_xref="taxon:32644"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCCTCCCTATC 1754
Db 2 CCCAACTCCTCCAGCTC 18

RESULT 163
I14568/c
LOCUS      I14568      18 bp      DNA      linear      PAT 26-SEP-1995
DEFINITION Sequence 45 from patent US 5451512.
ACCESSION  I14568
VERSION     I14568.1    GI:997051
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Apple, R. J., Bugawan, T. L. and Erlich, H. A.
TITLE       Methods and reagents for HLA class I A locus DNA typing
JOURNAL     Patent: US 5451512-A 45 19-SEP-1995;
FEATURES    Location/Qualifiers
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             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCCTCCCTATC 1754
Db 2 CCAACTCCTCCCTCTC 18
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Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1732 TTGGCTCCCAACTCTC 1748
Db 17 TAGGCTCTCAACTGCTC 1

RESULT 164
188615
LOCUS 188615 18 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 13 from patent US 5719021.
ACCESSION I88615
VERSION I88615.1 GI:3408555
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Inouye,M.
TITLE Protein activation
JOURNAL Patent: US 5719021-A 13 17-FEB-1998;
FEATURES
source
Location/Qualifiers
1..18
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1636 GGGCTTGTAGCAGAGG 1652
Db 2 GGGTTGTTTCAGAGG 18

RESULT 165
AR350406/c
LOCUS AR350406 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 20 from patent US 6586411.
ACCESSION AR350406
VERSION AR350406.1 GI:33751525
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Russell,S.J. and Morris,J.
TITLE System for monitoring the location of transgenes
JOURNAL Patent: US 6586411-A 20 01-JUL-2003;
FEATURES
source
Location/Qualifiers
1..18
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1717 GTACGAGATCGAGATT 1733
Db 17 GTAGGCAGATGAAGATT 1

RESULT 166
AR409159/c
LOCUS AR409159 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6632800.
ACCESSION AR409159
VERSION AR409159.1 GI:40159778
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Stamm,S., Wirth,B., Hofmann,Y., Androphy,E. and Lorson,C.
TITLE Substances for the treatment of spinal muscular atrophy
JOURNAL Patent: WO 0166129-A 10 13-SEP-2001;
FEATURES
source
Location/Qualifiers
1..18
/mol_type="synthetic construct"
/mol_type="unassigned DNA"

Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Russell,S.J. and Peng,K.W.
TITLE System for monitoring the expression of transgenes
JOURNAL Patent: US 6632800-A 16 14-OCT-2003;
FEATURES
source
Location/Qualifiers
1..18
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1717 GTACGAGATCGAGATT 1733
Db 17 GTAGGCAGATGAAGATT 1

RESULT 167
AX037486
LOCUS AX037486 18 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 111 from Patent WO0056922.
ACCESSION AX037486
VERSION AX037486.1 GI:11226913
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Norberg,L.T., Olaiasson,E., Jonsson,L., Lindstrom,P.H. and
Sanders,R.
TITLE Genetic polymorphism and polymorphic pattern for assessing disease
status, and compositions for use thereof
JOURNAL Patent: WO 0056922-A 111 28-SEP-2000;
NORBERG LEIF TOREJORN (SE) ; OLAISSON ERIK (SE) ; JONSSON LENA (SE)
; GEMINI GENOMICS AB (SE) ; LINDSTROM PER HARRY RUTGER (SE) ;
SANDERS RHANNON (SE)
FEATURES
source
Location/Qualifiers
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/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCTCCCTATC 1754
Db 2 CCAACCTCTCCCTCTC 18

RESULT 168
AX244626/c
LOCUS AX244626 18 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 10 from Patent WO0166129.
ACCESSION AX244626
VERSION AX244626.1 GI:15859527
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Stamm,S., Wirth,B., Hofmann,Y., Androphy,E. and Lorson,C.
TITLE Substances for the treatment of spinal muscular atrophy
JOURNAL Patent: WO 0166129-A 10 13-SEP-2001;
FEATURES
source
Location/Qualifiers
1..18
/mol_type="synthetic construct"
/mol_type="unassigned DNA"

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Query Match	8.8%;	Score 12.2;	DB 1;	Length 18;		
Best Local Similarity	82.4%;	Pred. No. 2e+02;				
Matches	14;	Conservative	0; Mismatches	3; Indels	0; Gaps	0;
QY	1731	ATTGGCTCCCAACTCCT	1747			
DB	18	ATGGCTCCCATCTCCT	2			
LOCUS	AX795173	18 bp	DNA	linear	PAT 04-OCT-2003	
DEFINITION	Sequence 3 from Patent EP1323825.					
ACCESSION	AX795173					
VERSION	AX795173.1	GI:37515934				
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	artificial sequences.					
REFERENCE	1					
AUTHORS	Giuliano,G., Rosati,C., Dharmapuri,S., Pallara,P. and Camara,B.					
TITLE	Recombinant plants and dna constructs					
JOURNAL	Patent: EP 1323825-A 3 02-JUL-2003;					
	ENEA ENTE PER LE NUOVE TECNOLOGIE, L'ENERGIA E L'AMBIENTE (IT) ;					
	Biogen S.r.l. (IT)					
FEATURES	Location/Qualifiers					
source	1. .18					
	/organism="synthetic construct"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:32630"					
	/note="Upstream primer used to detect the expression of					
	the gene Capsicu m annum B-Chy by RT-PCR"					
primer_bind	1. .18					
	/note="Ca-Chy Upstream Primer"					
Query Match	8.8%;	Score 12.2;	DB 1;	Length 18;		
Best Local Similarity	82.4%;	Pred. No. 2e+02;				
Matches	14;	Conservative	0; Mismatches	3; Indels	0; Gaps	0;
QY	1644	AGCAGAGGCGACGACC	1660			
DB	17	AGCACAAAGCAGCAGC	1			
LOCUS	BD075238	18 bp	DNA	linear	PAT 27-AUG-2002	
DEFINITION	Methods for assessing cardiovascular status and compositions for					
	use thereof.					
ACCESSION	BD075238					
VERSION	BD075238.1	GI:22620841				
KEYWORDS	JP 2001519660-A/111.					
SOURCE	synthetic construct					
ORGANISM	synthetic construct					
	artificial sequences.					
REFERENCE	1 (bases 1 to 18)					
AUTHORS	Norberg,J.T., Andersson,M.K. and Lindstrom,P.H.R.					
TITLE	Methods for assessing cardiovascular status and compositions for					
	use thereof					
JOURNAL	Patent: JP 2001519660-A 111 23-OCT-2001;					
	EURONA MEDICAL AB					
COMMENT	OS Artificial Sequence					
	PN JP 2001519660-A/111					
PD	23-OCT-2001					
FF	01-APR-1998	JP 1998542530				
PI	04-APR-1997	US 60/042930				
PR	LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON, PER HARRY PI					
	RUTGER LINDSTROM					
PC	CI201/68,C07K14/72,C07K14/575,C12N9/48					
CC	Description of Artificial Sequence: PCR PRIMER FH Key					

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Guida,M. and Hall,J.
TITLE Genetic typing of the human cytochrome P450 2A6 gene and related materials and methods
JOURNAL Patent: US 6492115-A 5 10-DEC-2002;
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1..16
/location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
Query Match 8.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1634 TGGGGCTGTAG 1645
Db 1 TGGGGCTGTAG 12
BD254997 17 bp DNA linear PAT 17-JUL-2003
LOCUS Regulation of repressor genes using nucleic acid molecules.
DEFINITION BD254997
ACCESSION BD254997
VERSION BD254997.1 GI:33064767
KEYWORDS JP 2002541795-A/2790.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and McSwiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2790 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
EN JP 2002541795-A/2790
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
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FT /organism='Eukaryote'.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 8.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1651 GGCAAGCACCAG 1662
Db 12 GGCAAGCACCAG 1
BD254997 17 bp DNA linear PAT 22-NOV-2002
LOCUS Regulation of repressor genes using nucleic acid molecules.
DEFINITION BD254997
ACCESSION BD254997
VERSION BD254997.1 GI:33064767
KEYWORDS JP 2002541795-A/2790.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and McSwiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2790 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
EN JP 2002541795-A/2790
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
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FT /organism='Eukaryote'.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 8.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1651 GGCAAGCACCAG 1662
Db 12 GGCAAGCACCAG 1
BD254997 17 bp DNA linear PAT 22-NOV-2002
LOCUS Regulation of repressor genes using nucleic acid molecules.
DEFINITION BD254997
ACCESSION BD254997
VERSION BD254997.1 GI:33064767
KEYWORDS JP 2002541795-A/2790.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and McSwiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2790 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
EN JP 2002541795-A/2790
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
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/organism="unidentified"
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AX531436
VERSION AX531436.1 GI:25254650
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 945 11-SEP-2002;
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1645 GCAGAAGGCAAG 1656
Db 6 GCAGAAGGCAAG 17
AX531437 17 bp DNA linear PAT 22-NOV-2002
LOCUS Sequence 946 from Patent EP1239051.
DEFINITION AX531437
ACCESSION AX531437
VERSION AX531437.1 GI:25254652
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 946 11-SEP-2002;
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/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1645 GCAGAAGGCAAG 1656
Db 5 GCAGAAGGCAAG 16
AX531438 17 bp DNA linear PAT 22-NOV-2002
LOCUS Sequence 947 from Patent EP1239051.
DEFINITION AX531438
ACCESSION AX531438
VERSION AX531438.1 GI:25254654
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 947 11-SEP-2002;

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Query Match
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  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1645 GCAGAGGCAAG 1656
Db 4 GCAGAGGCAAG 15

RESULT 177
AX531439
LOCUS
  AX531439 17 bp DNA linear PAT 22-NOV-2002
DEFINITION
  Sequence 948 from Patent EP1239051.
ACCESSION
  AX531439
VERSION
  AX531439.1 GI:25254656
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Shannon,M.
  TITLE
    Human posh-like protein 1
  JOURNAL
    Patent: EP 1239051-A 948 11-SEP-2002;
    Aecomica, Inc. (US)
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Query Match
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Qy 1645 GCAGAGGCAAG 1656
Db 1 GCAGAGGCAAG 12

RESULT 180
AX723858
LOCUS
  AX723858 17 bp DNA linear PAT 08-MAY-2003
DEFINITION
  Sequence 1545 from Patent WO03025176.
ACCESSION
  AX723858
VERSION
  AX723858.1 GI:30503201
KEYWORDS
  Mus musculus (house mouse)
SOURCE
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1
  AUTHORS
    Teleman,A., Anson,R. and Tuijnder,M.
  TITLE
    Sequences involved in phenomena of tumour suppression, tumour
    reversion, apoptosis and/or virus resistance and their use as
    medicines
  JOURNAL
    Patent: WO 03025176-A 1545 27-MAR-2003;
    Molecular Engines Laboratories (FR)
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:10090"

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Qy 1659 CCAGGCTCACAG 1670
Db 4 CCAGGCTCACAG 15

RESULT 181
AR169593
LOCUS
  AR169593 18 bp DNA linear PAT 17-DEC-2001
DEFINITION
  Sequence 9 from patent US 6291176.
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ACCESSION   AR169593
VERSION     AR169593.1  GI:17907465
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Harris,J.M. and You,Q.
TITLE       Identification of a DNA region potentially useful for the detection
            of mycobacterium kansasii
JOURNAL     Patent: US 6291176-A 9 18-SEP-2001;
FEATURES    Location/Qualifiers
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            1..18
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            /mol_type="unassigned DNA"

Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 CGGAGATGGAGAT 1732
Db 4 CGGAGATGGAGAT 15

RESULT 182
LOCUS       BD235157/c 18 bp DNA linear PAT 17-JUL-2003
DEFINITION  Oligonucleotide inhibitors of bcl-xL.
ACCESSION   BD235157
VERSION     BD235157.1  GI:33044927
KEYWORDS    JP 2002519048-A/9.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stein,C.A.
TITLE       Oligonucleotide inhibitors of bcl-xL.
JOURNAL     Patent: JP 2002519048-A 9 02-JUL-2002;
            THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT     OS Artificial Sequence
            PN JP 2002519048-A/9
            PD 02-JUL-2002
            PF 02-JUL-1999 JP 2000557839
            PR 02-JUL-1998 US 09/109614
            PI CY A STEIN
            PC C12N15/09,A61K9/127,A61K31/711,A61K31/712,A61K31/7125, PC
            A61K47/42.
            CC A61K47/48,A61K48/00,A61P35/00,C12N15/00
            CC ANTISENSE OLIGONUCLEOTIDE
            CC PHOSPHOROTHIATE LINKAGE
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Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 CGGAGATGGAGA 1731
Db 14 CGGAGATGGAGA 3

RESULT 184
LOCUS       BD235176/c 18 bp DNA linear PAT 17-JUL-2003
DEFINITION  Oligonucleotide inhibitors of bcl-xL.
ACCESSION   BD235176
VERSION     BD235176.1  GI:33044946
KEYWORDS    JP 2002519048-A/28.

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 18)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 28 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT     OS Artificial Sequence
           PN JP 2002519048-A/28
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC

C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
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FT misc binding (15)..(18).

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Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 CGGAGATGGAGA 1731
Db 14 CGGAGATGGAGA 3

RESULT 185
E33346
LOCUS      Identification of DNA region potentially efficacious in detecting
DEFINITION Mycobacterium kansaii.
ACCESSION  E33346
VERSION     E33346.1 GI:13026956
KEYWORDS   JP 199915589-A/9.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS    James,M.H. and Kimin,Y.
TITLE      Identification of DNA region potentially efficacious in detecting
JOURNAL    Patent: JP 199915589-A 9 15-JUN-1999;
           MYCOBACTERIUM KANSAL
COMMENT     OS Artificial Sequence
           PN JP 199915589-A/9
           PD 15-JUN-1999
           PF 22-SEP-1998 JP 1998267503
           PR 25-SEP-1997 US 08/937580
           PI JAMES M HARRIS,KIMIN YOU
           PC C12N15/09,C12Q1/04,C12Q1/68//(C12Q1/04,C12R1:32),C12N15/00 CC

FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.

SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 18)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    Patent: JP 2002519048-A 28 02-JUL-2002;
           THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT     OS Artificial Sequence
           PN JP 2002519048-A/28
           PD 02-JUL-2002
           PF 02-JUL-1999 JP 2000557839
           PR 02-JUL-1998 US 09/109614
           PI CY A STEIN
           PC

C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC PHOSPHOROTHIOATE LINKAGE
CC PHOSPHOROTHIOATE LINKAGE
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FEATURES             source
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Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 CGGAGATGGAGA 1731
Db 14 CGGAGATGGAGA 3

RESULT 185
E33346
LOCUS      Identification of DNA region potentially efficacious in detecting
DEFINITION Mycobacterium kansaii.
ACCESSION  E33346
VERSION     E33346.1 GI:13026956
KEYWORDS   JP 199915589-A/9.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS    James,M.H. and Kimin,Y.
TITLE      Identification of DNA region potentially efficacious in detecting
JOURNAL    Patent: JP 199915589-A 9 15-JUN-1999;
           MYCOBACTERIUM KANSAL
COMMENT     OS Artificial Sequence
           PN JP 199915589-A/9
           PD 15-JUN-1999
           PF 22-SEP-1998 JP 1998267503
           PR 25-SEP-1997 US 08/937580
           PI JAMES M HARRIS,KIMIN YOU
           PC C12N15/09,C12Q1/04,C12Q1/68//(C12Q1/04,C12R1:32),C12N15/00 CC

FH Key Location/Qualifiers
FT source 1..18
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Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 TAGGAGTACGGA 1723
Db 1 TAGGAGTACGGA 12

RESULT 187
A64217
LOCUS      Sequence 5 from Patent WO9727332.
DEFINITION A64217
ACCESSION  A64217
VERSION     A64217.1 GI:3717648
KEYWORDS   unidentifed
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE   1
AUTHORS    Stuyver,L., Louwagie,J. and Rossau,R.
TITLE      METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE
           TRANSCRIPTASE GENE
JOURNAL    Patent: WO 9727332-A 5 31-JUL-1997;
           INNOGENETICS NV (BE)
COMMENT     Other publication AU 144397 19970820.
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

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        /db_xref="taxon:32630"
        /note="Detection oligonucleotide for PITX2"

Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1712 TAGGAGTACGGA 1723
Db 1 TAGGAGTACGGA 12

RESULT 187
A64217
LOCUS      Sequence 5 from Patent WO9727332.
DEFINITION A64217
ACCESSION  A64217
VERSION     A64217.1 GI:3717648
KEYWORDS   unidentifed
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE   1
AUTHORS    Stuyver,L., Louwagie,J. and Rossau,R.
TITLE      METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE
           TRANSCRIPTASE GENE
JOURNAL    Patent: WO 9727332-A 5 31-JUL-1997;
           INNOGENETICS NV (BE)
COMMENT     Other publication AU 144397 19970820.
FEATURES    Location/Qualifiers
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Query Match      8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1717 GTACGAGATGGAGA 1731
Db 1 GTACAGAGATGGAAA 15

RESULT 188
AR011805/c
LOCUS AR011805 15 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 18 from patent US 5763172.
ACCESSION AR011805
VERSION AR011805.1 GI:3969795
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Magda,D., Sessler,J.L., Wright,M., Miller,R.A. and Dow,W.C.
TITLE Method of phosphate ester hydrolysis
JOURNAL Patent: US 5763172-A 18 09-JUN-1998;
FEATURES
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGCTG 1673
Db 15 CCCGGCTCACAGATG 1

RESULT 191
I36660/c
LOCUS I36660 15 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 4 from patent US 5607924.
ACCESSION I36660
VERSION I36660.1 GI:2066485
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Magda,D., Sessler,J.L., Iverson,B.L., Sansom,P.I. and Wright,M.
TITLE DNA photocleavage using texaphyrins
JOURNAL Patent: US 5607924-A 04-MAR-1997;
FEATURES
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGCTG 1673
Db 15 CCCGGCTCACAGATG 1

RESULT 192
I83457/c
LOCUS I83457 15 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 1 from patent US 5714328.
ACCESSION I83457
VERSION I83457.1 GI:3406987
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Magda,D. and Sessler,J.L.
TITLE RNA photocleavage using texaphyrins
JOURNAL Patent: US 5714328-A 1 03-FEB-1998;
FEATURES
source
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1717 GTACGAGATGGAGA 1731
Db 1 GTACAGAGATGGAAA 15

RESULT 190
I27821/c
LOCUS I27821 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 4 from patent US 5567687.
ACCESSION I27821
VERSION I27821.1 GI:1818597
KEYWORDS
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AUTHORS	Lieven,S., Joost,L. and Rudi,R.				
TITLE	Method for detection of drug-induced mutations in the reverse transcriptase gene				
JOURNAL	Patent: US 6331389-A 5 18-DEC-2001;				
FEATURES	Location/Qualifiers				
source	1..15				
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	/mol_type="genomic DNA"				
Query Match	8.5%; Score 11.8; DB 1; Length 15;				
Best Local Similarity	86.7%; Pred.No.1.8e+02;				
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
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QY	1717	GTACGGAGATGGAGA	1731		
Db	1	GTACACGATGGAAA	15		
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RESULT 196					
BD057672/c					
LOCUS	BD057672 15 bp DNA linear PAT 27-AUG-2002				
DEFINITION	Fusion proteins comprising bacteriophage coat protein and a single-chain T cell receptor.				
ACCESSION	BD057672				
VERSION	BD057672.1 GI:22603278				
KEYWORDS	JP 2001514503-A/48.				
SOURCE	Aspergillus tubingensis				
ORGANISM	Aspergillus tubingensis				
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;				
	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Weidanz,J.A., Card,K.F. and Wong,H.C.				
TITLE	Fusion proteins comprising bacteriophage coat protein and a single-chain T cell receptor				
JOURNAL	Patent: JP 2001514503-A 48 11-SEP-2001;				
COMMENT	SUNOL MOLECULAR CORP				
	PN JP 2001514503-A/48				
	PD 11-SEP-2001				
	PF 05-MAR-1998 JP 1998537984				
	PR 07-MAR-1997 US 08/813781				
	PI JON A WEIDANZ,KIMBERLIN F CARD,HING C WONG				
	PC Cl2Q1/68,Cl2N7/01,Cl2M15/70				
	CC Strandedness: Single;				
	CC Topology: Linear;				
FEH Key	Location/Qualifiers.				
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source	/organism="Aspergillus tubingensis"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:5068"				
Query Match	8.5%; Score 11.8; DB 1; Length 15;				
Best Local Similarity	86.7%; Pred.No.1.8e+02;				
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
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QY	1656	GCACCAGGCTCAG	1670		
Db	15	GAACCACTCACAG	1		
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RESULT 197					
BD081502/c					
LOCUS	BD081502 15 bp DNA linear PAT 27-AUG-2002				
DEFINITION	Soluble single-chain T-cell receptor proteins.				
ACCESSION	BD081502				
VERSION	BD081502.1 GI:22627105				
KEYWORDS	JP 2001519143-A/48.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Weidanz,J.A., Card,K.F. and Wong,H.C.				
TITLE	Soluble single-chain T-cell receptor proteins				
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QY	1659	CCAGGCTCACAGTG	1673		
Db	15	CCCGGCTCACAGT	1		
<hr/>					
RESULT 193					
I83461/c					
LOCUS	I83461 15 bp DNA linear PAT 10-AUG-1998				
DEFINITION	Sequence 5 from patent US 5714328.				
ACCESSION	I83461				
VERSION	I83461.1 GI:3406991				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Magda,D. and Sessler,J.L.				
TITLE	RNA photocleavage using texaphyrins				
JOURNAL	Patent: US 5714328-A 5 03-FEB-1998;				
FEATURES	Location/Qualifiers				
source	1..15				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	8.5%; Score 11.8; DB 1; Length 15;				
Best Local Similarity	86.7%; Pred.No.1.8e+02;				
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
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QY	1659	CCAGGCTCACAGTG	1673		
Db	15	CCCGGCTCACAGT	1		
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RESULT 194					
AR213614/c					
LOCUS	AR213614 15 bp DNA linear PAT 25-SEP-2002				
DEFINITION	Sequence 48 from patent US 6405989.				
ACCESSION	AR213614				
VERSION	AR213614.1 GI:23310893				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Davis,M.E., White,R.A., Saunders,C., Polin,R., Kristiansen,K., Ballone,M. and Grossman,G.				
TITLE	Rollable sports base				
JOURNAL	Patent: US 6405989-A 48 18-JUN-2002;				
FEATURES	Location/Qualifiers				
source	1..15				
	/organism="unknown"				
	/mol_type="genomic DNA"				
Query Match	8.5%; Score 11.8; DB 1; Length 15;				
Best Local Similarity	86.7%; Pred.No.1.8e+02;				
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
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QY	1656	GCACCAGGCTCACAG	1670		
Db	15	GAACCACTCACAG	1		
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RESULT 195					
AR262819					
LOCUS	AR262819 15 bp DNA linear PAT 29-JAN-2003				
DEFINITION	Sequence 5 from patent US 6331389.				
ACCESSION	AR262819				
VERSION	AR262819.1 GI:28074522				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 15)				
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AUTHORS	Lieven,S., Joost,L. and Rudi,R.
TITLE	Method for detection of drug-induced mutations in the reverse transcriptase gene
JOURNAL	Patent: US 6331389-A 5 18-DEC-2001;
FEATURES	Location/Qualifiers
source	1..15
Query Match	8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity	86.7%; Pred. No. 1.8e+02;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1717 GTACGGAGATGGAGA 1731
Db	1 GTACACAGATGGAAA 15
RESULT 196	
BD057672/c	
LOCUS	BD057672
DEFINITION	Fusion proteins comprising bacteriophage coat protein and a single-chain T cell receptor.
ACCESSION	BD057672.1 GI:22603278
VERSION	JP 2001514503-A/48.
KEYWORDS	Aspergillus tubingensis
SOURCE	Aspergillus tubingensis
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE	1 (bases 1 to 15)
AUTHORS	Weidanz,J.A., Card,K.F. and Wong,H.C.
TITLE	Fusion proteins comprising bacteriophage coat protein and a single-chain T cell receptor
JOURNAL	Patent: JP 2001514503-A 48 11-SEP-2001;
COMMENT	SUNOL MOLECULAR CORP
PD	JP 2001514503-A/48
PF	11-SEP-2001
PR	05-MAR-1998 JP 1998537984
PI	07-MAR-1997 US 08/813781
PC	JON A WEIDANZ,KIMBERLIN F CARD,HING C WONG
CC	C12Q1/68,C12N7/01,C12N15/70
CC	Strandedness: Single;
CC	Topology: Linear;
PH	Key Location/Qualifiers.
FEATURES	Location/Qualifiers
source	1..15
Query Match	8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity	86.7%; Pred. No. 1.8e+02;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1656 GCACCAGGCTCAG 1670
Db	15 GAACCACTCAG 1
RESULT 197	
BD081502/c	
LOCUS	BD081502
DEFINITION	Soluble single-chain T-cell receptor proteins.
ACCESSION	BD081502
VERSION	BD081502.1 GI:22627105
KEYWORDS	JP 2001519143-A/48.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1 (bases 1 to 15)
AUTHORS	Weidanz,J.A., Card,K.F. and Wong,H.C.
TITLE	Soluble single-chain T-cell receptor proteins

QY	1659 CCAGGCTCAGCTG 1673
Db	15 CCGGCTCAGATG 1
RESULT 193	
I83461/c	
LOCUS	I83461
DEFINITION	Sequence 5 from patent US 5714328.
ACCESSION	I83461
VERSION	I83461.1 GI:3406991
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	Magda,D. and Sessler,J.L.
TITLE	RNA photocleavage using texaphyrins
JOURNAL	Patent: US 5714328-A 5 03-FEB-1998;
FEATURES	Location/Qualifiers
source	1..15
Query Match	8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity	86.7%; Pred. No. 1.8e+02;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1659 CCAGGCTCAGCTG 1673
Db	15 CCGGCTCAGATG 1
RESULT 194	
AR213614/c	
LOCUS	AR213614
DEFINITION	Sequence 48 from patent US 6405989.
ACCESSION	AR213614
VERSION	AR213614.1 GI:23310893
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	Davis,M.E., White,R.A., Saunders,C., Polin,R., Kristiansen,K., Ballone,M. and Grossman,G.
TITLE	Rollable sports base
JOURNAL	Patent: US 6405989-A 48 18-JUN-2002;
FEATURES	Location/Qualifiers
source	1..15
Query Match	8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity	86.7%; Pred. No. 1.8e+02;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1656 GCACCAGGCTCAG 1670
Db	15 GAACCACTCAG 1
RESULT 195	
AR262819	
LOCUS	AR262819
DEFINITION	Sequence 5 from patent US 6331389.
ACCESSION	AR262819
VERSION	AR262819.1 GI:28074522
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
1 (bases 1 to 15)	

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JOURNAL Patent: JP 2001519143-A 48 23-OCT-2001;
SUNOL MOLECULAR CORP
OS Artificial Sequence
PN JP 2001519143-A/48
PD 23-OCT-2001
PF 28-SEP-1998 JP 2000514936
PR JON A WEIDANZ, KIMBERLYN F CARD, HING C WONG
PI 02-OCT-1997 US 08/943086
PC C12N15/09, A61K38/00, A61K39/395, A61P43/00, C07K14/725, C07K16/28,
PC C12P21/02//
PC C12P21/08, C12N15/00, A61K37/02
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..15
FT /organism='Artificial Sequence'.
FEATURES
source
1..15
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1656 GCACCGGCTCACAG 1670
Db 15 GAACGAGACTCACAG 1
RESULT 198
BD090530/c
LOCUS 15 bp DNA linear PAT 27-AUG-2002
DEFINITION Photocleavage of RNA using texaphylline.
ACCESSION BD090530
VERSION JP 2001316270-A/1.
KEYWORDS synthetic construct
SOURCE artificial sequences.
ORGANISM 1 (bases 1 to 15)
AUTHORS Magda, D. and Sessler, J.L.
TITLE Photocleavage of RNA using texaphylline
JOURNAL Patent: JP 2001316270-A 1 13-NOV-2001;
PHARMACYCLICS INC. BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM
COMMENT OS Artificial Sequence
PN JP 2001316270-A/1
PD 13-NOV-2001
PF 07-JUN-1995 US 08/484551
PR DARREN MAGDA, JONATHAN L SESSLER
PC A61K31/7125, A61K31/7135, A61K41/00, A61P35/00//C07H21/00 PC
PC C07H23/00, C12N15/09,
PC C12N15/00
CC Photocleavage of RNA using texaphylline
FH Key Location/Qualifiers
FT source 1..15
FT /organism='Artificial Sequence'.
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/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1659 CCAGGCTCACAGCTG 1673
Db 15 CCGGCTCACAGATG 1
RESULT 200
AR011801/c
LOCUS 16 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 14 from patent US 5763172.
ACCESSION AR011801
VERSION AR011801.1 GI:3969791
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Magda, D., Sessler, J.L., Wright, M., Miller, R.A. and Dow, W.C.
TITLE Method of phosphate ester hydrolysis
JOURNAL Patent: US 5763172-A 14 09-JUN-1998;
FEATURES
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1655 AGCACCAGGCTCACA 1669
Db 15 AACACCCGGCTCACA 1
RESULT 201
BD233058
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LOCUS      BD233058                      16 bp    DNA        linear        PAT 17-JUL-2003
DEFINITION Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION  BD233058
VERSION    BD233058.1 GI:33042828
KEYWORDS   JP 2002518065-A/154.
SOURCE     Aids-associated retrovirus
ORGANISM   Aids-associated retrovirus
REFERENCE  1 (bases 1 to 16)
AUTHORS    Stuyver,L.
TITLE      Method of detecting mutation selected by drug in HIV protease gene
JOURNAL    INNOGENETICS NV
COMMENT    OS Aids-associated retrovirus
           PN JP 2002518065-A/154
           PD 25-JUN-2002
           PF 22-JUN-1999 JP 2000556068
           PR 24-JUN-1998 EP 98870143.9
           PI LIEVEN STUYVER
           PC C12N15/09, C12Q1/68, C12Q1/70, C12N15/00
           CC Method of detecting mutation selected by drug in HIV protease
           FH Key gene Location/Qualifiers
           FT source 1..16
           FT Location/Qualifiers
           FT 1..16
           FT /organism='Aids-associated retrovirus'
           FT /mol_type='genomic DNA'
           FT /db_xref='taxon:11966'

Query Match      8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1721 GGAGTGGAGATTGG 1735
Db 2 GGAGTGGAGATTGG 16

RESULT 202
AX007612
LOCUS      AX007612                      16 bp    DNA        linear        PAT 06-SEP-2000
DEFINITION Sequence 154 from Patent WO9967428.
ACCESSION  AX007612
VERSION    AX007612.1 GI:9995309
KEYWORDS   Aids-associated retrovirus
SOURCE     Aids-associated retrovirus
ORGANISM   Aids-associated retrovirus
REFERENCE  1
AUTHORS    Stuyver,L.
TITLE      Method for detection of drug-selected mutations in the hiv protease
JOURNAL    INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES   source 1..16
           /organism='Aids-associated retrovirus'
           /mol_type='unassigned DNA'
           /db_xref='taxon:11966'

Query Match      8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1721 GGAGTGGAGATTGG 1735
Db 2 GGAGTGGAGATTGG 16

RESULT 203
BD234600
LOCUS      BD234600                      17 bp    DNA        linear        PAT 17-JUL-2003
DEFINITION Thymidine kinase mutants and fusion proteins having thymidine
ACCESSION  BD234600
VERSION    BD234600.1 GI:33044370
KEYWORDS   JP 2002516061-A/4.
SOURCE     unclassified
ORGANISM   unclassified
REFERENCE  1 (bases 1 to 17)
AUTHORS    Black,M.E.
TITLE      Thymidine kinase mutants and fusion proteins having thymidine
JOURNAL    Patent: JP 2002516061-A 4 04-JUN-2002;
           DARWIN MOLECULAR CORP
COMMENT    OS Unidentified
           PN JP 2002516061-A/4
           PD 04-JUN-2002
           PF 14-OCT-1998 JP 2000516019
           PR 14-OCT-1997 US 60/061812
           PI MARGARET E BLACK
           PC C12N15/09, A61K31/711, A61K35/76, A61K38/45, A61K48/00, A61K49/00,
           PC A61P31/00,
           PC A61P35/00, C12N5/10, C12N9/12, C12N15/00, A61K37/52, C12N5/00 CC
           CC Strandedness: Single;
           CC Topology: Linear;
           CC Thymidine kinase mutants and fusion proteins having thymidine
           CC kinase and
           CC Guanylate kinase activities
           FH Key Location/Qualifiers
           FT source 1..17
           FT Location/Qualifiers
           FT 1..17
           FT /organism='Unidentified'
           FT /mol_type='genomic DNA'
           FT /db_xref='taxon:32644'

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTGGT 1700
Db 1 CCCCTCCAGCGGT 15

RESULT 204
BD254104
LOCUS      BD254104                      17 bp    DNA        linear        PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD254104
VERSION    BD254104.1 GI:33063874
KEYWORDS   JP 2002541795-A/1897.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 17)
AUTHORS    Blatt,L., Zwick,M., Pavco,P. and Mcswigen,J.
TITLE      Regulation of repressor genes using nucleic acid molecules
JOURNAL    Patent: JP 2002541795-A 1897 10-DEC-2002;
           RIBOZYME PHARMACEUTICALS INC
COMMENT    OS Eukaryote
           PN JP 2002541795-A/1897
           PD 10-DEC-2002
           PF 11-APR-2000 JP 2000611654
           PR 12-APR-1999 US 60/129390
           PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGEN PC
           PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, C12N5/10, PC
           PC C12P21/02,
           PC
           PC C12P21/02, C12P21/02, //A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
           PC C12R1:91),

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PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17 /organism='Eukaryote'.
FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1681 GGTGCTCTCTCCAGC 1695
Db 2 GGGCTCTCTACAGC 16
RESULT 205
AR186388
LOCUS AR186388 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1876 from patent US 6346398.
ACCESSION AR186388
VERSION AR186388.1 GI:20232353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1876 12-FEB-2002;
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1745 CCTCCTATCCTATAA 1759
Db 3 CCTCCTATCCGAAA 17
RESULT 206
AR186389
LOCUS AR186389 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1877 from patent US 6346398.
ACCESSION AR186389
VERSION AR186389.1 GI:20232354
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1877 12-FEB-2002;
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17 /organism='Eukaryote'.
FT Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1681 GGTGCTCTCTCCAGC 1695
Db 2 GGGCTCTCTACAGC 16
RESULT 205
AR186388
LOCUS AR186388 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1876 from patent US 6346398.
ACCESSION AR186388
VERSION AR186388.1 GI:20232353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1876 12-FEB-2002;
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/mol_type="unassigned DNA"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1745 CCTCCTATCCTATAA 1759
Db 3 CCTCCTATCCGAAA 17
RESULT 206
AR186389
LOCUS AR186389 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1877 from patent US 6346398.
ACCESSION AR186389
VERSION AR186389.1 GI:20232354
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1877 12-FEB-2002;
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/mol_type="unassigned DNA"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1745 CCTCCTATCCTATAA 1759
Db 2 CCTCCTATCCGAAA 16
RESULT 207
AR230196
LOCUS AR230196 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 4 from patent US 6451571.
ACCESSION AR230196
VERSION AR230196.1 GI:27270251
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Loeb,L.A. and Black,M.E.
TITLE Thymidine kinase mutants
JOURNAL Patent: US 6451571-A 4 17-SEP-2002;
FEATURES
source
1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1686 CTCTCCAGCGTGCT 1700
Db 1 CCCCTCCAGCGCGT 15
RESULT 208
AR286032/c
LOCUS AR286032/c 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 404 from patent US 6528640.
ACCESSION AR286032
VERSION AR286032.1 GI:29723628
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 404 04-MAR-2003;
FEATURES
source
1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 3.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1660 CAGGCTCACAGCTGG 1674
Db 15 CGGGCGCACAGCTGG 1
RESULT 209
AR286132/c
LOCUS AR286132 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 504 from patent US 6528640.
ACCESSION AR286132
VERSION AR286132.1 GI:29723728
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.									
REFERENCE	1	(bases 1 to 17)							
AUTHORS	Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.								
TITLE	Synthetic ribonucleic acids with RNase activity								
JOURNAL	Patent: US 6528640-A 504 04-MAR-2003;								
FEATURES	Location/Qualifiers								
source	1..17								
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	/mol_type="unassigned RNA"								
Query Match	8.5%; Score 11.8; DB 1; Length 17;								
Best Local Similarity	86.7%; Pred. No. 2.2e+02;								
Matches	13;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1660	CAGGCTCACAGCTGG	1674						
Db	17	CAGTCACACAGCTGG	3						
RESULT 210									
AR286133/c									
LOCUS	AR286133			17 bp	RNA				
DEFINITION	Sequence 505 from patent US 6528640.								
ACCESSION	AR286133								
VERSION	AR286133.1	GI:29723729							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
	Unclassified.								
REFERENCE	1	(bases 1 to 17)							
AUTHORS	Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.								
TITLE	Synthetic ribonucleic acids with RNase activity								
JOURNAL	Patent: US 6528640-A 505 04-MAR-2003;								
FEATURES	Location/Qualifiers								
source	1..17								
	/organism="unknown"								
	/mol_type="unassigned RNA"								
Query Match	8.5%; Score 11.8; DB 1; Length 17;								
Best Local Similarity	86.7%; Pred. No. 2.2e+02;								
Matches	13;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1660	CAGGCTCACAGCTGG	1674						
Db	15	CAGTCACACAGCTGG	1						
RESULT 211									
AR286141/c									
LOCUS	AR286141			17 bp	RNA				
DEFINITION	Sequence 513 from patent US 6528640.								
ACCESSION	AR286141								
VERSION	AR286141.1	GI:29723737							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
	Unclassified.								
REFERENCE	1	(bases 1 to 17)							
AUTHORS	Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.								
TITLE	Synthetic ribonucleic acids with RNase activity								
JOURNAL	Patent: US 6528640-A 513 04-MAR-2003;								
FEATURES	Location/Qualifiers								
source	1..17								
	/organism="unknown"								
	/mol_type="unassigned RNA"								
Query Match	8.5%; Score 11.8; DB 1; Length 17;								
Best Local Similarity	86.7%; Pred. No. 2.2e+02;								
Matches	13;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 422 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1745 CCTCCCTATCCTAA 1759
Db 2 CCTCCTATCCGAA 16
RESULT 215
AR398022/c 17 bp RNA linear PAT 18-DEC-2003
LOCUS AR398022
DEFINITION Sequence 403 from patent US 6617438.
ACCESSION AR398022
VERSION AR398022.1 GI:40135497
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 403 09-SEP-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1660 CAGGCTCACAGCTGG 1674
Db 15 CGGGCGCACAGCTGG 1
RESULT 216
AR398122/c 17 bp RNA linear PAT 18-DEC-2003
LOCUS AR398122
DEFINITION Sequence 503 from patent US 6617438.
ACCESSION AR398122
VERSION AR398122.1 GI:40135673
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 503 09-SEP-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1660 CAGGCTCACAGCTGG 1674

Db 17 CAGTCACACAGCTG 3
RESULT 217
AR398123/c 17 bp RNA linear PAT 18-DEC-2003
LOCUS AR398123
DEFINITION Sequence 504 from patent US 6617438.
ACCESSION AR398123
VERSION AR398123.1 GI:40135675
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 504 09-SEP-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1660 CAGGCTCACAGCTGG 1674
Db 15 CAGTCACACAGCTGG 1
RESULT 218
AR398131/c 17 bp RNA linear PAT 18-DEC-2003
LOCUS AR398131
DEFINITION Sequence 512 from patent US 6617438.
ACCESSION AR398131
VERSION AR398131.1 GI:40135691
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 512 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 3.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 83.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1660 CAGGCTCACAGCTGG 1674
Db 17 CGGGCGCACAGCTGG 3
RESULT 219
AR398167 17 bp RNA linear PAT 18-DEC-2003
LOCUS AR398167
DEFINITION Sequence 548 from patent US 6617438.
ACCESSION AR398167
VERSION AR398167.1 GI:40135761
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)

AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
 Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
 TITLE Oligoribonucleotides with enzymatic activity
 JOURNAL Patent: US 6617438-A 548 09-SEP-2003;
 FEATURES Location/Qualifiers
 1. .17
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Query Match 8.5%; Score 11.8; DB 1; Length 17;
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QY 1677 CCTGTGTCCTCTC 1691
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 Db 2 CCTGTGTCCTCTC 16

RESULT 220
 AR401998
 LOCUS AR401998 17 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 338 from patent US 6623962.
 ACCESSION AR401998
 VERSION AR401998.1 GI:40149448
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
 TITLE Enzymatic nucleic acid treatment of diseases of conditions related
 to levels of epidermal growth factor receptors
 JOURNAL Patent: US 6623962-A 338 23-SEP-2003;
 FEATURES Location/Qualifiers
 1. .17
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Query Match 8.5%; Score 11.8; DB 1; Length 17;
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QY 1685 TCTCTCCAGCGTGG 1699
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 Db 3 TCTCTCCATCTCTG 17

RESULT 221
 AX039622
 LOCUS AX039622 17 bp DNA linear PAT 18-NOV-2000
 DEFINITION Sequence 11 from Patent WO0063441.
 ACCESSION AX039622
 VERSION AX039622.1 GI:11229651
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Herrnstadt,C. and Davis,R.E.
 TITLE Single nucleotide polymorphisms in mitochondrial genes that segreg
 ate with alzheimer's disease
 JOURNAL Patent: WO 0063441-A 11 26-OCT-2000;
 MITOKOR (US)

FEATURES Location/Qualifiers
 1. .17
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 /note="PCR primer"

Query Match 8.5%; Score 11.8; DB 1; Length 17;
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 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1652 GCAAGCACCAGGCTC 1666
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 Db 1 GCTATCACCAGGCTC 15

RESULT 222
 AX039652
 LOCUS AX039652 17 bp DNA linear PAT 18-NOV-2000
 DEFINITION Sequence 41 from Patent WO0063441.
 ACCESSION AX039652
 VERSION AX039652.1 GI:11229681
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Herrnstadt,C. and Davis,R.E.
 TITLE Single nucleotide polymorphisms in mitochondrial genes that segreg
 ate with alzheimer's disease
 JOURNAL Patent: WO 0063441-A 41 26-OCT-2000;
 MITOKOR (US)

FEATURES Location/Qualifiers
 1. .17
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 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1652 GCAAGCACCAGGCTC 1666
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 Db 1 GCTATCACCAGGCTC 15

RESULT 223
 AX263012
 LOCUS AX263012 17 bp DNA linear PAT 26-OCT-2001
 DEFINITION Sequence 403 from Patent WO0173002.
 ACCESSION AX263012
 VERSION AX263012.1 GI:16511811
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
 TITLE Targeted chromosomal genomic alterations with modified single
 stranded oligonucleotides
 JOURNAL Patent: WO 0173002-A 403 04-OCT-2001;
 UNIVERSITY OF DELAWARE (US)

FEATURES Location/Qualifiers
 1. .17
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QY 1695 CGTGGTGAAGTTGG 1709
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 Db 1 CGTGGATGAAGTTGG 15

RESULT 224
 AX263013/c
 LOCUS AX263013 17 bp DNA linear PAT 26-OCT-2001

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DEFINITION Sequence 404 from Patent WO0173002.
ACCESSION AX263013
VERSION AX263013.1 GI:16511812
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 404 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Best Local Similarity 86.7%; Pred. No. 2.2e+02;
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QY 1695 CGTGGTGAAGTTGG 1709
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Db 17 CGTGGATGAAGTTGG 3

RESULT 225
AX263016
LOCUS AX263016 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 407 from Patent WO0173002.
ACCESSION AX263016
VERSION AX263016.1 GI:16511815
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 407 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1695 CGTGGTGAAGTTGG 1709
||||| |||||||
Db 17 CGTGGATGAAGTTGG 3

RESULT 226
AX263017/c
LOCUS AX263017 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 408 from Patent WO0173002.
ACCESSION AX263017
VERSION AX263017.1 GI:16511816
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 408 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
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Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1695 CGTGGTGAAGTTGG 1709
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Db 2 CGTGGATGAAGTTGG 16

RESULT 227
AX266567
LOCUS AX266567 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3958 from Patent WO0173002.
ACCESSION AX266567
VERSION AX266567.1 GI:16515366
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 3958 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1695 CGTGGTGAAGTTGG 1709
||||| |||||||
Db 16 CGTGGATGAAGTTGG 2

RESULT 228
AX266568/c
LOCUS AX266568 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3959 from Patent WO0173002.
ACCESSION AX266568
VERSION AX266568.1 GI:16515367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 3959 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1661 AGGCTCACAGCTGGA 1675
      ||||| |||||
Db 16 AGGCTCCAGCTGGA 2

RESULT 229
AX422716/c
LOCUS AX422716 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1052 from Patent WO0188124.
ACCESSION AX422716
VERSION AX422716.1 GI:21526098
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 212 07-AUG-2002;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1675 AACCTCGTGTCTCC 1689
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Db 17 AACCTCGAGTCTCC 3

RESULT 230
AX498904
LOCUS AX498904 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 211 from Patent EP1229046.
ACCESSION AX498904
VERSION AX498904.1 GI:23381197
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 211 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
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Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGGCAAGCACC 1660
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Db 3 CGGAAGGCAAGCAGC 17

RESULT 231
AX498905
LOCUS AX498905 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 212 from Patent EP1229046.
ACCESSION AX498905
VERSION AX498905.1 GI:23381198
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 212 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
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Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGGCAAGCACC 1660
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Db 2 CGGAAGGCAAGCAGC 16

RESULT 232
AX498906
LOCUS AX498906 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 213 from Patent EP1229046.
ACCESSION AX498906
VERSION AX498906.1 GI:23381199
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 213 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
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Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGGCAAGCACC 1660
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Db 1 CGGAAGGCAAGCAGC 15

RESULT 233
AX499446
LOCUS AX499446 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 753 from Patent EP1229046.
ACCESSION AX499446
VERSION AX499446.1 GI:23381739
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 213 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
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source
1..17
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Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGGCAAGCACC 1660
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Db 1 CGGAAGGCAAGCAGC 15

RESULT 233
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LOCUS AX499446 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 753 from Patent EP1229046.
ACCESSION AX499446
VERSION AX499446.1 GI:23381739
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 213 07-AUG-2002;
Aeomica, Inc. (US)
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Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGGCAAGCACC 1660
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Db 3 CGGAAGGCAAGCAGC 17
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
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Patent: EP 1229046-A 753 07-AUG-2002;									
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Db 2 CTCACTGCTGGACCC 16									
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AX499447									
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DEFINITION									
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ACCESSION									
AX499447									
VERSION									
AX499447.1 GI:23381740									
KEYWORDS									
Homo sapiens (human)									
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
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Human testis expressed patched like protein									
Patent: EP 1229046-A 754 07-AUG-2002;									
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AX532098									
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AX532098									
VERSION									
AX532098.1 GI:25255958									
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Homo sapiens (human)									
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REFERENCE									
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Shannon, M.									
Human posh-like protein 1									
Patent: EP 1239051-A 1607 11-SEP-2002;									
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AX532251/c									
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ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
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Homo sapiens (human)									
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ACCESSION									
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VERSION									
AX532252.1 GI:25256289									
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ACCESSION									
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VERSION									
AX532252.1 GI:25256289									
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LOCUS AX672921 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 1366 from Patent WO0304526.
ACCESSION AX672921
VERSION AX672921.1 GI:29331269
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 0304526-A 1366 16-JAN-2003;
FEATURES Molecular Engines Laboratories (FR)
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QY 1735 GCTCCCAACTCTCTCC 1749
Db 1 GATCCCAACTGCTCC 15

RESULT 239
AX687558
LOCUS AX687558 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 290 from Patent EP1281758.
ACCESSION AX687558
VERSION AX687558.1 GI:29410254
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 290 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
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QY 1668 CAGCTGGAACCTCTGG 1682
Db 3 CAGCTGGACCCAGG 17

RESULT 240
AX687559
LOCUS AX687559 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 291 from Patent EP1281758.
ACCESSION AX687559
VERSION AX687559.1 GI:29410255
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 580 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
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REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 291 05-FEB-2003;
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Best Local Similarity 86.7%; Pred. No. 2.2e+02;
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QY 1668 CAGCTGGAACCTCTGG 1682
Db 2 CAGCTGGACCCAGG 16

RESULT 241
AX687560
LOCUS AX687560 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 292 from Patent EP1281758.
ACCESSION AX687560
VERSION AX687560.1 GI:29410256
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 292 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
source Location/Qualifiers
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Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCTCTGG 1682
Db 1 CAGCTGGACCCAGG 15

RESULT 242
AX687848/c
LOCUS AX687848 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 580 from Patent EP1281758.
ACCESSION AX687848
VERSION AX687848.1 GI:29410544
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 580 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
source Location/Qualifiers
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Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCCCTGG 1682
Db 17 CAGCTGGATGCTGG 3

RESULT 243
AX723249/c
LOCUS      AX723249/c      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 936 from Patent WO03025176.
ACCESSION  AX723249
VERSION     AX723249.1 GI:30423750
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 581 05-FEB-2003;
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Query Match      8.5%; Score 11.8; DB 1; Length 17;
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 16 CAGCTGGATGCTGG 2

RESULT 244
AX723249/c
LOCUS      AX723249/c      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 936 from Patent WO03025176.
ACCESSION  AX723249
VERSION     AX723249.1 GI:30423750
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 03025176-A 936 27-MAR-2003;
            Molecular Engines Laboratories (FR)
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Query Match      8.5%; Score 11.8; DB 1; Length 17;
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QY 1663 GCTCACAGCTGGAAC 1677
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RESULT 247

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QY 1724 GATGGAGATTGGCTC 1738
Db 15 GATGGACATTGGATC 1

RESULT 245
AX723448/c
LOCUS      AX723448/c      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 1135 from Patent WO03025176.
ACCESSION  AX723448
VERSION     AX723448.1 GI:30423949
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 03025176-A 1135 27-MAR-2003;
            Molecular Engines Laboratories (FR)
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Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1635 GGGGCTTGTCAGCAGA 1649
Db 17 GGGGTTGTATCAGA 3

RESULT 246
AX725456/c
LOCUS      AX725456/c      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 3143 from Patent WO03025176.
ACCESSION  AX725456
VERSION     AX725456.1 GI:30504799
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 03025176-A 3143 27-MAR-2003;
            Molecular Engines Laboratories (FR)
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/db_xref="taxon:10090"

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGGAAC 1677
Db 15 GCTCACAGTTGGATC 1

RESULT 247

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AX727005
LOCUS AX727005 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4692 from Patent WO03025176.
ACCESSION AX727005
VERSION AX727005.1 GI:30506348
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 4692 27-MAR-2003;
Molecular Engines Laboratories (FR)
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QY 1687 TCCTCCAGCGTGGTG 1701
Db 3 TCCTCCTGGTGCTG 17
RESULT 248
AX730367/c
LOCUS AX730367 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2001 from Patent WO03025175.
ACCESSION AX730367
VERSION AX730367.1 GI:30509710
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 2001 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Db 16 TAGGAGGAAGGAGAT 2
RESULT 249
AX732114/c
LOCUS AX732114 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3748 from Patent WO03025175.
ACCESSION AX732114
VERSION AX732114.1 GI:30511457
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 3748 27-MAR-2003;
Molecular Engines Laboratories (FR)
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QY 1702 GAAGTTGGGTTAGGA 1716
Db 17 GAAGATGTTAGGA 3
RESULT 250
AX734174
LOCUS AX734174 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5808 from Patent WO03025175.
ACCESSION AX734174
VERSION AX734174.1 GI:30513517
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 5808 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1735 GCTCCCAACTCTCC 1749
Db 1 GATCCCAACTCTCC 15
RESULT 251
AX734182
LOCUS AX734182 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5816 from Patent WO03025175.
ACCESSION AX734182
VERSION AX734182.1 GI:30513525
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
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Query Match	E.5%;	Score 11.8;	DB 1;	Length 17;
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Db 3 AATACGGTGTATGGAG 17				
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AX783895/c				
LOCUS	17 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Sequence 2226 from Patent WO03050284.			
ACCESSION	AX783895			
VERSION	AX783895.1	GI:32951744		
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 Guo,J.			
JOURNAL	Human prostate cancer candidate protein 1			
FEATURES	Patent: WO 03050284-A 2226 19-JUN-2003;			
source	Amersham Biosciences (SV) Corp. (US)			
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Matches 13;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY 1696 GTGGTGGAGTTGGG 1710				
Db 17 GAGCTGGAGTTGGG 3				
RESULT 255				
AX783896/c				
LOCUS	17 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Sequence 2227 from Patent WO03050284.			
ACCESSION	AX783896			
VERSION	AX783896.1	GI:32951745		
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 Guo,J.			
JOURNAL	Human prostate cancer candidate protein 1			
FEATURES	Patent: WO03050284-A 2227 19-JUN-2003;			
source	Amersham Biosciences (SV) Corp. (US)			
1..17	Location/Qualifiers			
Query Match	8.5%;	Score 11.8;	DB 1;	Length 17;
Best Local Similarity	86.7%;	Pred. No. 2.2e+02;		
Matches 13;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
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Db 16 GAGCTGGAGTTGGG 2				
RESULT 256				
AX783897/c				


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LOCUS AX783897 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2228 from Patent WO03050284.
ACCESSION AX783897
VERSION AX783897.1 GI:32951746
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2228 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
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Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1696 GTGTGGAGTTGGG 1710
Dn 15 GAGCTGGAGTTGGG 1
RESULT 257
BD067498 17 bp RNA linear PAT 27-AUG-2002
LOCUS BD067498
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067498
VERSION BD067498.1 GI:22613101
KEYWORDS JP 2001511003-A/338.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 338 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC.ASTON UNIV
COMMENT OS Unidentified
PN JP 2001511003-A/338
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476.04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: single;
CC Topology: linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
CC levels of epidermal growth factor receptors
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LOCUS AX783897 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2228 from Patent WO03050284.
ACCESSION AX783897
VERSION AX783897.1 GI:32951746
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2228 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
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Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1696 GTGTGGAGTTGGG 1710
Dn 15 GAGCTGGAGTTGGG 1
RESULT 257
BD067498 17 bp RNA linear PAT 27-AUG-2002
LOCUS BD067498
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067498
VERSION BD067498.1 GI:22613101
KEYWORDS JP 2001511003-A/338.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 338 07-AUG-2001;
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COMMENT OS Unidentified
PN JP 2001511003-A/338
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476.04-DEC-1997 US 08/985162 PI
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C12N9/00,C07K14/71
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CC Topology: linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
CC levels of epidermal growth factor receptors
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Query Match 8.5%; Score 11.8; DB 1; Length 17;
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QY 1685 TCTCCTCCAGCTGG 1699
Dn 15 GAGCTGGAGTTGGG 1

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Db 3 TCTCCTCCATCTCTGG 17
RESULT 258
BD197619 17 bp RNA linear PAT 17-JUL-2003
LOCUS BD197619
DEFINITION Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD197619
VERSION BD197619.1 GI:33007389
KEYWORDS JP 2002509721-A/645.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 645 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/645
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC participating in vasculogenic response
FH Key Location/Qualifiers
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Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1681 GGTGTCTCTCTCCAGC 1695
Dn 2 GGCATCTCTCTCCAGC 16
RESULT 259
BD198720 17 bp RNA linear PAT 17-JUL-2003
LOCUS BD198720
DEFINITION Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD198720
VERSION BD198720.1 GI:33008490
KEYWORDS JP 2002509721-A/1746.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
METHOD and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 1746 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)

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PN JP 2002509721-A/1746
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
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C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
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CC participating in vasculogenic response
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 17 GCAGTACAGAGATGG 3

RESULT 260
BD202828
LOCUS 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
ACCESSION BD202828
VERSION BD202828.1 GI:33012598
KEYWORDS JP 2002509721-A/5854.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 17)
Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
TITLE Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 5854 02-APR-2002; RIBOPYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/5854
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
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C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
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CC participating in vasculogenic response
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QY 1683 TGTCTCTCTCCAGCGT 1697
Db 1 TGCCTCTCTCCAGTGT 15

RESULT 261
AL7920
LOCUS 18 bp DNA linear PAT 20-APR-1994
DEFINITION oligonucleotide primer.
ACCESSION AL7920
VERSION AL7920.1 GI:513115
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
Meyer, U.A.
TITLE Detection of pocr metabolizers of drugs
JOURNAL Patent: EP 0463395-A 11 02-JAN-1992; F. HOFFMANN-LA ROCHE AG
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1665 TCACAGCTGGACCC 1679
Db 4 TCCAGCTGGATCC 18

RESULT 262
AB7622/c
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 19 from Patent WO9836089.
ACCESSION AB7622
VERSION AB7622.1 GI:6736262
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
Flohe, L. and Singh, M.
AUTHORS TEST KIT FOR TUBERCULOSIS DIAGNOSIS OR THE LIKE
TITLE Patent: WO 9836089-A 19 20-AUG-1998; FLOHE LEOPOLD (DE); SINGH MAHAVIR (DE)
JOURNAL
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QY 1688 CCTCCAGCTGGTGG 1702
Db 17 CCGCCAGCTGGTGG 3

RESULT 263
AR063222
LOCUS 18 bp DNA linear PAT 29-SEP-1999

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DEFINITION Sequence 1 from patent US 5844108.
ACCESSION AR063222
VERSION AR063222.1 GI:5990913
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Meyer,U.Albert.
TITLE Primers targeted to NAT2 gene for detection of poor metabolizers of
JOURNAL drugs
PATENT: US 5844108-A 1 01-DEC-1998;
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QY 1665 TCACAGCTGGAACCC 1679
Db 4 TCCACGCTGGAATCC 18
RESULT 264
AR095845
LOCUS AR095845 18 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 66 from patent US 6004814.
ACCESSION AR095845
VERSION AR095845.1 GI:10024100
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank. and Cowsert,L.M.
TITLE Antisense modulation of CD71 expression
JOURNAL Patent: US 6004814-A 66 21-DEC-1999;
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Best Local Similarity 86.7%; Pred. No. 2.4e+02;
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QY 1676 ACCCTGGTGCTCCT 1690
Db 3 AACCTGGTAICTCT 17
RESULT 265
BD274784
LOCUS BD274784 18 bp DNA linear PAT 17-JUL-2003
DEFINITION CANCER CELL VACCINE.
ACCESSION BD274784
VERSION BD274784.1 GI:33084552
KEYWORDS JP 2002531582-A/9.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kusu,M., Qiu,G. and Hunfreys,R.
TITLE CANCER CELL VACCINE
JOURNAL Patent: JP 2002531582-A 9 24-SEP-2002;
COMMENT ANTIGEN EXPRESS INC
OS Artificial Sequence
PN JP 2002531582-A/9
PD 24-SEP-2002
PF 24-NOV-1999 JP 2000586901

PR 04-DEC-1998 US 09/205995
PI minzhen kusu,gang qiu,robert hunfreys
CC Description of Artificial Sequence: antisense oligonucleotide
CC corresponding
CC to a specific region of the mouse li gene.
FH Key Location/Qualifiers.
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Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1656 GCACCAGGCTCACAG 1670
Db 3 GCACTGGCTCACAG 17
RESULT 266
I56123
LOCUS I56123 18 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5648482.
ACCESSION I56123
VERSION I56123.1 GI:2476917
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Meyer,U.Albert.
TITLE Primers targeted to CYP2D6 gene for detecting poor metabolizers of
JOURNAL drugs
PATENT: US 5648482-A 1 15-JUL-1997;
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Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1665 TCACAGCTGGAACCC 1679
Db 4 TCCACGCTGGAATCC 18
RESULT 267
AR205250
LOCUS AR205250 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 10 from patent US 6368855.
ACCESSION AR205250
VERSION AR205250.1 GI:21502786
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Xu,M., Qiu,G. and Humphreys,R.
TITLE MHC class II antigen presenting cells containing oligonucleotides
JOURNAL which inhibit Ii protein expression
PATENT: US 6368855-A 10 09-APR-2002;
FEATURES
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            /mol_type="unassigned DNA"
Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1665 TCACAGCTGGAACCC 1679
Db 4 TCCACGCTGGAATCC 18
RESULT 267
AR205250
LOCUS AR205250 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 10 from patent US 6368855.
ACCESSION AR205250
VERSION AR205250.1 GI:21502786
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Xu,M., Qiu,G. and Humphreys,R.
TITLE MHC class II antigen presenting cells containing oligonucleotides
JOURNAL which inhibit Ii protein expression
PATENT: US 6368855-A 10 09-APR-2002;
FEATURES
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        Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy 1656 GCACAGGCTACAG 1670
Db 3 GCATCTGGCTACAG 17

RESULT 268
LOCUS AR294317/c
DEFINITION Sequence 6052 from patent US 6537751.
ACCESSION AR294317
VERSION AR294317.1 GI:31681601
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
PATENT: US 6537751-A 6052 25-MAR-2003;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1721 GGAGTGGAGATTGG 1735
Db 18 GAAGTGGAGATTGG 4

RESULT 269
LOCUS AX022481
DEFINITION Sequence 8 from Patent WO9937763.
ACCESSION AX022481
VERSION AX022481.1 GI:10046078
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Flegel, W.A. and Wagner, F.F.
TITLE Novel nucleic acid molecules correlated with the rhesus weak d
JOURNAL phenotype
PATENT: WO 9937763-A 8 29-JUL-1999;
FLEGEL WILLY A (DE) ; WAGNER FRANZ F (DE) ; DRK BLUTSPENDEDIENST
BADEN WUE (DE)
FEATURES
Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1681 GGTGCTCTCCACG 1695
Db 2 GGTCCCTCTCCACG 16

RESULT 270
LOCUS AX103735
DEFINITION Sequence 52 from Patent WO0125458.
ACCESSION AX103735
VERSION AX103735.1 GI:13919945

Oy 1649 AAGGCAAGCACCAGG 1663
Db 17 ATGGGAAGCACCAGG 3

RESULT 272
LOCUS AX342470/c
DEFINITION Sequence 4 from Patent WO0198475.
ACCESSION AX342470
VERSION AX342470.1 GI:18151913
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Melms, A., Wienhold, W. and Tolosa, E.
TITLE Method for the detection of cathepsins, asparaginyl endopeptidases
and isozymes thereof and leukocystatin

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KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Olivier, J., Deslandes, L. and Marco, Y.
TITLE Novel class of proteins and uses thereof for plant resistance to
JOURNAL various pathogenic agents
PATENT: WO 0125458-A 52 12-APR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR) ;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1741 AACTCTCTCCATGCC 1755
Db 1 AACTCTCTCCATGCC 15

RESULT 271
LOCUS AX326967/c
DEFINITION Sequence 163 from Patent WO0178894.
ACCESSION AX326967
VERSION AX326967.1 GI:18097678
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Keith, T.
TITLE Novel human gene relating to respiratory diseases, obesity, and
JOURNAL inflammatory bowel disease
PATENT: WO 0178894-A 163 25-OCT-2001;
Genome Therapeutics Corp. (US)
FEATURES
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1649 AAGGCAAGCACCAGG 1663
Db 17 ATGGGAAGCACCAGG 3

RESULT 272
LOCUS AX342470/c
DEFINITION Sequence 4 from Patent WO0198475.
ACCESSION AX342470
VERSION AX342470.1 GI:18151913
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Melms, A., Wienhold, W. and Tolosa, E.
TITLE Method for the detection of cathepsins, asparaginyl endopeptidases
and isozymes thereof and leukocystatin

```

JOURNAL Patent: WO 0198475-A 4 27-DEC-2001;
Eberhard-Karls-Universitaet Tuebingen Universitaetsklinikum (DE)
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen Sequenz:
Nukleotidsequenz"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1733 TGGCTCCCAACTCT 1747
Db 17 TGGTGCCTCAACTCT 3

RESULT 273
AX352805
LOCUS AX352805 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 11 from Patent EP1174518.
ACCESSION AX352805
VERSION AX352805.1 GI:18617887
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Loukachov,V.V., van Gemen,B. and Goudsmit,J.
TITLE Collection of binding molecules
JOURNAL Patent: EP 1174518-A 11 23-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="position 41"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1717 GTACGGAGATGGAGA 1731
Db 1 GTACAGAGATGGAAA 15

RESULT 274
AX352808
LOCUS AX352808 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 14 from Patent EP1174518.
ACCESSION AX352808
VERSION AX352808.1 GI:18617890
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Loukachov,V.V., van Gemen,B. and Goudsmit,J.
TITLE Collection of binding molecules
JOURNAL Patent: EP 1174518-A 14 23-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="position 41"

Query Match 8.5%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1717 GTACGGAGATGGAGA 1731
Db 1 GTACAGAAATGGAGA 15

RESULT 275
AX362650
LOCUS AX362650 18 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 11 from Patent WO0208463.
ACCESSION AX362650
VERSION AX362650.1 GI:18694790
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Loukachov,V.V., Goudsmit,J. and van Gemen,B.
TITLE Collection of binding molecules
JOURNAL Patent: WO 0208463-A 11 31-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="position 41"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1717 GTACGGAGATGGAGA 1731
Db 1 GTACAGAGATGGAAA 15

RESULT 276
AX362653
LOCUS AX362653 18 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 14 from Patent WO0208463.
ACCESSION AX362653
VERSION AX362653.1 GI:18694793
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Loukachov,V.V., Goudsmit,J. and van Gemen,B.
TITLE Collection of binding molecules
JOURNAL Patent: WO 0208463-A 14 31-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="position 41"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1717 GTACGGAGATGGAGA 1731
Db 1 GTACAGAAATGGAGA 15

RESULT 277
BD006224/c
LOCUS BD006224 18 bp DNA linear PAT 31-JAN-2002

FEATURES	source	Location/Qualifiers
Query Match		8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity		86.7%; Pred. No. 2.4e+02;
Matches 13;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
QY	1689	CTCCAGCGTGGTGGG 1703
DB	2	CTCCAGCGTCATGGA 16
RESULT 279		
BD103926/c		18 bp DNA linear PAT 27-AUG-2002
LOCUS		
DEFINITION		Kit and method for determining HLA type.
ACCESSION		BD103926
VERSION		BD103926.1 GI:22649500
KEYWORDS		WO 0192572-A/30.
SOURCE		synthetic construct
ORGANISM		artificial sequences.
REFERENCE		1 (bases 1 to 18)
AUTHORS		Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE		Kit and method for determining HLA type
JOURNAL		Patent: WO 0192572-A 30 06-DEC-2001;
		NISSHINO INDUSTRIES INC.SYSTEM RESEARCH INC.HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA,MICHIO NISHIDA
COMMENT		OS Artificial Sequence
		PN WO 0192572-A/30
		PD 06-DEC-2001
		PF 01-JUN-2001 WO 2001JP004662
		PR 01-JUN-2000 JP 00P 164798
		PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI MATSUMURA, MATSUMURA,
		PI SHOGO MORIYA,MICHIO NISHIDA
		PC C1201/68,C12M1/00,C12N15/09,G01N33/53
		CC Description of Artificial Sequence:capture
		FH Key Location/Qualifiers
		FT source 1..18
		FT /organism='Artificial Sequence'.
FEATURES		
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		1..18
		/organism="synthetic construct"
		/mol_type="genomic DNA"
		/db_xref="taxon:32630"
Query Match		8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity		86.7%; Pred. No. 2.4e+02;
Matches 13;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
QY	1650	AGGCAGCACCGGC 1664
DB	18	AGGCAGCACCGAGAC 4
RESULT 280		
BD124069		18 bp DNA linear PAT 18-SEP-2002
LOCUS		
DEFINITION		Novel nucleic acid molecule correlating to Rhesus weak D phenotype
ACCESSION		BD124069
VERSION		BD124069.1 GI:33219014
KEYWORDS		JP 2002500884-A/8.
SOURCE		unidentified
ORGANISM		unclassified.
REFERENCE		1 (bases 1 to 18)
AUTHORS		Fregel,V.A. and Wagner,F.F.

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TITLE Novel nucleic acid molecule correlating to Rhesus weak D phenotype
JOURNAL Patent: JP 2002500884-A 8 15-JAN-2002;
COMMENT DRK BL0TSPENDEDIENST BADEN WUERTEMBERG GGBMH
PN Unidentified
PD JP 2002500884-A/8
PF 15-JAN-2002
PR 18-DEC-1998 JP 2000528671
PI 23-JAN-1998 EP 98101203.2
PI VILLY A FREGEL, FRANZ F WAGNER
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12P21/08, C12Q1/02, C12Q1/68, G01N33/566, C12N15/00, PC
C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'oligonucleotide'
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
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1..18
/organism="Unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTGTCCTCTCCAGC 1695
DB 2 GGTCTCTCTCCAGC 16

RESULT 281
AB067849
LOCUS AB067849 18 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-D1S243 at
lp36.
ACCESSION AB067849
VERSION AB067849.1 GI:15128653
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
and Soeda, E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 18)
AUTHORS Horii, A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES
source
1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

misc_feature 1..18
/note="reverse primer for human STS sts-D1S243 at lp36
sts-D1S243 obtained from clones B83K22, B47P3, B43E2,
B123D13, B290B2 and B82D16, B226P2, Human BAC library
RPC1-11"

Novel nucleic acid molecule correlating to Rhesus weak D phenotype
Patent: JP 2002500884-A 8 15-JAN-2002;
DRK BL0TSPENDEDIENST BADEN WUERTEMBERG GGBMH
Unidentified
JP 2002500884-A/8
15-JAN-2002
18-DEC-1998 JP 2000528671
23-JAN-1998 EP 98101203.2
VILLY A FREGEL, FRANZ F WAGNER
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12P21/08, C12Q1/02, C12Q1/68, G01N33/566, C12N15/00, PC
C12N5/00
Strandedness: Single;
Topology: Linear;
/desc = 'oligonucleotide'
Key Location/Qualifiers
source 1..18
Location/Qualifiers
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source
1..18
/organism="Unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTGTCCTCTCCAGC 1695
DB 2 GGTCTCTCTCCAGC 16

RESULT 281
AB067849
LOCUS AB067849 18 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-D1S243 at
lp36.
ACCESSION AB067849
VERSION AB067849.1 GI:15128653
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
and Soeda, E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 18)
AUTHORS Horii, A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES
source
1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

misc_feature 1..18
/note="reverse primer for human STS sts-D1S243 at lp36
sts-D1S243 obtained from clones B83K22, B47P3, B43E2,
B123D13, B290B2 and B82D16, B226P2, Human BAC library
RPC1-11"

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Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1689 CTCGAGCGTGGTGA 1703
DB 2 CTCGAGCGTGGTGA 16

RESULT 282
AX250715/c
LOCUS AX250715 20 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 7 from Patent WO0168670.
ACCESSION AX250715
VERSION AX250715.1 GI:15984453
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lazdunski, M., Lesage, F. and Maingret, F.
TITLE Novel family of mechanically sensitive human potassium channels
activated by polyunsaturated fatty acids and use thereof
JOURNAL Patent: WO 0168670-A 7 20-SEP-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
source 1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1..20
/note="Oligonucleotide utilise pour l'analyse des blots,
marque au P32"

Query Match 8.5%; Score 11.8; DB 1; Length 20;
Best Local Similarity 86.7%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCTCG 1682
DB 15 CAGCTGCGAGCCTGG 1

RESULT 283
AX007253
LOCUS AX007253 15 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 15 from Patent WO0000593.
ACCESSION AX007253
VERSION AX007253.1 GI:9995109
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Zaehringer, U., Heinz, E., Schmidt, H. and Sperling, P.
TITLE Sphingolipid-desaturase
JOURNAL Patent: WO 0000593-A 15 06-JAN-2000;
ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); SCHMIDT HERMANN (DE);
SPERLING PETRA (DE); GVS GES FUER ERWERB UND VERWER (DE)
FEATURES
source 1..15
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="degenerierter forward Primer aus Hlianthus annuus"

Query Match 8.3%; Score 11.6; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1694 GCGTGGTGAAGTTG 1708

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1: |||||:|:|
1 GSNTGCTGGARTGG 15

RESULT 284
LOCUS AR175362/c 13 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 85 from patent US 6309823.
ACCESSION AR175362
VERSION AR175362.1 GI:17916661
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Cronin,M.T., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A.,
Huang,X.C., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and
Sheldon,E.L.
TITLE Arrays of nucleic acid probes for analyzing biotransformation genes
and methods of using the same
JOURNAL Patent: US 6309823-A 85 30-OCT-2001;
FEATURES
source
1. .13
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1649 AAGGCAAGCACCA 1661
Db 13 AGGGCAAGCACCA 1

RESULT 285
LOCUS AR285094/c 13 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 17 from patent US 6528268.
ACCESSION AR285094
VERSION AR285094.1 GI:29722011
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Andersson,M.K., Berglund,L.G.T., Reneland,R.H. and Adam,G.I.R.
TITLE Reagents and methods for detection of heart failure
JOURNAL Patent: US 6528268-A 17 04-MAR-2003;
FEATURES
source
1. .13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGG 1674
Db 13 GGCTCAGCTGG 1

RESULT 286
LOCUS AR285104 13 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 27 from patent US 6528268.
ACCESSION AR285104
VERSION AR285104.1 GI:29722021
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 13)
AUTHORS Andersson,M.K., Berglund,L.G.T., Reneland,R.H. and Adam,G.I.R.
TITLE Reagents and methods for detection of heart failure
JOURNAL Patent: US 6528268-A 17 04-MAR-2003;
FEATURES
source
1. .13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGG 1674
Db 13 GGCTCAGCTGG 1

RESULT 287
LOCUS A64221 14 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 9 from Patent WO9727332.
ACCESSION A64221
VERSION A64221.1 GI:3717652
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Stuyver,L., Louwagie,J. and Rossau,R.
TITLE METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE
TRANSCRIPTASE GENE
JOURNAL Patent: WO 9727332-A 9 31-JUL-1997;
COMMENT INNOGENETICS NV (BE)
Other publication AU 144397 19970820.
FEATURES
source
1. .14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 8.2%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1717 GTACGAGATGGA 1729
Db 1 GTACGAGATGGA 13

RESULT 288
LOCUS AR102520 14 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6087093.
ACCESSION AR102520
VERSION AR102520.1 GI:12814108
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Lieven,S., Joost,L. and Rudi,R.
TITLE Method for detection of drug-induced mutations in the reverse
transcriptase gene
JOURNAL Patent: US 6087093-A 9 11-JUL-2000;
FEATURES
source
1. .14
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.2%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGG 1674
Db 13 GGCTCAGCTGG 1

RESULT 289
LOCUS AR102520 14 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6087093.
ACCESSION AR102520
VERSION AR102520.1 GI:12814108
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Lieven,S., Joost,L. and Rudi,R.
TITLE Method for detection of drug-induced mutations in the reverse
transcriptase gene
JOURNAL Patent: US 6087093-A 9 11-JUL-2000;
FEATURES
source
1. .14
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.2%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGG 1674
Db 13 GGCTCAGCTGG 1
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Qy 1717 GTACGGAGATGGA 1729
 Db 1 GTACAGATGGA 13

RESULT 289
 LOCUS AR262823 14 bp DNA linear PAT 29-JAN-2003
 DEFINITION Sequence 9 from patent US 6331389.
 ACCESSION AR262823
 VERSION AR262823.1 GI:28074526
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Lieven, S., Joost, L. and Rudi, R.
 TITLE Method for detection of drug-induced mutations in the reverse transcriptase gene
 JOURNAL Patent: US 6331389-A 9 18-DEC-2001;
 FEATURES Location/Qualifiers
 source 1..14
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 1.9e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1717 GTACGGAGATGGA 1729
 Db 1 GTACAGATGGA 13

RESULT 290
 LOCUS AX802880/c 14 bp DNA linear PAT 24-NOV-2003
 DEFINITION Sequence 11 from Patent WO03057909.
 ACCESSION AX802880
 VERSION AX802880.1 GI:38501577
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Berlin, K.
 TITLE Method for detecting cytosine-methylation patterns by exponential ligation of hybridised probe oligo-nucleotides (mla)
 JOURNAL Patent: WO 03057909-A 11 17-JUL-2003;
 FEATURES Epigenomics AG (DE)
 source Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

Query Match 8.2%; Score 11.4; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 1.9e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1634 TGGGGCTTGAGC 1646
 Db 14 TGGGGCTTGACG 2

RESULT 291
 LOCUS BD061635/c 14 bp DNA linear PAT 27-AUG-2002
 DEFINITION Human Lafora type epilepsy causal gene full-length sequence and use of mutation thereof.
 ACCESSION BD061635

VERSION BD061635.1 GI:22607240
 KEYWORDS JP 2001299350-A/26.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Yamakawa, K. and Excweta, A.D.
 TITLE Human Lafora type epilepsy causal gene full-length sequence and use of mutation thereof
 JOURNAL Patent: JP 2001299350-A 26 30-OCT-2001;
 COMMENT THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
 OS Homo sapiens (human)
 PN JP 2001299350-A/26
 PD 30-OCT-2001
 PF 19-APR-2000 JP 2000118361
 PI KAZUHIRO YAMAKAWA, ANTONIO DELGARD EXCWETA
 PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, C12N15/00 CC
 FH Key Location/Qualifiers

FEATURES
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 1.9e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1746 CTCCTATCTTAA 1758
 Db 14 CTCCTATCTTAA 2

RESULT 292
 LOCUS AR000458/c 15 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 17 from patent US 5736365.
 ACCESSION AR000458
 VERSION AR000458.1 GI:3962989
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Walker, G. Terrance., Nadeau, J. G., Spears, P. Anne., Nycz, C. M., Shank, D. Dee., Schram, J. L. and Jurgensen, S. Russel.
 TITLE Multiplex nucleic acid amplification
 JOURNAL Patent: US 5736365-A 17 07-APR-1998;
 FEATURES Location/Qualifiers
 source 1..15
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 2.2e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCACAG 1670
 Db 14 ACCAGGCTCACAG 2

RESULT 293
 LOCUS AR008358 15 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 16 from patent US 5753481.
 ACCESSION AR008358
 VERSION AR008358.1 GI:3967467
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 15)
AUTHORS Niwa,M., Saito,Y., Ishii,Y., Yoshida,M. and Suzuki,H.
TITLE L-sorbose dehydrogenase and novel L-sorbose dehydrogenase
JOURNAL obtained from gluconobacter oxydans T-100
FEATURES Patent: US 5753481-A 16 19-MAY-1998;
          Location/Qualifiers
          source
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              /mol_type="unassigned DNA"
Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGC 1736
Db 2 GATGGAGATTGGC 14

RESULT 294
AR030667 LOCUS 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5861292.
ACCESSION AR030667
VERSION AR030667.1 GI:5943881
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Niwa,M., Saito,Y., Ishii,Y., Yoshida,M. and Suzuki,H.
TITLE L-sorbose dehydrogenase and novel L-sorbose dehydrogenase
JOURNAL obtained from Gluconobacter oxydans T-100
FEATURES Patent: US 5861292-A 16 19-JAN-1999;
          Location/Qualifiers
          source
            1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGC 1736
Db 2 GATGGAGATTGGC 14

RESULT 295
AR033686 LOCUS 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 452 from patent US 5869253.
ACCESSION AR033686
VERSION AR033686.1 GI:5949291
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 452 09-FEB-1999;
FEATURES Location/Qualifiers
          source
            1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGC 1736
Db 2 GATGGAGATTGGC 14

RESULT 296
AR033773 LOCUS 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5834263.
ACCESSION AR053773
VERSION AR053773.1 GI:5978635
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Niwa,M., Saito,Y., Ishii,Y., Yoshida,M. and Hayashi,H.
TITLE Method for producing 2-keto-L-gulonic acid
JOURNAL Patent: US 5834263-A 17 10-NOV-1998;
FEATURES Location/Qualifiers
          source
            1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGC 1736
Db 2 GATGGAGATTGGC 14

RESULT 297
AR113508 LOCUS 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 452 from patent US 6132966.
ACCESSION AR113508
VERSION AR113508.1 GI:14093830
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 452 17-OCT-2000;
FEATURES Location/Qualifiers
          source
            1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1686 CTCCTCCACGGTG 1698
Db 3 CTCCTCCACGGTG 15

RESULT 298
AR137837 LOCUS 15 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 16 from patent US 6197562.
ACCESSION AR137837
VERSION AR137837.1 GI:14479346
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Niwa,M., Saito,Y., Ishii,Y., Yoshida,M. and Suzuki,H.
TITLE L-sorbose dehydrogenase and novel L-sorbose dehydrogenase
          obtained from gluconobacter oxydans T-100
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JOURNAL Patent: US 6197562-A 16 06-MAR-2001;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1724 GATGAGATTGGC 1736
Db 2 GATGAGATTGGC 14
|||||

RESULT 299
LOCUS I15710/c 15 bp DNA linear PAT 02-APR-1996
DEFINITION Sequence 17 from patent US 5470723.
ACCESSION I15710
VERSION I15710.1 GI:1250618
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Walker,G.F., Nadeau,J.G., Spears,P.A., Nycz,C.M., Shank,D.D.,
Schram,J.L. and Jurgensen,S.R.
TITLE Detection of mycobacteria by multiplex nucleic acid amplification
JOURNAL Patent: US 5470723-A 17 28-NOV-1995;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCAG 1670
Db 14 ACCAGGCTCAG 2
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RESULT 300
LOCUS I26924/c 15 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 17 from patent US 5561044.
ACCESSION I26924
VERSION I26924.1 GI:1606794
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Walker,G.T., Nadeau,J.G., Spears,P.A., Nycz,C.M., Shank,D.D.,
Schram,J.L. and Jurgensen,S.R.
TITLE Detection of mycobacteria by multiplex strand displacement nucleic
acid amplification
JOURNAL Patent: US 5561044-A 17 01-OCT-1996;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCAG 1670
Db 14 ACCAGGCTCAG 2
|||||

RESULT 301
LOCUS I57915 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 452 from patent US 5610054.
ACCESSION I57915
VERSION I57915.1 GI:2482979
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL Patent: US 5610054-A 452 11-MAR-1997;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTG 1698
Db 3 CTCCTCCAGCGTG 15
|||||

RESULT 302
LOCUS BD207419 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD207419
VERSION BD207419.1 GI:33017189
KEYWORDS JP 2002512791-A/1009.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 1009 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/1009
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO.
PI DENNIS MACEJAX
PC C12N9/00,A61K31/7105,A61K38/21,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
hepatitis C virus infection.
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1. .15
/organism='Hepatitis virus (hepatitis C FT
virus)',
Location/Qualifiers
1. .15
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;

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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTG 1698
Db 3 CTCCTCCAGCGTG 15

RESULT 303
LOCUS AX26037
DEFINITION polynucleotide 16C17.
ACCESSION A26037
VERSION A26037.1 GI:904809
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 16)
AUTHORS
JOURNAL
FEATURES
    source
        Patent: FR 2680520-A 32 26-FEB-1993;
        Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 8.2%; Score 11.4; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1655 AGCACCAGGCTCA 1667
Db 1 AGACACAGGCTCA 13

RESULT 304
LOCUS I26247
DEFINITION Sequence 32 from patent US 5556955.
ACCESSION I26247
VERSION I26247.1 GI:1606117
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Vernaud,G.
TITLE Process for detection of new polymorphic loci in a DNA sequence,
nucleotide sequences forming hybridization probes and their
applications
JOURNAL Patent: US 5556955-A 32 17-SEP-1996;
FEATURES
    source
        Location/Qualifiers
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 8.2%; Score 11.4; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1655 AGCACCAGGCTCA 1667
Db 1 AGACACAGGCTCA 13

RESULT 305
LOCUS AX266567/c
DEFINITION Sequence 3958 from Patent WO0173002.
ACCESSION AX266567
VERSION AX266567.1 GI:16515366
KEYWORDS
SOURCE Homo sapiens (human)

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTG 1698
Db 3 CTCCTCCAGCGTG 15

RESULT 306
LOCUS AX266568
DEFINITION Sequence 3959 from Patent WO0173002.
ACCESSION AX266568
VERSION AX266568.1 GI:16515367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 3958 04-OCT-2001;
FEATURES
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        Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAGCCCT 1680
Db 14 CAGCTGGAGCCCT 2

RESULT 306
LOCUS AX266568
DEFINITION Sequence 3959 from Patent WO0173002.
ACCESSION AX266568
VERSION AX266568.1 GI:16515367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 3958 04-OCT-2001;
FEATURES
    source
        Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAGCCCT 1680
Db 4 CAGCTGGAGCCCT 16

RESULT 307
LOCUS AR019338/c
DEFINITION Sequence 5 from patent US 5783416.
ACCESSION AR019338
VERSION AR019338.1 GI:3974452
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Thim,L., Norris,K., Norris,F., Bj.o slashedren,Erik.,
Christensen,M. and Nielsen,P.Franklin.
TITLE Human spasmodic polypeptide in glycosylated form
JOURNAL Patent: US 5783416-A 5 21-JUL-1998;
FEATURES
    source
        Location/Qualifiers
            1..17
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 CCCTGGTGTCTCC 1698
    |||||
Db 14 CCCTGGTGTCTCC 2

RESULT 308
AR161494/c
LOCUS AR161494 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 16 from patent US 6255467.
ACCESSION AR161494
VERSION AR161494.1 GI:16227404
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Lindner,L.E. and MacPhee,K.
TITLE Human blood bacterium
JOURNAL Patent: US 6255467-A 16 03-JUL-2001;
FEATURES
    source
        location/Qualifiers
            1..17
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GGTGGAAGTGGG 1710
    |||||
Db 16 GGTGGAAGTGGG 4

RESULT 309
BD231535/c
LOCUS BD231535 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Chromosome 17q-linked prostate cancer susceptibility gene.
ACCESSION BD231535
VERSION BD231535.1 GI:33041305
KEYWORDS JP 2002529065-A/87.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 17)
AUTHORS Tavtigian,S.V., Teng,D.H.F., Simard,J. and Rommens,J.M.
TITLE Chromosome 17q-linked prostate cancer susceptibility gene
JOURNAL Patent: JP 2002529065-A 87 10-SEP-2002;
COMMENT MYRIAD GENETICS INC,THE HOSPITAL FOR SICK CHILDREN
OS Homo sapiens (human)
PN JP 2002529065-A/87
PD 10-SEP-2002
PF 05-NOV-1999 JP 2000581041
PR 06-NOV-1998 US 60/107468
PI SEAN V TAVTIGIAN,DAVID H F TENG,JACQUES SIMARD,JOHANNA M PI ROMMENS
PC C12N15/09,A61K31/713,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
PC A61P35/00,
PC C07K14/47,C07K16/18,C07K16/44,C12N1/15,C12N1/19,C12N1/21,C12N5/10,
PC C12E21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566,
PC G01N33/577,
PC G01N37/00,C12N15/00,A61K37/02,C12N5/00
CC Chromosome 17q-linked prostate cancer susceptibility gene FH
KEY Location/Qualifiers

/organism="Homo sapiens (human)"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1657 CACCAGGCTCACA 1669
    |||||
Db 17 CACCAGGCTGACA 5

RESULT 310
BD254457/c
LOCUS BD254457 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254457
VERSION BD254457.1 GI:33064227
KEYWORDS JP 2002541795-A/2250.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2250 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2250
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1/91),(C12P21/02, PC C12R1/91),
PC (C12P21/02,C12R1/91),(C12P21/02,C12R1/91),C12N15/00,C12N5/00, PC A61K37/02,
PC (C12N5/00,C12R1/91)
CC Regulation of repressor genes using nucleic acid molecules FH
KEY Location/Qualifiers
FT source
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Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1686 CTCCTCCAGCGTG 1698
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Db 17 CTCCTCCAGAGTG 5

RESULT 311
AR187364
LOCUS AR187364 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2852 from patent US 6346398.
ACCESSION AR187364
VERSION AR187364.1 GI:20233329
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2852 12-FEB-2002;
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QY 1725 ATGGAGATTGGCT 1737
Db 3 ATGGATATTGGCT 15
RESULT 312
LOCUS AR187365 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2853 from patent US 6346398.
ACCESSION AR187365
VERSION AR187365.1 GI:20233330
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2853 12-FEB-2002;
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QY 1725 ATGGAGATTGGCT 1737
Db 1 ATGGATATTGGCT 13
RESULT 313
LOCUS AR195588/c 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 53 from patent US 6350934.
ACCESSION AR195588
VERSION AR195588.1 GI:20245025
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 53 26-FEB-2002;
FEATURES
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        Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1725 ATGGAGATTGGCT 1737
Db 1 ATGGATATTGGCT 13
RESULT 314
LOCUS AR286088 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 460 from patent US 6528640.
ACCESSION AR286088
VERSION AR286088.1 GI:29723684
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 460 04-MAR-2003;
FEATURES
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                /mol_type="unassigned RNA"
    Query Match
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QY 1663 GTCACAGCTGGA 1675
Db 2 GTCACAGCTGGA 14
RESULT 315
LOCUS AR323974 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1376 from patent US 6566127.
ACCESSION AR323974
VERSION AR323974.1 GI:33709782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1376 20-MAY-2003;
FEATURES
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                /mol_type="unassigned RNA"
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QY 1725 ATGGAGATTGGCT 1737
Db 3 ATGGATATTGGCT 15
RESULT 316
LOCUS AR323975 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1377 from patent US 6566127.
ACCESSION AR323975
VERSION AR323975.1 GI:33709783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.
1 (bases 1 to 17)
REFERENCE Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
AUTHORS Method and reagent for the treatment of diseases or conditions
TITLE related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1377 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1725 ATGGAGATTGGCT 1737
Db 1 ATGGATATTGGCT 13

RESULT 317
AR327590/c
LOCUS AR327590 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4992 from patent US 6566127.
ACCESSION AR327590
VERSION AR327590.1 GI:33713398
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6566127-A 4992 20-MAY-2003;
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGA 1676
Db 17 CCCACAGCTGGA 5

RESULT 318
AR398078
LOCUS AR398078 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 459 from patent US 6617438.
ACCESSION AR398078
VERSION AR398078.1 GI:40135598
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 459 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGAGA 1731
Db 14 ACAGAGATGGAGA 2

RESULT 321
AX272713/c
LOCUS AX272713 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 282 from Patent WO0162911.
ACCESSION AX272713
VERSION AX272713.1 GI:16545450
KEYWORDS

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QY 1663 GCTCACAGCTGGA 1675
Db 2 GCTCACTGCTGGA 14

RESULT 319
AR401959
LOCUS AR401959 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 299 from patent US 6623962.
ACCESSION AR401959
VERSION AR401959.1 GI:40149409
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related
JOURNAL to levels of epidermal growth factor receptors
FEATURES Patent: US 6623962-A 299 23-SEP-2003;
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1729 AGATTGGCTCCCA 1741
Db 5 ATATTGGCTCCCA 17

RESULT 320
AX272527/c
LOCUS AX272527 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 96 from Patent WO0162911.
ACCESSION AX272527
VERSION AX272527.1 GI:16545264
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 96 30-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGAGA 1731
Db 14 ACAGAGATGGAGA 2

RESULT 321
AX272713/c
LOCUS AX272713 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 282 from Patent WO0162911.
ACCESSION AX272713
VERSION AX272713.1 GI:16545450
KEYWORDS

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE      Method and reagent for the inhibition of grid
JOURNAL    Patent: WO 0162911-A 282 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   Location/Qualifiers
source     1..17
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Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGAGA 1731
Db 17 ACAGAGATGGAGA 5

RESULT 322
AX272714/c
LOCUS      AX272714      17 bp      RNA      linear      PAT 29-OCT-2001
DEFINITION Sequence 283 from Patent WO0162911.
ACCESSION  AX272714
VERSION     AX272714.1 GI:16545451
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE      Method and reagent for the inhibition of grid
JOURNAL    Patent: WO 0162911-A 283 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   Location/Qualifiers
source     1..17
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Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGAGA 1731
Db 16 ACAGAGATGGAGA 4

RESULT 323
AX272715/c
LOCUS      AX272715      17 bp      RNA      linear      PAT 29-OCT-2001
DEFINITION Sequence 284 from Patent WO0162911.
ACCESSION  AX272715
VERSION     AX272715.1 GI:16545452
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE      Method and reagent for the inhibition of grid
JOURNAL    Patent: WO 0162911-A 284 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   Location/Qualifiers
source     1..17
            /organism="Homo sapiens"
            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGAGA 1731
Db 16 ACAGAGATGGAGA 4

RESULT 324
AX393384/c
LOCUS      AX393384      17 bp      DNA      linear      PAT 23-MAR-2002
DEFINITION Sequence 314 from Patent WO0210217.
ACCESSION  AX393384
VERSION     AX393384.1 GI:19701366
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
St Croix,B., Kinzler,K.W. and Vogelstein,B.
TITLE      Endothelial cell expression patterns
JOURNAL    Patent: WO 0210217-A 314 07-FEB-2002;
The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
source     1..17
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Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1678 CCTGGTGCTCTCCT 1690
Db 14 CCTGGTGCTCTCCT 2

RESULT 325
AX498902
LOCUS      AX498902      17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 209 from Patent EPI229046.
ACCESSION  AX498902
VERSION     AX498902.1 GI:23381195
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Zhan,J.
TITLE      Human testis expressed patched like protein
JOURNAL    Patent: EP 1229046-A 209 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
source     1..17
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Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1678 CCTGGTGCTCTCCT 1690
Db 14 CCTGGTGCTCTCCT 2
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QY	1646	CAGAAGGCAAGCA	1658		
Db	5	CGGAAGGCAAGCA	17		
RESULT 326					
LOCUS	AX498903	Sequence 210 from Patent EP1229046.	17 bp DNA linear	PAT 27-SEP-2002	
DEFINITION	AX498903				
ACCESSION	AX498903				
VERSION	AX498903.1	GI:23381196			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Zhan,J.				
AUTHORS	Human testis expressed patched like protein				
TITLE	Patent: BP 1229046-A 210 07-AUG-2002;				
JOURNAL	Aeomica, Inc. (US)				
FEATURES	Location/Qualifiers				
source	1..17				
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Query Match	Best Local Similarity	8.2%; Score 11.4; DB 1; Length 17;			
	Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1646	CAGAAGGCAAGCA	1658		
Db	4	CGGAAGGCAAGCA	16		
RESULT 327					
LOCUS	AX498907	Sequence 214 from Patent EP1229046.	17 bp DNA linear	PAT 27-SEP-2002	
DEFINITION	AX498907				
ACCESSION	AX498907				
VERSION	AX498907.1	GI:23381200			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Zhan,J.				
AUTHORS	Human testis expressed patched like protein				
TITLE	Patent: BP 1229046-A 214 07-AUG-2002;				
JOURNAL	Aeomica, Inc. (US)				
FEATURES	Location/Qualifiers				
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Query Match	Best Local Similarity	8.2%; Score 11.4; DB 1; Length 17;			
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QY	1646	CAGAAGGCAAGCA	1658		
Db	4	CGGAAGGCAAGCA	16		
RESULT 328					
LOCUS	AX498908	Sequence 215 from Patent EP1229046.	17 bp DNA linear	PAT 27-SEP-2002	
DEFINITION	AX498908				
ACCESSION	AX498908				
VERSION	AX498908.1	GI:23381201			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Zhan,J.				
AUTHORS	Human testis expressed patched like protein				
TITLE	Patent: BP 1229046-A 215 07-AUG-2002;				
JOURNAL	Aeomica, Inc. (US)				
FEATURES	Location/Qualifiers				
source	1..17				
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	/db_xref="taxon:9606"				
Query Match	Best Local Similarity	8.2%; Score 11.4; DB 1; Length 17;			
	Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1648	GAAGGCAAGCACC	1660		
Db	2	GAAGGCAAGCAGC	14		
RESULT 329					
LOCUS	AX499429	Sequence 736 from Patent EPI229046.	17 bp DNA linear	PAT 27-SEP-2002	
DEFINITION	AX499429				
ACCESSION	AX499429				
VERSION	AX499429.1	GI:23381722			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Zhan,J.				
AUTHORS	Human testis expressed patched like protein				
TITLE	Patent: Ep 1229046-A 736 07-AUG-2002;				
JOURNAL	Aeomica, Inc. (US)				
FEATURES	Location/Qualifiers				
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	Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1684	GTCCTCTCCAGCG	1696		
Db	5	GTCCTCTACAGCG	17		
RESULT 330					
LOCUS	AX499430	Sequence 737 from Patent EPI229046.	17 bp DNA linear	PAT 27-SEP-2002	
DEFINITION	AX499430				
ACCESSION	AX499430				
VERSION	AX499430.1	GI:23381723			
KEYWORDS			</		

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/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696
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Db 4 GTCTCTACAGCG 16

RESULT 331
AX499431
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 738 from Patent EP1229046.
ACCESSION AX499431
VERSION AX499431.1 GI:23381724
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 738 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696
|||||
Db 3 GTCTCTACAGCG 15

RESULT 332
AX499432
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 739 from Patent EP1229046.
ACCESSION AX499432
VERSION AX499432.1 GI:23381725
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 739 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696
|||||
Db 1 GTCTCTACAGCG 13

RESULT 333
AX499433
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 740 from Patent EP1229046.
ACCESSION AX499433
VERSION AX499433.1 GI:23381726
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 740 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696
|||||
Db 1 GTCTCTACAGCG 13

RESULT 334
AX531787/c
LOCUS      17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1296 from Patent EP1239051.
ACCESSION AX531787
VERSION AX531787.1 GI:25255351
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1296 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAA 1676
|||||
Db 17 CACACAGCTGGAA 5

RESULT 335
AX531788/c
LOCUS      17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1297 from Patent EP1239051.
ACCESSION AX531788
VERSION AX531788.1 GI:25255353
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1297 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1664 CTCACAGCTGGAA 1676
Db 16 CACACAGCTGGAA 4

RESULT 336
AX531789/c
LOCUS AX531789 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1298 from Patent EP1239051.
ACCESSION AX531789
VERSION AX531789.1 GI:25255355
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1298 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1664 CTCACAGCTGGAA 1676
Db 15 CACACAGCTGGAA 3

RESULT 337
AX531790/c
LOCUS AX531790 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1299 from Patent EP1239051.
ACCESSION AX531790
VERSION AX531790.1 GI:25255357
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1299 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1664 CTCACAGCTGGAA 1676
Db 14 CACACAGCTGGAA 2

RESULT 338
AX531791/c
LOCUS AX531791 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1300 from Patent EP1239051.
ACCESSION AX531791
VERSION AX531791.1 GI:25255359
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1300 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1664 CTCACAGCTGGAA 1676
Db 13 CACACAGCTGGAA 1

RESULT 339
AX532249/c
LOCUS AX532249 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1758 from Patent EP1239051.
ACCESSION AX532249
VERSION AX532249.1 GI:25256283
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1758 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1753 TCCTAAAGTCCCA 1765
Db 17 TCCTAAAGTCCCA 5
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RESULT 340
AX532250/c
LOCUS          17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION     Sequence 1759 from Patent EP1239051.
ACCESSION      AX532250
VERSION        AX532250.1  GI:25256285
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Human posh-like protein 1
JOURNAL       Patent: EP 1239051-A 1759 11-SEP-2002;
               Aeomica, Inc. (US)
FEATURES       source
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               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1753 TCCTAAGGCCCA 1765
Db 16 TCCTAAGTCCCA 4

RESULT 341
AX616595
LOCUS          17 bp      DNA      linear      PAT 20-FEB-2003
DEFINITION     Sequence 4 from Patent EP1262534.
ACCESSION      AX616595
VERSION        AX616595.1  GI:28447578
KEYWORDS       synthetic construct
               synthetic construct
               artificial sequences.
SOURCE         Lever,A.M. and Hunter,E.
ORGANISM       Defective packaging non-oncoviral vectors based on mpv and hiv
               Patent: EP 1262534-A 4 04-DEC-2002;
               SYNGENIX LIMITED (GB)
FEATURES       Location/Qualifiers
               1..17
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Plasmid sequence"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1715 GACTACGGAGATG 1727
Db 5 GAGTACTGAGATG 17

RESULT 342
AX687668
LOCUS          17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION     Sequence 400 from Patent EP1281758.
ACCESSION      AX687668
VERSION        AX687668.1  GI:29410364
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
               mdz12
JOURNAL       Patent: EP 1281758-A 400 05-FEB-2003;
               Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
               1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
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REFERENCE      1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
               mdz12
JOURNAL       Patent: EP 1281758-A 400 05-FEB-2003;
               Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
               1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1744 TCCTCCCTATCCT 1756
Db 4 TCCTCACTATCCT 16

RESULT 343
AX687669
LOCUS          17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION     Sequence 401 from Patent EP1281758.
ACCESSION      AX687669
VERSION        AX687669.1  GI:29410365
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
               mdz12
JOURNAL       Patent: EP 1281758-A 401 05-FEB-2003;
               Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
               1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1744 TCCTCCCTATCCT 1756
Db 3 TCCTCACTATCCT 15

RESULT 344
AX687670
LOCUS          17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION     Sequence 402 from Patent EP1281758.
ACCESSION      AX687670
VERSION        AX687670.1  GI:29410366
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
               mdz12
JOURNAL       Patent: EP 1281758-A 402 05-FEB-2003;
               Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
               1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
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/organism="Homo sapiens"
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Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1744 TCCTCCCTATCCT 1756
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Db 2 TCCTCACTATCCT 14

RESULT 345
AX691854
LOCUS AX691854 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 403 from Patent EP1281758.
ACCESSION AX687671
VERSION AX687671.1 GI:29410367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 403 05-FEB-2003;
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    Location/Qualifiers
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            /mol_type="unassigned DNA"
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Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1744 TCCTCCCTATCCT 1756
      ||||| |||||
Db 1 TCCTCACTATCCT 13

RESULT 346
AX691853
LOCUS AX691853 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 4585 from Patent EP1281758.
ACCESSION AX691853
VERSION AX691853.1 GI:29414794
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 4585 05-FEB-2003;
FEATURES
source
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        1..17
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Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 GTACGACAGGCA 1654
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Db 3 GTACGACAGGAA 15

RESULT 349
AX691856
LOCUS AX691856 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 4588 from Patent EP1281758.
ACCESSION AX691856

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VERSION      AX691856.1  GI:29414797
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
              mdz12
JOURNAL     Patent: EP 1281758-A 4588 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
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                /organism="Homo sapiens"
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              Query Match      8.2%; Score 11.4; DB 1; Length 17;
              Best Local Similarity 92.3%; Pred. No. 2.6e+02;
              Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1642 GTAGCAGAAGGCA 1654
Db      2 GTAGCAGAAGGAA 14

RESULT 350
LOCUS    AX691857
DEFINITION Sequence 4589 from Patent EP1281758.
ACCESSION AX691857
VERSION   AX691857.1  GI:29414798
KEYWORDS .
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
              mdz12
JOURNAL   Patent: EP 1281758-A 4589 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES  Location/Qualifiers
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          Best Local Similarity 92.3%; Pred. No. 2.6e+02;
          Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1642 GTAGCAGAAGGCA 1654
Db      1 GTAGCAGAAGGAA 13

RESULT 351
LOCUS    AX725940
DEFINITION Sequence 3627 from Patent WO03025176.
ACCESSION AX725940
VERSION   AX725940.1  GI:30505283
KEYWORDS .
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          Telerman,A., Anson,R. and Tuijnder,M.
          Sequences involved in phenomena of tumour suppression, tumour
          reversion, apoptosis and/or virus resistance and their use as
          medicines
          Patent: WO 03025176-A 1251 27-MAR-2003;
          Molecular Engines Laboratories (FR)
          Location/Qualifiers
          1..17
            /organism="Homo sapiens"

JOURNAL   reversion, apoptosis and/or virus resistance and their use as
              medicines
              Patent: WO 03025176-A 3627 27-MAR-2003;
              Molecular Engines Laboratories (FR)
              Location/Qualifiers
              1..17
                /organism="Mus musculus"
                /mol_type="unassigned DNA"
                /db_xref="taxon:10090"
              Query Match      8.2%; Score 11.4; DB 1; Length 17;
              Best Local Similarity 92.3%; Pred. No. 2.6e+02;
              Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1752 ATCCTAAAGGCC 1764
Db      2 ATCCTAAAGCCCC 14

RESULT 352
LOCUS    AX726324
DEFINITION Sequence 4011 from Patent WO03025176.
ACCESSION AX726324
VERSION   AX726324.1  GI:30505667
KEYWORDS .
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          Telerman,A., Anson,R. and Tuijnder,M.
          Sequences involved in phenomena of tumour suppression, tumour
          reversion, apoptosis and/or virus resistance and their use as
          medicines
          Patent: WO 03025176-A 4011 27-MAR-2003;
          Molecular Engines Laboratories (FR)
          Location/Qualifiers
          1..17
            /organism="Mus musculus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:10090"
          Query Match      8.2%; Score 11.4; DB 1; Length 17;
          Best Local Similarity 92.3%; Pred. No. 2.6e+02;
          Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1693 ACGGTGGTGAAG 1705
Db      2 ATCGTGGTGAAG 14

RESULT 353
LOCUS    AX729617
DEFINITION Sequence 1251 from Patent WO03025175.
ACCESSION AX729617
VERSION   AX729617.1  GI:30508960
KEYWORDS .
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          Telerman,A., Anson,R. and Tuijnder,M.
          Sequences involved in phenomena of tumour suppression, tumour
          reversion, apoptosis and/or virus resistance and their use as
          medicines
          Patent: WO 03025175-A 1251 27-MAR-2003;
          Molecular Engines Laboratories (FR)
          Location/Qualifiers
          1..17
            /organism="Homo sapiens"

JOURNAL   reversion, apoptosis and/or virus resistance and their use as
              medicines
              Patent: WO 03025175-A 1251 27-MAR-2003;
              Molecular Engines Laboratories (FR)
              Location/Qualifiers
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                /organism="Homo sapiens"

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/mol_type="unassigned DNA" /db_xref="taxon:9606"					
QY	1714 GGAGTACGGAGAT 1726 14 GGAGTAGGAGAT 2				
Db					
Query Match	8.2%; Score 11.4; DB 1; Length 17;				
Best Local Similarity	92.3%; Pred. No. 2.6e+02;				
Matches	12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1685 TCTCCTCAAGCGT 1697 3 TCTCCTCAAGCGT 15				
Db					
RESULT 354					
LOCUS	AX730112	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 1746 from Patent WO03025175.				
ACCESSION	AX730112				
VERSION	AX730112.1 GI:30509455				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 Telerman,A., Anson,R. and Tuijnder,M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines Patent: WO 03025175-A 1746 27-MAR-2003; Molecular Engines Laboratories (FR) Location/Qualifiers				
AUTHORS	1..17				
TITLE	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"				
JOURNAL					
FEATURES	source				
Query Match	8.2%; Score 11.4; DB 1; Length 17;				
Best Local Similarity	92.3%; Pred. No. 2.6e+02;				
Matches	12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1679 CTGGTGTCCTCCTC 1691 4 CTGGTGTCCTCCTC 16				
Db					
RESULT 355					
LOCUS	AX732381/c	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 4015 from Patent WO03025175.				
ACCESSION	AX732381				
VERSION	AX732381.1 GI:30511724				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 Telerman,A., Anson,R. and Tuijnder,M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines Patent: WO 03025175-A 4015 27-MAR-2003; Molecular Engines Laboratories (FR) Location/Qualifiers				
AUTHORS	1..17				
TITLE	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"				
JOURNAL					
FEATURES	source				
Query Match	8.2%; Score 11.4; DB 1; Length 17;				
Best Local Similarity	92.3%; Pred. No. 2.6e+02;				
Matches	12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1679 CTGGTGTCCTCCTC 1691 4 CTGGTGTCCTCCTC 16				
Db					
RESULT 356					
LOCUS	AX752612	17 bp	DNA	linear	PAT 20-JUN-2003
DEFINITION	Sequence 7 from Patent WO03035884.				
ACCESSION	AX752612				
VERSION	AX752612.1 GI:32134550				
KEYWORDS	synthetic construct artificial sequences.				
SOURCE	1 Kueper,J.H., Meyer,R., Meyer-Ficca,M. and Kuhn,A. Transient immortalization Patent: WO 03035884-A 7 01-MAY-2003; Heart Biosystems GmbH (DE) Location/Qualifiers				
ORGANISM	1..17				
REFERENCE	/organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Primer zur Gewinnung von ueberlappenden PCR-Fragmenten"				
AUTHORS					
TITLE					
JOURNAL					
FEATURES	source				
Query Match	8.2%; Score 11.4; DB 1; Length 17;				
Best Local Similarity	92.3%; Pred. No. 2.6e+02;				
Matches	12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1679 CTGGTGTCCTCCTC 1691 2 CTGGTGTCCTCCTC 14				
Db					
RESULT 358					
LOCUS	AX753719	17 bp	DNA	linear	PAT 23-JUN-2003
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
Query Match	8.2%; Score 11.4; DB 1; Length 17;				
Best Local Similarity	92.3%; Pred. No. 2.6e+02;				
Matches	12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				

AUTHORS	Telerman,A., Amson,R. and Tuijnder,M.
TITLE	Sequences involved in tumoral suppression, apoptotic and/or viral resistance phenomena and their use as medicines
JOURNAL	Patent: WO 03040369-A 264 15-MAY-2003;
FEATURES	Molecular Engines Laboratories (FR)
source	Location/Qualifiers 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity	92.3%; Pred.No. 2.6e+02;
Matches 12;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1637 GGCTGTGACAGCAGA 1649
Dd	 15 GGTITGTAGCACA 3
RESULT 361	
AX759131	Linear PAT 25-JUN-2003
LOCUS	AX759131 17 bp DNA
DEFINITION	Sequence 2452 from Patent W003040369.
ACCESION	AX759131
VERSION	AX759131.1 GI:32253747
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1
AUTHORS	Telerman,A., Amson,R. and Tuijnder,M.
TITLE	Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL	Patent: WO 03040369-A 2452 15-MAY-2003;
FEATURES	Molecular Engines Laboratories (FR) Location/Qualifiers 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
source	
Query Match	8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity	92.3%; Pred.No. 2.6e+02;
Matches 12;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1679 CTGGTGTCTCCTC 1691
Dd	 4 CTGGTGTCTCCTC 16
RESULT 362	
AX761322/C	Linear PAT 25-JUN-2003
LOCUS	AX761322 17 bp DNA
DEFINITION	Sequence 4643 from Patent W003040369.
ACCESION	AX761322
VERSION	AX761322.1 GI:32255938
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1
AUTHORS	Telerman,A., Amson,R. and Tuijnder,M.
TITLE	Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL	Patent: WO 03040369-A 4643 15-MAY-2003;
FEATURES	Molecular Engines Laboratories (FR) Location/Qualifiers

source 1. .17
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Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGAAC 1677
|||||||
13 TCACAGCTGGATC 1

Db 13 TCACAGCTGGATC 1

RESULT 363
AX783893/c
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2224 from Patent WO03050284.
ACCESSION AX783893
VERSION AX783893.1 GI:32951742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2224 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GGTGGAAGTTGGG 1710
|||||||
17 GCTGGAAGTTGGG 5

Db 17 GCTGGAAGTTGGG 5

RESULT 364
AX783894/c
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2225 from Patent WO03050284.
ACCESSION AX783894
VERSION AX783894.1 GI:32951743
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2225 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GGTGGAAGTTGGG 1710
|||||||
17 GCTGGAAGTTGGG 5

Db 17 GCTGGAAGTTGGG 5

RESULT 365
BD067459
LOCUS 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.
ACCESSION BD067459
VERSION BD067459.1 GI:22613062
KEYWORDS JP 2001511003-A/299.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 299 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT OS Unidentified
PN JP 2001511003-A/299
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: linear;
CC Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1. .17
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FEATURES
source
1. .17
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1729 ACATTGGCTCCCA 1741
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5 ATATTGGCTCCCA 17

Db 5 ATATTGGCTCCCA 17

RESULT 366
BD104949/c
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104949
VERSION BD104949.1 GI:22650523
KEYWORDS WO 0192572-A/1053.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 1053 06-DEC-2001;
NISHINOBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA, SHOGO MORIYA,MICHIO NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/1053
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798

QY 1698 GGTGGAAGTTGGG 1710
|||||||
17 GCTGGAAGTTGGG 5

```

PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
MATSUMURA,
PI SHOGO MORIYA,MICHIO NISHIDA
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
CC Description of Artificial Sequence:capture
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
    source
        1..17
            /organism='Artificial Sequence'.
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match
Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1661 AGGCTCAGCTG 1673
Db 17 AGGCTCAGCTG 5
RESULT 367
BD105056/c
LOCUS BD105056 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD105056
VERSION BD105056.1 GI:22650630
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 1160 06-DEC-2001;
NISHINEO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/1160
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
MATSUMURA,
PI SHOGO MORIYA,MICHIO NISHIDA
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
CC Description of Artificial Sequence:capture
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
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            /organism='Artificial Sequence'.
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match
Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1661 AGGCTCAGCTG 1673
Db 17 AGGCTCAGCTG 5
RESULT 368
BD132027/c
LOCUS BD132027 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Human blood bacterium.

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ACCESSION BD132027
VERSION BD132027.1 GI:23226972
KEYWORDS JP 2002502583-A/16.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Lindner,L. and Macphree,K.
TITLE Human blood bacterium
JOURNAL Patent: JP 2002502583-A 16 29-JAN-2002;
COMMENT PATHBIOTEK INC
OS Artificial Sequence
PN JP 2002502583-A/16
PD 29-JAN-2002
PF 06-NOV-1998 JP 2000519605
PR 06-NOV-1997 US 60/064472
PI LUTHER LINDNER,KATHLEEN MACPHEE
PC C12N15/09,A61K31/18,A61K31/395,A61K31/424,A61K31/431 PC
,A61K31/47,A61K31/4709.
PC A61K31/65,A61K31/7036,A61K31/704,A61K31/7048,A61K31/7052, PC
A61K39/00.
PC A61P31/04,C07H21/04,C12N1/20,C12Q1/06,C12Q1/69,C12N15/00 CC
primer specific for intergenic spacer region
(IGS) sequence of
CC a new human
CC blood bacterium
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
    source
        1..17
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match
Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1698 GGTGGAAGTTGG 1710
Db 16 GGTGGAAGTTGG 4
RESULT 369
BD198719/c
LOCUS BD198719 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
ACCESSION BD198719
VERSION BD198719.1 GI:33008489
KEYWORDS JP 2002509721-A/1745.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 1745 02-APR-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
PN JP 2002509721-A/1745
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT, JAMES A MCSWIGGEN
PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00.
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC

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RESULT 371
I31522/c
LOCUS       I31522             20 bp    DNA        linear     PAT 06-FEB-1997
DEFINITION   Sequence 434 from patent US 5582979.
ACCESSION    I31522
VERSION      I31522.1 GI:1822313
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Weber,J.B.
TITLE        Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL      Patent: US 5582979-A 434 10-DEC-1996;
FEATURES     Location/Qualifiers
source       1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match          8.2%; Score 11.4; DB 1; Length 20;
Best Local Similarity 92.3%; Pred.No. 3.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1735 GCTCCCAACTCT 1747
Dbs 13 GTCCTTAATCTCT 1

RESULT 372
A09974
LOCUS       A09974             16 bp    DNA        linear     PAT 28-FEB-1994
DEFINITION   Probe HBV.
ACCESSION    A09974
VERSION      A09974.1 GI:490630
KEYWORDS     .
SOURCE       synthetic construct
               synthetic construct
               artificial sequences.
ORIGIN       1 (bases 1 to 16)
AUTHORS      Vijg,J. and Uitterlinden,A.G.
TITLE        A method for the simultaneous determination of DNA sequence variations at a large number of sites, and a kit therefor
JOURNAL      Patent: EP 0349024-A 9 03-JAN-1990;
               NEDERLANDSE ORGANISATIE VOOR TOEGEPAST-NATUURWETENSCHAPPELIJK ONDERZOEK TWO
FEATURES     Location/Qualifiers
source       1..16
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

Query Match          8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No. 2.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1702 GAAGTTGGGTAGGAG 1717
Dbs  1 GGAGTTGGGGAGGAG 16

RESULT 373
AR105448/c
LOCUS       AR105448           16 bp    DNA        linear     PAT 14-FEB-2001
DEFINITION   Sequence 11 from patent US 6096549.
ACCESSION    AR105448
VERSION      AR105448.1 GI:12819045
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Pellicic.V., Reyrat,J.-M., Gicquel,B., Guilhot,C. and Jackson,M.
```

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TITLE      Method of selection of allelic exchange mutants
JOURNAL    Patent: US 6096549-A 11 01-AUG-2000;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1754 CCTAAGGCCCACTGG 1769
Db 16 CCTAATGGCCTAATGG 1

RESULT 374
LOCUS      AR328255                16 bp    RNA
DEFINITION Sequence 5657 from patent US 6566127.
ACCESSION  AR328255
VERSION     AR328255.1 GI:33714063
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 5657 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGACCCCTG 1681
Db 16 CACAGCAGGACCCCG 1

RESULT 375
LOCUS      AR328256                16 bp    RNA
DEFINITION Sequence 5658 from patent US 6566127.
ACCESSION  AR328256
VERSION     AR328256.1 GI:33714064
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 5658 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCAGCTGGGAACC 1678
Db 16 GCGCAGCAGGAGGCC 1

RESULT 376
LOCUS      AR328552                16 bp    RNA
DEFINITION Sequence 5954 from patent US 6566127.
ACCESSION  AR328552
VERSION     AR328552.1 GI:33714360
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 5954 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1661 AGGCTCACAGCTGGAA 1676
Db 16 AGGTCACAGCTGGGA 1

RESULT 377
LOCUS      AR435895                16 bp    RNA
DEFINITION Sequence 154 from patent US 6656731.
ACCESSION  AR435895
VERSION     AR435895.1 GI:40198979
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Eckstein,F., Ludwig,J. and Beigelman,L.
TITLE     Nucleic acid catalysts with endonuclease activity
          Patent: US 6656731-A 154 02-DEC-2003;
JOURNAL   Patent: US 6656731-A 154 02-DEC-2003;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1654 AAGCACACAGGCTCACA 1669
Db 16 AAGCTCAAGGTTTACA 1

RESULT 378
LOCUS      AX255727                16 bp    DNA
DEFINITION Sequence 148 from Patent WO0170982.
ACCESSION  AX255727
VERSION     AX255727.1 GI:16074782
KEYWORDS   synthetic construct
          synthetic construct
          artificial sequences.
SOURCE     1
ORGANISM   Beger,C., Barber,J. and Wong-Staal,F.
REFERENCE  Brca-1 regulators and methods of use
          Patent: WO 0170982-A 148 27-SEP-2001;
          Immusol Incorporated (US) ; Beger, Carmela (DE)
```

Query Match 8.1%; Score 11.2; DB 1; Length 16;

<p> JOURNAL Patent: WO 925815-A 24 27-MAY-1999; FEATURES HERRMANN BERNHARD (DE); MAX PLANCK GESELLSCHAFT (DE) Location/Qualifiers 1. .17 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644" </p>		<p> Query Match 8.1%; Score 11.2; DB 1; Length 17; Best Local Similarity 81.2%; Pred. NO. 2.9e+02; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0; </p>
<p> QY 1690 TCCAGCGTGGTGAAG 1705 Db 16 TCCAGCCAGGGGAG 1 </p>		
<p> RESULT 386 AR022370 LOCUS AR022370 17 bp DNA linear PAT 05-DEC-1998 DEFINITION Sequence 16 from patent US 5792833. ACCESSION AR022370 VERSION AR022370.1 GI:3976432 KEYWORDS . SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 17) AUTHORS Androphy,E.J. and Breiding,D.E. TITLE E2 binding proteins JOURNAL Patent: US 5792833-A 16 11-AUG-1998; FEATURES Location/Qualifiers 1. .17 /organism="unknown" /mol_type="unassigned DNA" </p>		
<p> Query Match 8.1%; Score 11.2; DB 1; Length 17; Best Local Similarity 81.2%; Pred. NO. 2.9e+02; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0; </p>		
<p> QY 1691 CCAGCGTGGTGAAGT 1706 Db 1 CCAGGGTGTAGAGT 16 </p>		
<p> RESULT 387 AR046570/c LOCUS AR046570 17 bp DNA linear PAT 29-SEP-1999 DEFINITION Sequence 1363 from patent US 5817796. ACCESSION AR046570 VERSION AR046570.1 GI:5968035 KEYWORDS . SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 17) AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T. TITLE C-myb ribozymes having 2'-5',-linked adenylyate residues JOURNAL Patent: US 5817796-A 1363 06-OCT-1998; FEATURES Location/Qualifiers 1. .17 /organism="unknown" /mol_type="unassigned DNA" </p>		
<p> Query Match 8.1%; Score 11.2; DB 1; Length 17; Best Local Similarity 85.2%; Pred. NO. 2.9e+02; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0; </p>		
<p> QY 1715 GAGTACGAGATGGAG 1730 Db 16 GAGAGCTGAGATGGAG 1 </p>		

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RESULT 388
AR057466/c
LOCUS AR057466 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1670 from patent US 5837542.
ACCESSION AR057466
VERSION AR057466.1 GI:5983043
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Inter cellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1670 17-NOV-1998;
FEATURES
Location/Qualifiers
1..17
/mol_type="unassigned DNA"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1704 AGTTGGGTTAGGAGTA 1719
Db 17 AGTGGGTGAGGGGTA 2
RESULT 389
AR057770/c
LOCUS AR057770 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1974 from patent US 5837542.
ACCESSION AR057770
VERSION AR057770.1 GI:5983347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Inter cellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1974 17-NOV-1998;
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1704 AGTTGGGTTAGGAGTA 1719
Db 17 AGTGGGTGAGGGGTA 2
RESULT 390
AR099617/c
LOCUS AR099617 17 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 28 from patent US 6077934.
ACCESSION AR099617
VERSION AR099617.1 GI:12809383
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
Grilley,M., Watkins,M. and Hillyard,D.R.
TITLE Contryphan peptides
JOURNAL Patent: US 6077934-A 28 20-JUN-2000;
FEATURES
Location/Qualifiers
1..17
/mol_type="unassigned DNA"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 76.9%; Pred. No. 2.9e+02;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1673 GGACCCCTGGTCT 1685
Db 15 GGARCCNTGGTGY 3
RESULT 391
AR100616
LOCUS AR100616 17 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 12 from patent US 6080727.
ACCESSION AR100616
VERSION AR100616.1 GI:12811064
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zupi,G.
TITLE Oligonucleotide treatments and compositions for human melanoma
JOURNAL Patent: US 6080727-A 12 27-JUN-2000;
FEATURES
Location/Qualifiers
1..17
/mol_type="unassigned DNA"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1731 ATTGGCTCCCAACTCC 1746
Db 2 ATTGTTTCCCACTCC 17
RESULT 392
AR115224/c
LOCUS AR115224 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1670 from patent US 6132967.
ACCESSION AR115224
VERSION AR115224.1 GI:14095546
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1670 17-OCT-2000;
FEATURES
Location/Qualifiers
1..17
/mol_type="unassigned DNA"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1704 AGTTGGGTTAGGAGTA 1719
Db 17 AGTGGGTGAGGGGTA 2
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TITLE		Expression systems comprising chimeric promoters with binding sites for recombinant transcription factors	
JOURNAL		Patent: JP 2002538759-A 4 19-NOV-2002; AVENTIS PHARMA DEUTSCHLAND GMBH	
COMMENT		OS Saccharomyces cerevisiae (yeast) PN JP 2002538759-A/4 PD 19-NOV-2002 PF 01-JUL-1999 JP 2000560275 PR 14-JUL-1998 DE 198 31 420.5 PI ROLF MUELLER,DIRK NETTLEBECK,HANS HARALD SEDLACEK PC C12N15/09,C12Q1/68//C12N15/09,C12R1:92),C12N15/00,(C12N15/00,PC C12R1:92) CC Expression systems comprising chimeric promoters with binding sites for recombinant transcription factors FH Key Location/Qualifiers FT source 1..17 /organism='Saccharomyces cerevisiae (yeast)'. FT Location/Qualifiers 1..17 /organism="Saccharomyces cerevisiae" /mol_type="genomic DNA" /db_xref="taxon:4932"	
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Best Local Similarity		81.2%; Pred. No. 2.9e+02;	
Matches		13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	1734	GGCTCCCAACTCCTCC	1749
DB	17	GGCTCCCAACACCTGC	2
RESULT 396		BD244486 17 bp DNA linear PAT 17-JUL-2003	
LOCUS		BD244486 New triplex forming oligonucleotides and their use in anti-HBV.	
DEFINITION		BD244486	
ACCESSION		BD244486.1 GI:33054256	
VERSION		JP 2002511384-A/4.	
KEYWORDS		synthetic construct synthetic construct artificial sequences.	
SOURCE		1 (bases 1 to 17) Lu,C.	
REFERENCE		New triplex forming oligonucleotides and their use in anti-HBV	
AUTHORS		Patent: JP 2002511384-A 4 16-APR-2002;	
TITLE		SHANGHAI INSTITUTE OF BIOCHEMISTRY CHINESE ACADEMY OF SCIENCES	
JOURNAL		OS Artificial Sequence	
COMMENT		PN JP 2002511384-A/4 PD 16-APR-2002 PF 19-OCT-1998 JP 2000516982 PR 21-OCT-1997 CN 97 1 06667.1 PI CHANGDE LU PC A61K31/711,A61K48/00,A61P31/20,C12N15/09,C12N15/00 CC Description of Artificial Sequence: Triplex forming CC oligonucleotide CC This oligo may or may not be 3'-monophosphorylated FH Key Location/Qualifiers FT source 1..17 FT /organism='Artificial Sequence'. FT Location/Qualifiers 1..17 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"	
FEATURES		source	
Query Match		8.1%; Score 11.2; DB 1; Length 17;	
Best Local Similarity		85.2%; Pred. No. 2.9e+02;	
Matches		13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	1736	CTCCCAACTCCTCCT	1751


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Db 16 CTCCTCTCTCTCTCT 1

RESULT 397
BD254012/c
LOCUS BD254012 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254012
VERSION BD254012.1 GI:33063782
KEYWORDS JP 2002541795-A/1805.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 1805 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/1805
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1..17 Location/Qualifiers
FT /organism='Eukaryote'.
FEATURES
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1..17
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/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1647 AGAAGGCAAGCACCAG 1662
||| ||| ||| ||| |||
Db 16 AGCAGGCAAGCCCG 1
||| ||| ||| ||| |||

RESULT 399
E07498/c
LOCUS E07498 17 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA for probe.
ACCESSION E07498
VERSION E07498.1 GI:2175636
KEYWORDS JP 1994133799-A/7.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Yamanishi,K., Yamamoto,T. and Mori,H.
TITLE ANALYSIS OF HUMAN HERPES VIRUS 6 TYPE @ (3754/24) HHV-6) DNA AND
DISCRIMINATION OF SUB-TYPE
JOURNAL Patent: JP 1994133799-A 7 17-MAY-1994;
INTERNAIL REAGENTS CORP
COMMENT OS None
OC Artificial sequences.
PN JP 1994133799-A/7
PD 17-MAY-1994
PF 27-OCT-1992 JP 1992311416
PI YAMANISHI KOICHI, YAMAMOTO TAKESHI, MORI HIROYUKI PC
C12Q1/68, C12Q1/68, C12N15/11, C12N15/38;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT source 1..17
/organism='Artificial sequences'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1665 TCACAGCTGGAACCT 1680
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Db 16 TCACAGATGGAAGACT 1
||| ||| ||| ||| |||

RESULT 400

Db 16 CTCCTCTCTCTCTCT 1

RESULT 397
BD254012/c
LOCUS BD254012 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254012
VERSION BD254012.1 GI:33063782
KEYWORDS JP 2002541795-A/1805.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 1805 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/1805
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1..17 Location/Qualifiers
FT /organism='Eukaryote'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1638 GCTTGTAGCAGAGGC 1653
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Db 17 GCTTGTAGTAGAGGCC 2
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RESULT 398
BD255189/c
LOCUS BD255189 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255189
VERSION BD255189.1 GI:33064959
KEYWORDS JP 2002541795-A/2982.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2982 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2982
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
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E24413/c	E24413	17 bp	DNA	linear	PAT 18-JUN-2001
LOCUS	Pharmacologically controllable self-accelerating expression system.				
DEFINITION	E24413				
ACCESSION	E24413.1	GI:13024640			
VERSION	JP 1999000176-A/7.				
KEYWORDS	unidentified				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Rolf,M. and Hansharald,S.				
TITLE	Pharmacologically controllable self-accelerating expression system				
JOURNAL	Patent: JP 1999000176-A 7 06-JAN-1999;				
COMMENT	HOECHST AG				
OS	Unidentified				
PN	JP 1999000176-A/7				
PD	06-JAN-1999				
PF	11-DEC-1997	JP 1997341728			
PR	11-DEC-1996	DE			
PI	ROLF MUELLER,HANS-HARALD SEDLACEK				
PC	C12N15/09,A61K31/70,A61K31/70,A61K31/70,A61K31/70,A61K31/70,				
PC	A61K31/70,				
PC	A61K31/70,A61K31/70,A61K31/70,A61K38/00,A61K48/00,C07K16/18,				
PC	C07K19/00,				
PC	C12N5/10,C12P21/02,C12N15/00,A61K37/02,C12N5/00	CC			
Strandedness:	Single;				
CC	Topology: Linear;				
PH	Key	Location/Qualifiers			
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FT		/organism='Unidentified'.			
FEATURES	source	Location/Qualifiers			
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		/db_xref="taxon:32644"			
Query Match	8.1%;	Score 11.2;	DB 1;	Length 17;	
Best Local Similarity	81.2%;	Pred. No. 2.9e+02;			
Matches	13;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	1734	GGCTCCCAACTCTCC	1749		
Db	17	GGCTCCCAACACTGC	2		
RESULT 401					
E27450/c	E27450	17 bp	DNA	linear	PAT 18-JUN-2001
LOCUS	cdc25B Gene promoter, preparation thereof and utilization of the				
DEFINITION	same.				
ACCESSION	E27450				
VERSION	E27450.1	GI:13025267			
KEYWORDS	JP 1999000181-A/1.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Kathryn,K., Rolf,M. and Hansharald,S.				
TITLE	cdc25B Gene promoter, preparation thereof and utilization of the				
JOURNAL	Patent: JP 1999000181-A 1 06-JAN-1999;				
COMMENT	HOECHST AG				
OS	Unidentified				
PN	JP 1999000181-A/1				
PD	06-JAN-1999	JP 1998084995			
PF	16-MAR-1998	JP 1998084995			
PR	14-MAR-1997	DE			
PI	KATHRYN KERUNA,ROLF MUELLER,HANS-HARALD SEDLACEK	PC			
C12N15/09,A61K48/00,C12P21/02,C12N9/12,C12P21/02,C12N5/10,					
C12R1:91),					
PC	(C12N9/12,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,				
PC	(C12N5/00,C12R1:91)				
CC	Strandedness: Single;				
CC	Topology: Linear;				
PH	Key	Location/Qualifiers			
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FEATURES	source	Location/Qualifiers			
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Query Match	8.1%;	Score 11.2;	DB 1;	Length 17;	
Best Local Similarity	81.2%;	Pred. No. 2.9e+02;			
Matches	13;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	1734	GGCTCCCAACTCTCC	1749		
Db	17	GGCTCCCAACACTGC	2		
RESULT 402					
E39008/c	E39008	17 bp	DNA	linear	PAT 18-JUN-2001
LOCUS	Nucleic acid construction for gene therapy affected in activity by				
DEFINITION	cyclin-dependent kinase inhibitor.				
ACCESSION	E39008				
VERSION	E39008.1	GI:13017670			
KEYWORDS	JP 1999308997-A/7.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Martin,A., Andrea,B. and Hansharald,S.				
TITLE	Nucleic acid construction for gene therapy affected in activity by				
JOURNAL	cyclin-dependent kinase inhibitor				
COMMENT	Patent: JP 1999308997-A 7 09-NOV-1999;				
	HOECHST MARION ROUSSEL DEUTSCHLAND GMBH				
OS	Homo sapiens (human)				
PN	JP 1999308997-A/7				
PD	09-NOV-1999				
PF	21-DEC-1998	JP 1998376131			
PR	20-DEC-1997	DE 197 56 975.7			
PI	MARTIN AIRASU,ANDREA BUAGIN,HANS-HARALD SEDLACEK	PC			
C12N15/09,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,					
A61K31/00,					
PC	A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K38/00,A61K38/22,				
PC	A61K38/43,				
PC	A61K39/395,A61K48/00,C12N15/00,A61K37/02,A61K37/24,A61K37/465				
CC					
PH	Key	Location/Qualifiers			
FT	source	1..17			
FT		/organism='Homo sapiens (human)'.			
FEATURES	source	Location/Qualifiers			
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		/mol_type="genomic DNA"			
		/db_xref="taxon:9606"			
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Best Local Similarity	81.2%;	Pred. No. 2.9e+02;			
Matches	13;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	1734	GGCTCCCAACTCTCC	1749		
Db	17	GGCTCCCAACACTGC	2		
RESULT 403					
E64351/c	E64351	17 bp	DNA	linear	PAT 31-JAN-2002
LOCUS	Single-stranded multiple antigen-binding molecule and method for				
DEFINITION	producing it and use.				
ACCESSION	E64351				
VERSION	E64351.1	GI:18628512			
KEYWORDS	JP 2000201678-A/2.				

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 17)
AUTHORS    Kontaman,R., Sedlacek,H.H. and Mueller,R.
TITLE      Single-stranded multiple antigen-binding molecule and method for
JOURNAL    producing it and use
COMMENT    Patent: JP 200201678-A 2 25-JUL-2000;
          HORCHST MARION ROUSSEL DEUTSCHLAND GMBH
          OS Artificial Sequence
          PN JP 200201678-A/2
          PD 25-JUL-2000
          PF 09-APR-1999 JP 1999102595
          PR
          PI ROLAND KONTAMAN, HANS HARALD SEDLACEK, ROLF MUELLER PC
          C12N15/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00, PC
          A61K35/74,
          PC A61K35/76,A61K38/00,C07K16/46,C12N1/19,C12N1/21,C12N5/10, PC
          C12N15/00,
          PC A61K37/02,C12N5/00
          CC
          FH Key Location/Qualifiers
          FT source 1..17
          FT Location/Qualifiers
          FT 1..17 /organism='Artificial Sequence'
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              /mol_type='genomic DNA'
              /db_xref='taxon:32630'
            Query Match 8.1%; Score 11.2; DB 1; Length 17;
            Best Local Similarity 81.2%; Pred. No. 2.9e+02;
            Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
          Qy 1734 GGCTCCCAACTCCCTCC 1749
            | ||||| |||||
            Db 17 GGCTCCCAACACCTGC 2
          RESULT 404
          LOCUS 150743 17 bp DNA linear PAT 07-OCT-1997
          DEFINITION Sequence 25 from patent US 5643724.
          ACCESSION I50743
          VERSION I50743.1 GI:2472446
          KEYWORDS
          SOURCE Unknown.
          ORGANISM Unclassified.
          REFERENCE 1 (bases 1 to 17)
          AUTHORS Fildes,N.Jane. and Reynolds,R.Lynne.
          TITLE Methods and reagents for Glycophorin A typing
          JOURNAL Patent: US 5643724-A 25 01-JUL-1997;
          FEATURES
            source
              1..17 /organism='unknown'
              /mol_type='unassigned DNA'
            Query Match 8.1%; Score 11.2; DB 1; Length 17;
            Best Local Similarity 81.2%; Pred. No. 2.9e+02;
            Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
          Qy 1670 GCTGGAACTCTGGTGT 1685
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            Db 1 GGTGGAACTCTGGTGT 16
          RESULT 405
          LOCUS I53622 17 bp DNA linear PAT 07-OCT-1997
          DEFINITION Sequence 1363 from patent US 5646042.
          ACCESSION I53622
          VERSION I53622.1 GI:2474825

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KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1363 08-JUL-1997;
FEATURES
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    /mol_type='unassigned DNA'
  Query Match 8.1%; Score 11.2; DB 1; Length 17;
  Best Local Similarity 81.2%; Pred. No. 2.9e+02;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  Qy 1715 GAGTACCGGAGATGGAG 1730
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    Db 16 GAGAGCTGAGATGGAG 1
  RESULT 406
  LOCUS AR185989/c 17 bp DNA linear PAT 20-APR-2002
  DEFINITION Sequence 1477 from patent US 6346398.
  ACCESSION AR185989
  VERSION AR185989.1 GI:20231954
  KEYWORDS
  SOURCE Unknown.
  ORGANISM Unclassified.
  REFERENCE 1 (bases 1 to 17)
  AUTHORS Payco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE Method and reagent for the treatment of diseases or conditions
  JOURNAL related to levels of vascular endothelial growth factor receptor
  FEATURES Patent: US 6346398-A 1477 12-FEB-2002;
    Location/Qualifiers
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        1..17 /organism='unknown'
        /mol_type='unassigned DNA'
    Query Match 8.1%; Score 11.2; DB 1; Length 17;
    Best Local Similarity 81.2%; Pred. No. 2.9e+02;
    Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
    Qy 1666 CACAGCTGGAACTCGT 1681
      ||||| ||||| |||||
      Db 17 CACAGCAGGACCCCGG 2
  RESULT 407
  LOCUS AR186749/c 17 bp DNA linear PAT 20-APR-2002
  DEFINITION Sequence 2237 from patent US 6346398.
  ACCESSION AR186749
  VERSION AR186749.1 GI:20232714
  KEYWORDS
  SOURCE Unknown.
  ORGANISM Unclassified.
  REFERENCE 1 (bases 1 to 17)
  AUTHORS Payco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE Method and reagent for the treatment of diseases or conditions
  JOURNAL related to levels of vascular endothelial growth factor receptor
  FEATURES Patent: US 6346398-A 2237 12-FEB-2002;
    Location/Qualifiers
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        /mol_type='unassigned DNA'
    Query Match 8.1%; Score 11.2; DB 1; Length 17;
    Best Local Similarity 81.2%; Pred. No. 2.9e+02;

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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1661 AGGTCACAGCTGGAA 1676
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Db 16 AGGTCACAGCTGGGA 1

RESULT 408
LOCUS AR190210 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 5698 from patent US 6346398.
ACCESSION AR190210
VERSION AR190210.1 GI:20236175
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5698 12-FEB-2002;
FEATURES Location/Qualifiers
    source
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 81.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAACCCCTG 1681
    |||||
Db 16 CCCAGCAGAAACCCCTG 1

RESULT 411
LOCUS AR190586 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 6074 from patent US 6346398.
ACCESSION AR190586
VERSION AR190586.1 GI:20236551
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6074 12-FEB-2002;
FEATURES Location/Qualifiers
    source
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 81.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1642 CTAGCAGAGGCAAGC 1657
    |||||
Db 16 GCATCATAGGCAAGC 1

RESULT 409
LOCUS AR190567/c 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 6055 from patent US 6346398.
ACCESSION AR190567
VERSION AR190567.1 GI:20236532
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6055 12-FEB-2002;
FEATURES Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 81.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAACCCCTG 1681
    |||||
Db 17 CCCAGCAGAAACCCCTG 2

RESULT 410
LOCUS AR190568/c 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 6056 from patent US 6346398.
ACCESSION AR190568
VERSION AR190568.1 GI:20236533
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6056 12-FEB-2002;
FEATURES Location/Qualifiers
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 81.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1661 AGGTCACAGCTGGAA 1676
    |||||
Db 16 AGGTCACAGCTGGGA 1

RESULT 408
LOCUS AR190210 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 5698 from patent US 6346398.
ACCESSION AR190210
VERSION AR190210.1 GI:20236175
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5698 12-FEB-2002;
FEATURES Location/Qualifiers
    source
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 81.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAACCCCTG 1681
    |||||
Db 16 CCCAGCAGAAACCCCTG 1

RESULT 411
LOCUS AR190586 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 6074 from patent US 6346398.
ACCESSION AR190586
VERSION AR190586.1 GI:20236551
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6074 12-FEB-2002;
FEATURES Location/Qualifiers
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 81.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAAGTCCTCCTAT 1753
    |||||
Db 2 CCCAAGTCCTCCTAT 17

RESULT 412
LOCUS AR196222/c 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 687 from patent US 6350934.
ACCESSION AR196222
VERSION AR196222.1 GI:20245659
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P. Ann.Owens.,
Guo,L., Skokut,J.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase,
JOURNAL Patent: US 6350934-A 687 26-FEB-2002;
FEATURES Location/Qualifiers
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 81.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1733 TGGCTCCCAACTCTCC 1748
Db 17 TGGCTGCCAACACTTC 2

RESULT 413
AR209224/c
LOCUS AR208224 17 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 3 from patent US 6380170.
ACCESSION AR208224
VERSION AR208224.1 GI:21508185
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Muller,R., Liu,N., Zwicker,J. and Sedlacek,H.-H.
TITLE Nucleic acid construct for the cell cycle regulated expression of structural genes
JOURNAL Patent: US 6380170-A 3 30-APR-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GCCTCCCAACTCTCC 1749
Db 17 GCCTCCCAACACTTC 2

RESULT 414
AR262374
LOCUS AR262374 17 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 10 from patent US 6323184.
ACCESSION AR262374
VERSION AR262374.1 GI:28073805
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Zalewski,A. and Shi,Y.
TITLE Arteriovenous and venous graft treatments: methods and compositions
JOURNAL Patent: US 6323184-A 10 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCAACTCC 1746
Db 2 ATTGTTTCCAACTCC 17

RESULT 415
AR286208
LOCUS AR286208 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 580 from patent US 6528640.
ACCESSION AR286208
VERSION AR286208.1 GI:29723804
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 580 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1677 CCTGTGTCTCTCTCC 1692
Db 1 CGCTGGGGCTCTCTCC 16

RESULT 416
AR322620/c
LOCUS AR322620 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 22 from patent US 6566127.
ACCESSION AR322620
VERSION AR322620.1 GI:33708428
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 22 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAACTCTG 1681
Db 17 CACAGCAGGACCCCG 2

RESULT 417
AR323380/c
LOCUS AR323380 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 782 from patent US 6566127.
ACCESSION AR323380
VERSION AR323380.1 GI:33709188
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 782 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1661 AGGCTCACAGCTGGAA 1676

Db 16 CACAGCAGGACCCGG 1

RESULT 423
LOCUS AR326803 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4205 from patent US 6566127.
ACCESSION AR326803
VERSION AR326803.1 GI:33712611
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4205 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGACCC 1679
Db 17 CGCAGCAGGACCC 2

RESULT 424
LOCUS AR327651 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5053 from patent US 6566127.
ACCESSION AR327651
VERSION AR327651.1 GI:33713459
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5053 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGACCC 1679
Db 17 CGCAGCAGGACCC 2

RESULT 425
LOCUS AR327652 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5054 from patent US 6566127.
ACCESSION AR327652
VERSION AR327652.1 GI:33713460
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Favco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5054 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1654 AAGCACCAGGCTCACA 1669
Db 16 AAGCAGCTGGCTCCCA 1

RESULT 426
LOCUS AR327765/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5167 from patent US 6566127.
ACCESSION AR327765
VERSION AR327765.1 GI:33713573
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5167 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1661 AGGCTCAGCTGGAA 1676
Db 17 AGGCTCAGCTGGGA 2

RESULT 427
LOCUS AR398198 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 579 from patent US 6617438.
ACCESSION AR398198
VERSION AR398198.1 GI:40135816
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 579 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1677 CCCTGGGTCTCTCC 1692
Db 1 CGCTGGGGGTCTCTCC 16

thereof
JOURNAL Patent: US 6642339-A 24 04-NOV-2003;
FEATURES Location/Qualifiers
source
1.17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1690 TCCAGCGTGTGGGAG 1705
||||| |||||
Db 16 TCCAGCCAGGGGGAAG 1

RESULT 431
AR432062 17 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 4 from patent US 6653119.
ACCESSION AR432062
VERSION AR432062.1 GI:40194267
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kondo,R., Sakai,K. and Wakao,K.
TITLE White rot fungi and method for decomposing dioxins using them
JOURNAL Patent: US 6653119-A 4 25-NOV-2003;
FEATURES Location/Qualifiers
source
1.17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1648 GAAGGCAAGCACCAGG 1663
||||| |||||
Db 16 GAAGGGCACCACCAGG 1

RESULT 432
AR432063 17 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 5 from patent US 6653119.
ACCESSION AR432063
VERSION AR432063.1 GI:40194268
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kondo,R., Sakai,K. and Wakao,K.
TITLE White rot fungi and method for decomposing dioxins using them
JOURNAL Patent: US 6653119-A 5 25-NOV-2003;
FEATURES Location/Qualifiers
source
1.17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1648 GAAGGCAAGCACCAGG 1663
||||| |||||
Db 2 GAAGGGCACCACCAGG 17

RESULT 433

AR401960 17 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 300 from patent US 6623962.
ACCESSION AR401960
VERSION AR401960.1 GI:40149410
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 300 23-SEP-2003;
FEATURES Location/Qualifiers
source
1.17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCACTCC 1746
||||| |||||
Db 2 ATTGGCTCCCACTCC 17

RESULT 429
AR402031 17 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 371 from patent US 6623962.
ACCESSION AR402031
VERSION AR402031.1 GI:40149481
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 371 23-SEP-2003;
FEATURES Location/Qualifiers
source
1.17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1694 CGGTGGTGAAGTTGG 1709
||||| |||||
Db 17 GCACGGTAGAAGTTGG 2

RESULT 430
AR429221 17 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 24 from patent US 6642369.
ACCESSION AR429221
VERSION AR429221.1 GI:40189370
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herrmann,B., Koschorz,B. and Kispert,A.
TITLE Nucleic acids involved in the responder phenotype and applications


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AX002552/c
LOCUS AX002552 17 bp DNA linear PAT 13-MAR-2000
DEFINITION Sequence 1 from Patent EP0864651.
ACCESSION AX002552
VERSION AX002552.1 GI:7242096
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Koerner, K. and Mueller, R.P.
TITLE Promoter of the cdc25B gene, its preparation and use
JOURNAL Patent: EP 0864651-A 1 16-SEP-1998;
HOECHST AG (DE)
FEATURES
LOCATION/Qualifiers
SOURCE 1..17
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1734 GGCTCCCAACTCTCTCC 1749
Db 17 GCCTCCCAACACCTGC 2

RESULT 434
AX002607/c
LOCUS AX002607 17 bp DNA linear PAT 10-MAR-2000
DEFINITION Sequence 3 from Patent EP0859008.
ACCESSION AX002607
VERSION AX002607.1 GI:7242114
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Liu, N. and Mueller, R.P.
TITLE Nucleic acid construct for the cell cycle regulated expression of
structural genes
JOURNAL Patent: EP 0859008-A 3 19-AUG-1998;
HOECHST AG (DE)
FEATURES
LOCATION/Qualifiers
SOURCE 1..17
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

promoter
1..17

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1734 GGCTCCCAACTCTCTCC 1749
Db 17 GCCTCCCAACACCTGC 2

RESULT 435
AX006344/c
LOCUS AX006344 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 4 from Patent WO0004178.
ACCESSION AX006344
VERSION AX006344.1 GI:9994493
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Eilers, M.P., Buerger, A. and Sedlacek, H.H.
TITLE Nucleic acid constructs for gene therapy, whose activity is
influenced by inhibitors of cyclin-dependent kinases
JOURNAL Patent: EP 0926237-A 7 30-JUN-1999;
HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES
LOCATION/Qualifiers
SOURCE 1..17
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

AX002552/c
LOCUS AX002552 17 bp DNA linear PAT 13-MAR-2000
DEFINITION Sequence 1 from Patent EP0864651.
ACCESSION AX002552
VERSION AX002552.1 GI:7242096
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Koerner, K. and Mueller, R.P.
TITLE Promoter of the cdc25B gene, its preparation and use
JOURNAL Patent: EP 0864651-A 1 16-SEP-1998;
HOECHST AG (DE)
FEATURES
LOCATION/Qualifiers
SOURCE 1..17
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1734 GGCTCCCAACTCTCTCC 1749
Db 17 GCCTCCCAACACCTGC 2

RESULT 436
AX015204/c
LOCUS AX015204 17 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 4 from Patent EP0952218.
ACCESSION AX015204
VERSION AX015204.1 GI:10041245
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kontermann, R.D., Mueller, R.P. and Sedlacek, H.H.
TITLE Single chain, multiple antigen-binding molecule, its preparation
and use
JOURNAL Patent: EP 0952218-A 4 27-OCT-1999;
HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES
LOCATION/Qualifiers
SOURCE 1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="VE-Box (Myo D binding site)"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1734 GGCTCCCAACTCTCTCC 1749
Db 17 GCCTCCCAACACCTGC 2

RESULT 437
AX022637/c
LOCUS AX022637 17 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 7 from Patent EP0926237.
ACCESSION AX022637
VERSION AX022637.1 GI:10046194
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Eilers, M.P., Buerger, A. and Sedlacek, H.H.
TITLE Nucleic acid constructs for gene therapy, whose activity is
influenced by inhibitors of cyclin-dependent kinases
JOURNAL Patent: EP 0926237-A 7 30-JUN-1999;
HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES
LOCATION/Qualifiers
SOURCE 1..17
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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exon
1. 17
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GCCTCCCACTCTCC 1749
Db 17 GCCTCCCACTCTCC 1749

RESULT 438
AX215133
LOCUS AX215133 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 575 from Patent WO0159103.
ACCESSION AX215133
VERSION AX215133.1 GI:15525176
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
FEATURES
source
1. 17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1704 AGTTGGTTAGGAGTA 1719
Db 2 AGTTGGTTAGGAGTA 1719

RESULT 439
AX216004
LOCUS AX216004 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1446 from Patent WO0159103.
ACCESSION AX216004
VERSION AX216004.1 GI:15526047
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
FEATURES
source
1. 17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1705 GTTGGTTAGGAGTAC 1720
Db 17 GTTGGTTAGGAGTAC 1720

exon
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Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GCCTCCCACTCTCC 1749
Db 17 GCCTCCCACTCTCC 1749

RESULT 440
AX217394
LOCUS AX217394 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2836 from Patent WO0159103.
ACCESSION AX217394
VERSION AX217394.1 GI:15527455
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
FEATURES
source
1. 17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1647 AGAAGGCCAACGACG 1662
Db 17 AGAAGGCCAACGATCAG 2

RESULT 441
AX217395/c
LOCUS AX217395/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2837 from Patent WO0159103.
ACCESSION AX217395
VERSION AX217395.1 GI:15527456
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
FEATURES
source
1. 17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1647 AGAAGGCCAACGACG 1662
Db 16 AGAAGGCCAACGATCAG 1

RESULT 442
AX217770/c
LOCUS AX217770 17 bp RNA linear PAT 07-SEP-2001
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DEFINITION Sequence 3212 from Patent WO0159103.
ACCESSION AX217770
VERSION AX217770.1 GI:15527831
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 3212 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1706 TTGGGTAGGAGTACG 1721
Db 17 TTGGGCTGGAGCAG 2

RESULT 443
AX217771/c
LOCUS AX217771 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3213 from Patent WO0159103.
ACCESSION AX217771
VERSION AX217771.1 GI:15527832
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 3213 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1706 TTGGGTAGGAGTACG 1721
Db 16 TTGGGCTGGAGCAG 1

RESULT 444
AX264312/c
LOCUS AX264312 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1703 from Patent WO0173002.
ACCESSION AX264312
VERSION AX264312.1 GI:16513111
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., Hamblin,P.A. and
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 119 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
Location/Qualifiers

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL stranded oligonucleotides
PATENT: WO 0173002-A 1703 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGTGCTCTCC 1689
Db 16 GAACCTGCAGTCTGC 1

RESULT 445
AX264313
LOCUS AX264313 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1704 from Patent WO0173002.
ACCESSION AX264313
VERSION AX264313.1 GI:16513112
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL stranded oligonucleotides
PATENT: WO 0173002-A 1704 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGTGCTCTCC 1689
Db 2 GAACCTGCAGTCTGC 17

RESULT 446
AX272550/c
LOCUS AX272550 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 119 from Patent WO0162911.
ACCESSION AX272550
VERSION AX272550.1 GI:16545287
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., Hamblin,P.A. and
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 119 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
Location/Qualifiers

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., Hamblin,P.A. and
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 119 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
Location/Qualifiers

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., Hamblin,P.A. and
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 119 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGGC 1736
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Db 17 GGAGATGGAATTGTC 2

RESULT 447
AX272551/c
LOCUS AX272551 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 120 from Patent WO0162911.
ACCESSION AX272551
VERSION AX272551.1 GI:16545288
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
AUTHORS Method and reagent for the inhibition of grid
TITLE Patent: WO 0162911-A 120 30-AUG-2001;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..17
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGGC 1736
|||||
Db 16 GGAGATGGAATTGTC 1

RESULT 448
AX272840
LOCUS AX272840 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 409 from Patent WO0162911.
ACCESSION AX272840
VERSION AX272840.1 GI:16545577
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
AUTHORS Method and reagent for the inhibition of grid
TITLE Patent: WO 0162911-A 409 30-AUG-2001;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1632 GATGGGGCTTGATGCA 1647
|||||
Db 2 GATGGGCTTGTGGCA 17

RESULT 449
AX273034/c
LOCUS AX273034 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 603 from Patent WO0162911.
ACCESSION AX273034
VERSION AX273034.1 GI:16545771
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
AUTHORS Method and reagent for the inhibition of grid
TITLE Patent: WO 0162911-A 603 30-AUG-2001;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1753 TCCTAAAGGCCCACTG 1768
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Db 17 TCCACAGCCCACTG 2

RESULT 450
AX326513
LOCUS AX326513 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2651 from Patent WO0192512.
ACCESSION AX326513
VERSION AX326513.1 GI:18097277
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
REFERENCE 1 Kmiec, E.B., Gampfer, H.B., Rice, M.C. and Kim, J.
AUTHORS Targeted chromosomal genomic alterations in plants using modified
TITLE single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 2651 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
Location/Qualifiers
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/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1642 GTAGCAGAGCGCAGC 1657
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Db 2 GGAGCAGTAGCGCAGC 17

RESULT 451
AX326514/c
LOCUS AX326514 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2652 from Patent WO0192512.

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ACCESSION AX326514
VERSION AX226514.1 GI:18097278
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
REFERENCE 1
AUTHORS Kmiec,B.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 2652 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
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1. .17
/organism="Triticum aestivum"
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/db_xref="taxon:4565"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1642 GTAGCAGAGGCGAAGC 1657
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Db 16 GGACGAGTAGCGGAGC 1

RESULT 452
AX393401
LOCUS AX393401 17 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 331 from Patent WO0210217.
ACCESSION AX393401
VERSION AX393401.1 GI:19701383
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 331 07-FEB-2002;
The Johns Hopkins University (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1741 AACTCCCTCCCTATCCT 1756
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Db 2 ACCACCTCCCTTCCT 17

RESULT 453
AX423730
LOCUS AX423730 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 2066 from Patent WO0188124.
ACCESSION AX423730
VERSION AX423730.1 GI:21527112
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 2066 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1710 GTTAGGAGTAGCGAGA 1725
| | | | | | | | | | | | | | |
Db 2 GTTAGGAGAGGAGACA 17

RESULT 455
AX475293
LOCUS AX475293 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 514 from Patent WO0224750.
ACCESSION AX475293
VERSION AX475293.1 GI:22214578
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang,J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 514 28-MAR-2002;
Acomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAGACC 1679
Db 2 CTCACAGCTGGAGACC 17

RESULT 456
AX475294
LOCUS AX475294 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 515 from Patent WO224750.
ACCESSION AX475294
VERSION AX475294.1 GI:22214579
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 515 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAGACC 1679
Db 1 CTCACAGCTGGAGACC 16

RESULT 457
AX498962
LOCUS AX498962 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 269 from Patent EPI229046.
ACCESSION AX498962
VERSION AX498962.1 GI:23381255
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 269 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 CTGGAACCTGGTCTC 1686
Db 2 CAGGACCCCTGGGCTC 17

RESULT 458
AX498963
LOCUS AX498963 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 270 from Patent EPI229046.
ACCESSION AX498963
VERSION AX498963.1 GI:23381256
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 270 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 CTGGAACCTGGTCTC 1686
Db 1 CAGGACCCCTGGGCTC 16

RESULT 459
AX499444
LOCUS AX499444 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 751 from Patent EPI229046.
ACCESSION AX499444
VERSION AX499444.1 GI:23381737
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 751 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGGAGAC 1677
Db 2 GACTCACTGCTGGACC 17

RESULT 460
AX531276
LOCUS AX531276 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 785 from Patent EPI239051.
ACCESSION AX531276
VERSION AX531276.1 GI:25254340
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
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TITLE      Human posh-like protein 1
JOURNAL    Patent: EP 1239051-A 785 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES   source
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           Location/Qualifiers
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           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CCAGCGTGGTGGAGT 1706
Db 2 CCAGCTCCGTGGAGT 17

RESULT 461
AX531277
LOCUS      AX531277
DEFINITION Sequence 786 from Patent EP1239051.
ACCESSION AX531277
VERSION    AX531277.1 GI:25254341
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Shannon,M.
TITLE     Human posh-like protein 1
JOURNAL   Patent: EP 1239051-A 786 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES   source
           1..17
           Location/Qualifiers
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           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CCAGCGTGGTGGAGT 1706
Db 1 CCAGCTCCGTGGAGT 16

RESULT 462
AX532096
LOCUS      AX532096
DEFINITION Sequence 1605 from Patent EP1239051.
ACCESSION AX532096
VERSION    AX532096.1 GI:25255955
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Shannon,M.
TITLE     Human posh-like protein 1
JOURNAL   Patent: EP 1239051-A 1605 11-SEP-2002;
           Aeomica, Inc. (US)
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           /db_xref="taxon:9606"

Query Match
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CCAGCGTGGTGGAGT 1706
Db 1 CCAGCTCCGTGGAGT 16

RESULT 463
AX532100
LOCUS      AX532100
DEFINITION Sequence 1609 from Patent EP1239051.
ACCESSION AX532100
VERSION    AX532100.1 GI:25255987
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Shannon,M.
TITLE     Human posh-like protein 1
JOURNAL   Patent: EP 1239051-A 1609 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES   source
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGTCTCC 1689
Db 1 GAGCCCTGGTCTCTAC 16

RESULT 464
AX532102
LOCUS      AX532102
DEFINITION Sequence 1611 from Patent EP1239051.
ACCESSION AX532102
VERSION    AX532102.1 GI:25255991
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Shannon,M.
TITLE     Human posh-like protein 1
JOURNAL   Patent: EP 1239051-A 1611 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES   source
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Query Match
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGTCTCC 1689
Db 1 GAGCCCTGGTCTCTAC 16

RESULT 465
AX532104
LOCUS      AX532104
DEFINITION Sequence 1613 from Patent EP1239051.
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1677 CCCTGGTGTCTCTCC 1692
Db 2 CCCTGGTGTCTCTAC 17
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ACCESSION AX532104
VERSION AX532104.1 GI:25255995
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1613 11-SEP-2002;
FEATURES
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1. .17
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1678 CCTGCTCTCTCCCA 1693
Db 1 CCTGGTCTTACCA 16
RESULT 466
AX532255/c
LOCUS AX532255 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1764 from Patent EP1239051.
ACCESSION AX532255
VERSION AX532255.1 GI:25256295
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1764 11-SEP-2002;
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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1678 CCTGCTCTCTCCCA 1693
Db 1 CCTGGTCTTACCA 16
RESULT 467
AX532275/c
LOCUS AX532275 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1784 from Patent EP1239051.
ACCESSION AX532275
VERSION AX532275.1 GI:25256333
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1784 11-SEP-2002;
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/db_xref="taxon:9606"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1748 CCTATCTCTAAGGCC 1763
Db 16 CCTGTCTTAAGTCC 1
RESULT 468
AX532276/c
LOCUS AX532276 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1785 from Patent EP1239051.
ACCESSION AX532276
VERSION AX532276.1 GI:25256335
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1785 11-SEP-2002;
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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1743 CTCTCTCTCTCTCTAA 1758
Db 16 CTCCGCCCTTTCGAA 1
RESULT 469
AX532448
LOCUS AX532448 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1957 from Patent EP1239051.
ACCESSION AX532448
VERSION AX532448.1 GI:25256670
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1957 11-SEP-2002;
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1. .17
/organism="Homo sapiens"
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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1743 CTCTCTCTCTCTCTAA 1758
Db 16 CTCCGCCCTTTCGAA 1
RESULT 470
AX532448
LOCUS AX532448 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1957 from Patent EP1239051.
ACCESSION AX532448
VERSION AX532448.1 GI:25256670
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1957 11-SEP-2002;
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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1743 CTCTCTCTCTCTCTAA 1758
Db 16 CTCCGCCCTTTCGAA 1
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QY 1696 GTGGTGAAGTTGGGT 1711
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Db 2 GTGGTGAAGTTGGGT 17

RESULT 470
AX532449
LOCUS AX532449 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1958 from Patent EP1239051.
ACCESSION AX532449
VERSION AX532449.1 GI:25256672
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1958 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1696 GTGGTGAAGTTGGGT 1711
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Db 1 GTGGTGAAGTTGGGT 16

RESULT 471
AX532450
LOCUS AX532450 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1959 from Patent EP1239051.
ACCESSION AX532450
VERSION AX532450.1 GI:25256674
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1959 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGCTCC 1739
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Db 2 GTGGAGATGGGTCCA 17

RESULT 474
AX532453
LOCUS AX532453 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1962 from Patent EP1239051.
ACCESSION AX532453
VERSION AX532453.1 GI:25256680
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1962 11-SEP-2002;
Aeomica, Inc. (US)
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Location/Qualifiers
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Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1726 TGGAGATTGGCTCCA 1741
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Db 2 TGGAGATGGGTCCA 17

RESULT 474
AX532453
LOCUS AX532453 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1962 from Patent EP1239051.
ACCESSION AX532453
VERSION AX532453.1 GI:25256680
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1962 11-SEP-2002;
Aeomica, Inc. (US)
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Location/Qualifiers
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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1726 TGGAGATTGGCTCCA 1741
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Db 2 TGGAGATGGGTCCA 17

RESULT 474
AX532453
LOCUS AX532453 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1962 from Patent EP1239051.
ACCESSION AX532453
VERSION AX532453.1 GI:25256680
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1962 11-SEP-2002;
Aeomica, Inc. (US)
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Location/Qualifiers
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/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGCTCC 1739
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Db 2 GTGGAGATGGGTCCA 17

RESULT 474
AX532453
LOCUS AX532453 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1960 from Patent EP1239051.
ACCESSION AX532451
VERSION AX532451.1 GI:25256676
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Query Match
8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1726 TGGAGATTGGCTCCCA 1741
Db 1 TGGAGATGGGTCCCA 16

RESULT 475
AX578661
LOCUS AX578661 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 499 from Patent WO0211674.
ACCESSION AX578661
VERSION AX578661.1 GI:27647863
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Patent: WO 0211674-A 499 14-FEB-2002;
Thompson, James (US)
FEATURES
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Location/Qualifiers
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Query Match
8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCTAA 1758
Db 1 CTGCTCCTTGCTCTAA 16

RESULT 476
AX579336
LOCUS AX579336 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1174 from Patent WO0211674.
ACCESSION AX579336
VERSION AX579336.1 GI:27648538
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Patent: WO 0211674-A 1174 14-FEB-2002;
Thompson, James (US)
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Query Match
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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCTAA 1758
Db 2 CTGCTCCTTGCTCTAA 17

RESULT 477
AX615330/c
LOCUS AX615330 17 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 137 from Patent EP1262488.
ACCESSION AX615330
VERSION AX615330.1 GI:28446229
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu, Y. and Nguyen, C.T.
TITLE Human lcc1-domain containing protein
JOURNAL Patent: EP 1262488-A 137 04-DEC-2002;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
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Query Match
8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1753 TCCTAAAGGCCCACTG 1768
Db 17 TCCTCATGGTCCACTG 2

RESULT 478
AX615331/c
LOCUS AX615331 17 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 138 from Patent EP1262488.
ACCESSION AX615331
VERSION AX615331.1 GI:28446230
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu, Y. and Nguyen, C.T.
TITLE Human lcc1-domain containing protein
JOURNAL Patent: EP 1262488-A 138 04-DEC-2002;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
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Query Match
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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1753 TCCTAAAGGCCCACTG 1768
Db 16 TCCTCATGGTCCACTG 1

RESULT 479
AX615842/c

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LOCUS AX615842 17 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 649 from Patent EP1262488.
ACCESSION AX615842
VERSION AX615842.1 GI:28446888
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu.Y. and Nguyen,C.T.
TITLE Human lcc1-domain containing protein
JOURNAL Patent: EP 1262488-A 649 04-DEC-2002;
Aeomica, Inc. (US)
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Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1696 GTGGTGAAGTTGGGT 1711
Db 17 GTGGGGAGGTTGGTT 2
RESULT 480
AX615843/c
LOCUS AX615843 17 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 650 from Patent EP1262488.
ACCESSION AX615843
VERSION AX615843.1 GI:28446889
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu.Y. and Nguyen,C.T.
TITLE Human lcc1-domain containing protein
JOURNAL Patent: EP 1262488-A 650 04-DEC-2002;
Aeomica, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
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Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1696 GTGGTGAAGTTGGGT 1711
Db 16 GTGGGGAGGTTGGTT 1
RESULT 481
AX634562/c
LOCUS AX634562 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1701 from Patent EP1260586.
ACCESSION AX634562
VERSION AX634562.1 GI:28470176
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 1934 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
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/db_xref="taxon:32644"

Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 1701 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1704 AGTGGGTTAGGAGTA 1719
Db 17 AGGTGGGTGAGGGTA 2
RESULT 482
AX634795/c
LOCUS AX634795 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1934 from Patent EP1260586.
ACCESSION AX634795
VERSION AX634795.1 GI:28470409
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 1934 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1704 AGTGGGTTAGGAGTA 1719
Db 17 AGGTGGGTGAGGGTA 2
RESULT 483
AX648876
LOCUS AX648876 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 716 from Patent EP1273660.
ACCESSION AX648876
VERSION AX648876.1 GI:29151694
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 716 08-JAN-2003;
Aeomica, Inc. (US)

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QY 1679 CTGGTGTCTCCCTCCAG 1694
Db 2 CTGATGTCGTCTACAG 17

RESULT 484
AX649489/c
LOCUS AX649489 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1329 from Patent EP1273660.
ACCESSION AX649489
VERSION AX649489.1 GI:29152307
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS Gu, Y.
  TITLE Human sodium-hydrogen exchanger like protein 1
  JOURNAL Patent: EP 1273660-A 1329 08-JAN-2003;
  Aeomica, Inc. (US)
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QY 1679 CTGGTGTCTCCCTCCAG 1694
Db 1 CTGATGTCGTCTACAG 16

RESULT 485
AX649489/c
LOCUS AX649489 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1329 from Patent EP1273660.
ACCESSION AX649489
VERSION AX649489.1 GI:29152307
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS Gu, Y.
  TITLE Human sodium-hydrogen exchanger like protein 1
  JOURNAL Patent: EP 1273660-A 1329 08-JAN-2003;
  Aeomica, Inc. (US)
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QY 1713 AGGAGTACGGAGATGG 1728
Db 2 ATCAACAGGCTTACAG 17

RESULT 488
AX671735/c
LOCUS AX671735 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 180 from Patent WO03004526.
ACCESSION AX671735

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Db 17 AGGAGGAGGAGAGG 2

RESULT 486
AX649490/c
LOCUS AX649490 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1330 from Patent EP1273660.
ACCESSION AX649490
VERSION AX649490.1 GI:29152308
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS Gu, Y.
  TITLE Human sodium-hydrogen exchanger like protein 1
  JOURNAL Patent: EP 1273660-A 1330 08-JAN-2003;
  Aeomica, Inc. (US)
FEATURES
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QY 1713 AGGAGTACGGAGATGG 1728
Db 16 AGGAGGAGGAGAGG 1

RESULT 487
AX671672
LOCUS AX671672 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 117 from Patent WO03004526.
ACCESSION AX671672
VERSION AX671672.1 GI:29330020
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS Telerman, A., Amson, R. and Tuijthof, M.
  TITLE Sequences involved in phenomena of tumour suppression, tumour
  JOURNAL reversal, apoptosis and/or resistance to viruses and their use as
  keywords
  Patent: WO 03004526-A 117 16-JAN-2003;
  Molecular Engines Laboratories (FR)
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
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  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670
Db 2 ATCAACAGGCTTACAG 17

RESULT 488
AX671735/c
LOCUS AX671735 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 180 from Patent WO03004526.
ACCESSION AX671735

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VERSION      AX671735.1  GI:29330083
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
JOURNAL      Molecular Engines Laboratories (FR)
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Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGGAAC 1677
Db 16 GTCTCAGCTTGATC 1

RESULT 489
AX672964
LOCUS      AX672964      17 bp      DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 1409 from Patent WO03004526.
ACCESSION  AX672964
VERSION     AX672964.1  GI:29331312
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
JOURNAL      Molecular Engines Laboratories (FR)
FEATURES     source
            1. .17
            /organism="Homo sapiens"
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Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCCTCCC 1750
Db 1 GATCCGAGCTGACC 16

RESULT 490
AX672965
LOCUS      AX672965      17 bp      DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 1410 from Patent WO03004526.
ACCESSION  AX672965
VERSION     AX672965.1  GI:29331313
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
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JOURNAL      Molecular Engines Laboratories (FR)
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Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCCTCCC 1750
Db 1 GATCCGAGCTGACC 16

RESULT 491
AX672967
LOCUS      AX672967      17 bp      DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 1412 from Patent WO03004526.
ACCESSION  AX672967
VERSION     AX672967.1  GI:29331315
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
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JOURNAL      Molecular Engines Laboratories (FR)
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Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCCTCCC 1750
Db 1 GATCCGAGCTGACC 16

RESULT 492
AX684195
LOCUS      AX684195      17 bp      DNA      linear      PAT 29-MAR-2003
DEFINITION Sequence 46 from Patent WO0246386.
ACCESSION  AX684195
VERSION     AX684195.1  GI:29371095
KEYWORDS
SOURCE      Aspergillus ochraceus
            Aspergillus ochraceus
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE    1
AUTHORS      Bolton,S., Clayton,R., Easton,A., Engel,L. and Messing,D.
TITLE       Aspergillus ochraceus 11 alpha hydroxylase and oxidoreductase
            Patent: WO 0246386-A 46 13-JUN-2002;
            Pharmacia Corporation (US) ; Bolton, Suzanne (US) ; Clayton, Robert
            (US) ; Easton, Alan (US) ; Engel, Leslie (US) ; Messing, Dean (US)
            Location/Qualifiers
            1. .17
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Query Match
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1722 GAGATGGAGATTGGCT 1737
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Db 1 GAGATCAAGATTGCCT 16

RESULT 493
AX687045/c
LOCUS AX687045 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 19 from Patent EP1281755.
ACCESSION AX687045
VERSION AX687045.1 GI:29409546
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Milos,P.M. and Webb,S.M.
TITLE Variants of the human cyp2d6 gene
JOURNAL Patent: EP 1281755-A 19 05-FEB-2003;
Pfizer Products Inc. (US)
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Location/Qualifiers
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Query Match
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAG 1670
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Db 17 AGCACAAAGCTCATAG 2

RESULT 494
AX687046
LOCUS AX687046 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 20 from Patent EP1281755.
ACCESSION AX687046
VERSION AX687046.1 GI:29409547
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Milos,P.M. and Webb,S.M.
TITLE Variants of the human cyp2d6 gene
JOURNAL Patent: EP 1281755-A 20 05-FEB-2003;
Pfizer Products Inc. (US)
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 17 AGCACAAAGCTCATAG 2

RESULT 494
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LOCUS AX687046 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 20 from Patent EP1281755.
ACCESSION AX687046
VERSION AX687046.1 GI:29409547
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Milos,P.M. and Webb,S.M.
TITLE Variants of the human cyp2d6 gene
JOURNAL Patent: EP 1281755-A 20 05-FEB-2003;
Pfizer Products Inc. (US)
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RESULT 494
AX687046
LOCUS AX687046 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 20 from Patent EP1281755.
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VERSION AX687046.1 GI:29409547
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Milos,P.M. and Webb,S.M.
TITLE Variants of the human cyp2d6 gene
JOURNAL Patent: EP 1281755-A 20 05-FEB-2003;
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QY 1655 AGCACCAGGCTCACAG 1670
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RESULT 493
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LOCUS AX687045 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 19 from Patent EP1281755.
ACCESSION AX687045
VERSION AX687045.1 GI:29409546
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Milos,P.M. and Webb,S.M.
TITLE Variants of the human cyp2d6 gene
JOURNAL Patent: EP 1281755-A 19 05-FEB-2003;
Pfizer Products Inc. (US)
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1740 CAACTCTCTCCCTATCC 1755
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Db 2 CAGTTCTCTCACTATCC 17

RESULT 496
AX687742/c
LOCUS AX687742 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 474 from Patent EP1281758.
ACCESSION AX687742
VERSION AX687742.1 GI:29410438
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 474 05-FEB-2003;
Aeomica, Inc. (US)
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Query Match
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QY 1740 CAACTCTCTCCCTATCC 1755
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Db 2 CAGTTCTCTCACTATCC 17

RESULT 496
AX687742/c
LOCUS AX687742 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 474 from Patent EP1281758.
ACCESSION AX687742
VERSION AX687742.1 GI:29410438
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 474 05-FEB-2003;
Aeomica, Inc. (US)
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1687 TCCTCCAGCGTGGTGG 1702
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Db 17 TCCTCCACCATGCGG 2

RESULT 497
AX687743/c
LOCUS AX687743 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 475 from Patent EP1281758.
ACCESSION AX687743
VERSION AX687743.1 GI:29410439
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KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1687 TCCTCCAGCGTGGTGG 1702
Db 16 TCCTCCACCATGCGG 1
RESULT 498
AX687812/c
LOCUS
DEFINITION Sequence 544 from Patent EP1281758. PAT 31-MAR-2003
ACCESSION AX687812
VERSION AX687812.1 GI:29410508
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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source
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1687 TCCTCCAGCGTGGTGG 1702
Db 16 TCCTCCACCATGCGG 1
RESULT 499
AX687813/c
LOCUS
DEFINITION Sequence 545 from Patent EP1281758. PAT 31-MAR-2003
ACCESSION AX687813
VERSION AX687813.1 GI:29410509
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
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Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 17 TGCTGTTCCTCTCTGC 2
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DEFINITION Sequence 583 from Patent EP1281758. PAT 31-MAR-2003
ACCESSION AX687851
VERSION AX687851.1 GI:29410549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1666 CACAGCTGGACCCCTG 1681
Db 16 CCCAGCTGGATCCCTG 1
RESULT 501
AX691734
LOCUS
DEFINITION Sequence 4466 from Patent EP1281758. PAT 31-MAR-2003
ACCESSION AX691734
VERSION AX691734.1 GI:29414675
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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source
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1666 CACAGCTGGACCCCTG 1681
Db 16 CCCAGCTGGATCCCTG 1

JOURNAL Patent: EP 1281758-A 545 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1680 TGGTGTCTCTCCAGC 1695
Db 16 TGCTGTTCCTCTCTGC 1
RESULT 500
AX687851/c
LOCUS
DEFINITION Sequence 583 from Patent EP1281758. PAT 31-MAR-2003
ACCESSION AX687851
VERSION AX687851.1 GI:29410549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1666 CACAGCTGGACCCCTG 1681
Db 16 CCCAGCTGGATCCCTG 1
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DEFINITION Sequence 4466 from Patent EP1281758. PAT 31-MAR-2003
ACCESSION AX691734
VERSION AX691734.1 GI:29414675
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1666 CACAGCTGGACCCCTG 1681
Db 16 CCCAGCTGGATCCCTG 1

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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCAGCTGGAACC 1678
Db 2 GCTCAAGCTGGGATC 17

RESULT 502
AX691735
LOCUS AX691735 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 4467 from Patent EP1281758.
ACCESSION AX691735
VERSION AX691735.1 GI:29414676
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 4467 05-FEB-2003;
mdz12
Aeomica, Inc. (US)
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Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCAGCTGGAACC 1678
Db 1 GCTCAAGCTGGGATC 16

RESULT 503
AX692741/c
LOCUS AX692741 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5473 from Patent EP1281758.
ACCESSION AX692741
VERSION AX692741.1 GI:29415699
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 5473 05-FEB-2003;
mdz12
Aeomica, Inc. (US)
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Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1716 AGTACGAGATCGAGA 1731
Db 17 AGTCAGGAGATCGAGA 2

RESULT 504
AX692741/c
LOCUS AX692741 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5473 from Patent EP1281758.
ACCESSION AX692741
VERSION AX692741.1 GI:29415699
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 5473 05-FEB-2003;
mdz12
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1716 AGTACGAGATCGAGA 1731
Db 17 AGTCAGGAGATCGAGA 2

RESULT 504
AX692741/c
LOCUS AX692741 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5473 from Patent EP1281758.
ACCESSION AX692741
VERSION AX692741.1 GI:29415700
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 5474 05-FEB-2003;
mdz12
Aeomica, Inc. (US)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1716 AGTACGAGATCGAGA 1731
Db 16 AGTCAGGAGATCGAGA 1

RESULT 505
AX723798/c
LOCUS AX723798 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1485 from Patent WO03025176.
ACCESSION AX723798
VERSION AX723798.1 GI:30503141
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apop-osis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 1485 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1697 TGCTGAAGTTGGGAT 1712
Db 17 TGCTGAAGTTGGGAT 2

RESULT 506
AX724082
LOCUS AX724082 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1769 from Patent WO03025176.
ACCESSION AX724082
VERSION AX724082.1 GI:30503425
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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JOURNAL Patent: WO 03025176-A 2961 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1752 ATCTAAAGGCCACT 1767
Db 2 ATCCCAACACCCACT 17
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/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

RESULT 507
AX724176/c
LOCUS AX724176 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1863 from Patent WO03025176.
ACCESSION AX724176
VERSION AX724176.1 GI:30503519
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 1863 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1717 GTCCGATATGGAGAT 1732
Db 17 GTCCGATATGGAGAT 2
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/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

RESULT 508
AX725274
LOCUS AX725274 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2961 from Patent WO03025176.
ACCESSION AX725274
VERSION AX725274.1 GI:30504617
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines

JOURNAL Patent: WO 03025176-A 2961 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCACAGCTG 1673
Db 2 ATCAGGCCACAGCCG 17
||||| |||||
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

RESULT 509
AX725621/c
LOCUS AX725621 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3308 from Patent WO03025176.
ACCESSION AX725621
VERSION AX725621.1 GI:30504964
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 3308 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1651 GGCAAGCACAGGCTC 1666
Db 16 GGGAAGAACCAAGGATC 1
||||| |||||
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

RESULT 510
AX726666
LOCUS AX726666 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4353 from Patent WO03025176.
ACCESSION AX726666
VERSION AX726666.1 GI:30506009
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 4353 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

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Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCAGCTGGAAC 1678
Db 1 GATCAGCTGGAAC 16

RESULT 511
AX727148/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025176-A 4835 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGGAAC 1677
Db 16 GGTAACAGCTGATC 1

RESULT 512
AX727322/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025176-A 5009 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGGAAC 1677
Db 1 GGTAACAGCTGATC 1

RESULT 513
AX727322/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025176-A 5009 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGGAAC 1677
Db 16 GGTAACAGCTGATC 1

RESULT 514
AX731553
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3187 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGACAT 1732
Db 17 GGATGGGATGGACAT 2

RESULT 515
AX731553
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3187 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1752 ATCCTAAAGGCCACT 1767
Db 2 ATCATAAAGGCCACT 17

RESULT 516
AX731661/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3187 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1752 ATCCTAAAGGCCACT 1767
Db 2 ATCATAAAGGCCACT 17

RESULT 517
AX731661/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3187 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1752 ATCCTAAAGGCCACT 1767
Db 2 ATCATAAAGGCCACT 17
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ACCESSION AX731661
VERSION AX731661.1 GI:30511004
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 3295 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1717 GTACGGAGTGGAGAT 1732
Db 17 GGAAGGAGCTGGAGAT 2
RESULT 516
AX731671/c
LOCUS AX731671 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3305 from Patent WO03025175.
ACCESSION AX731671
VERSION AX731671.1 GI:30511014
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 3305 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1717 GTACGGAGTGGAGAT 1732
Db 17 GGAAGGAGCTGGAGAT 2
RESULT 517
AX731671/c
LOCUS AX731671 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3305 from Patent WO03025175.
ACCESSION AX731671
VERSION AX731671.1 GI:30511014
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 3305 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1717 TTAGGAGTACGGAGAT 1726
Db 17 TCAGAGGCCGGAGAT 2
RESULT 517
AX732733/c
LOCUS AX732733 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4367 from Patent WO03025175.
ACCESSION AX732733
VERSION AX732733.1 GI:30512076
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 4367 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1651 GGCAAGCAGCCAGGCTC 1666
Db 16 GTCCAGCAGCAGGATC 1
RESULT 518
AX734016/c
LOCUS AX734016 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5650 from Patent WO03025175.
ACCESSION AX734016
VERSION AX734016.1 GI:30513359
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 5650 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1663 GCTCAGCTGGAGACC 1678
Db 16 GTCACACTGCTGGATC 1
RESULT 519
AX734043/c
LOCUS AX734043 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5677 from Patent WO03025175.
ACCESSION AX734043
VERSION AX734043.1 GI:30513386
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 5677 27-MAR-2003;
Molecular Engines Laboratories (FR)
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FEATURES
source
  Location/Qualifiers
  1. .17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670
Db 2 ATCAACAGGCTTACG 17

RESULT 520
AX736388/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Telerman, A., Anson, R. and Tuijinder, M.
  TITLE
    Sequences involved in phenomena of tumour suppression, tumour
    reversion, apoptosis and/or resistance to viruses and the use
    thereof as medicaments
  JOURNAL
    Patent: WO 03025177-A 1978 27-MAR-2003;
    Molecular Engines Laboratories (FR)
FEATURES
source
  1. .17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1711 TTAGGAGTATGCGAT 1726
Db 17 TTAGGAGTATGCGAT 2

RESULT 521
AX738496
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Telerman, A., Anson, R. and Tuijinder, M.
  TITLE
    Sequences involved in phenomena of tumour suppression, tumour
    reversion, apoptosis and/or resistance to viruses and the use
    thereof as medicaments
  JOURNAL
    Patent: WO 03025177-A 4086 27-MAR-2003;
    Molecular Engines Laboratories (FR)
FEATURES
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Query Match
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670
Db 2 ATCAACAGGCTTACG 17

RESULT 522
AX756774
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Telerman, A., Anson, R. and Tuijinder, M.
  TITLE
    Sequences involved in tumoral suppression, tumoral reversion,
    apoptosis and/or viral resistance phenomena and their use as
    medicines
  JOURNAL
    Patent: WO 03040369-A 95 15-MAY-2003;
    Molecular Engines Laboratories (FR)
FEATURES
source
  1. .17
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGGACC 1678
Db 1 GATCACAGCGGGAPAC 16

RESULT 523
AX757120/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Telerman, A., Anson, R. and Tuijinder, M.
  TITLE
    Sequences involved in tumoral suppression, tumoral reversion,
    apoptosis and/or viral resistance phenomena and their use as
    medicines
  JOURNAL
    Patent: WO 03040369-A 441 15-MAY-2003;
    Molecular Engines Laboratories (FR)
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Query Match
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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1711 TTAGGAGTACGGAGAT 1726
Db 17 TTAGGAGTATGCGAT 2

RESULT 524
AX757120/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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  ORGANISM
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Telerman, A., Anson, R. and Tuijinder, M.
  TITLE
    Sequences involved in tumoral suppression, tumoral reversion,
    apoptosis and/or viral resistance phenomena and their use as
    medicines
  JOURNAL
    Patent: WO 03040369-A 441 15-MAY-2003;
    Molecular Engines Laboratories (FR)
FEATURES
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1711 TTAGGAGTACGGAGAT 1726
Db 17 TTAGGAGTATGCGAT 2
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KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Telerman,A., Amson,R. and Tuijnder,M.				
TITLE	Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines				
JOURNAL	Patent: WO 03040369-A 5181 15-MAY-2003;				
FEATURES	Molecular Engines Laboratories (FR) Location/Qualifiers				
source	1..17				
Query Match	8.1%; Score 11.2; DB 1; Length 17;				
Best Local Similarity	81.2%; Pred.No. 2.9e+02;				
Matches	13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1723 AGATGGAGATTGGCTC 1738				
Db	 16 AATGGAATTGCATC 1				
RESULT 527					
AX762374					
LOCUS	AX762374 17 bp DNA linear PAT 25-JUN-2003				
DEFINITION	Sequence 5695 from Patent WO03040369.				
ACCESSION	AX762374				
VERSION	AX762374.1 GI:32256990				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Telerman,A., Amson,R. and Tuijnder,M.				
TITLE	Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines				
JOURNAL	Patent: WO 03040369-A 5695 15-MAY-2003;				
FEATURES	Molecular Engines Laboratories (FR) Location/Qualifiers				
source	1..17				
Query Match	8.1%; Score 11.2; DB 1; Length 17;				
Best Local Similarity	81.2%; Pred.No. 2.9e+02;				
Matches	13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1655 AGCACACGGCTTCACAG 1670				
Db	 2 ATCAACACGGCTTACAG 17				
RESULT 528					
AX762744/c					
LOCUS	AX762744 17 bp DNA linear PAT 25-JUN-2003				
DEFINITION	Sequence 6065 from Patent WO03040369.				
ACCESSION	AX762744				
VERSION	AX762744.1 GI:32257360				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Telerman,A., Amson,R. and Tuijnder,M.				

TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 6065 15-MAY-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1. .17
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGAGAT 1732
Db 17 GGATGGGATGGAGAT 2

RESULT 529
BD067460
LOCUS 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.
ACCESSION BD067460
VERSION BD067460.1 GI:22613063
KEYWORDS JP 2001511003-A/300.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 300 07-AUG-2001;
COMMENT RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
OS Unidentified
PN JP 2001511003-A/300
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
FH Key Location/Qualifiers
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/organism='Unidentified'.
FEATURES source
1. .17
/organism="unidentified"
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/db_xref="taxon:32644"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCACTCC 1746
Db 2 ATTGGCTCCCACTCC 17

RESULT 530
BD067531
LOCUS 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.
ACCESSION BD067531

BD067531.1 GI:22613134
JP 2001511003-A/371.
unidentified
unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 371 07-AUG-2001;
COMMENT RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
OS Unidentified
PN JP 2001511003-A/371
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
FH Key Location/Qualifiers
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/organism='Unidentified'.
FEATURES source
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/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1694 GCGTGTGGAAGTTGG 1709
Db 17 GCACGGTAGAGTTGG 2

RESULT 531
BD091426/c
LOCUS 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Nucleic acids involved in the responder phenotype and applications thereof.
ACCESSION BD091426
VERSION BD091426.1 GI:22637037
KEYWORDS JP 2001523449-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herrmann,B., Koschorz,B. and Kispert,A.
TITLE Nucleic acids involved in the responder phenotype and applications thereof
JOURNAL Patent: JP 2001523449-A 15 27-NOV-2001;
COMMENT MAX PLANCK GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN EV
OS Artificial sequence
PN JP 2001523449-A/15
PD 27-NOV-2001
PF 18-NOV-1998 JP 2000521181
PR 18-NOV-1997 EP 97120190,0.02-MAR-1998 EP 98103596.7 PI
BERNHARD HERMANN,BIRGIT KOSCHORZ,ANDREAS KISPERT PC
C12N15/09,A01K67/027,A61K31/7088,A61K38/45,A61K39/395,A61K48/PC
00,A61P15/16,
PC C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/12 PC
,C12Q1/68//A61K35/12,
PC C12P21/08,C.2N15/00,A61K37/52,C12N5/00
CC Description of Artificial Sequence: synthetic no-natural
FH Key origin
FT source Location/Qualifiers
1. .17

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AUTHORS      Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
              Nishida,M.
TITLE         Kit and method for determining HLA type
JOURNAL       Patent: WO 0192572-A 1161 06-DEC-2001;
              NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
              KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
              NISHIDA
COMMENT       OS Artificial Sequence
              PN WO 0192572-A/1161
              PD 06-DEC-2001
              PF 01-JUN-2001 WO 2001JP004662
              PR 01-JUN-2000 JP 00P 164798
              PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
              MATSUMURA,
              PC SHOGO MORIYA,MICHIO NISHIDA
              PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
              CC Description of Artificial Sequence:capture
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              /db_xref="taxon:32630"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred.No.2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1690 TCCAGCGTGGTGGAG 1705
Db 16 TCCAGCCAGGGGGAAG 1
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RESULT 532
LOCUS      BD104174
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104174
VERSION    BD104174.1 GI:22649748
KEYWORDS   WO 0192572-A/278.
SOURCE     synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
              Nishida,M.
TITLE      Kit and method for determining HLA type
JOURNAL    Patent: WO 0192572-A 278 06-DEC-2001;
              NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
              KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
              NISHIDA
COMMENT     OS Artificial Sequence
              PN WO 0192572-A/278
              PD 06-DEC-2001
              PF 01-JUN-2001 WO 2001JP004662
              PR 01-JUN-2000 JP 00P 164798
              PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
              MATSUMURA,
              PC SHOGO MORIYA,MICHIO NISHIDA
              PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
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              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred.No.2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1716 ACTACGAGATGGAGA 1731
Db 2 ACTACGGAGTGGTGA 17
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RESULT 533
LOCUS      BD105057/c
DEFINITION Kit and method for determining HLA type.
ACCESSION BD105057
VERSION    BD105057.1 GI:22650631
KEYWORDS   WO 0192572-A/1161.
SOURCE     synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 17)

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AUTHORS      Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
              Nishida,M.
TITLE         Kit and method for determining HLA type
JOURNAL       Patent: WO 0192572-A 1161 06-DEC-2001;
              NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
              KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
              NISHIDA
COMMENT       OS Artificial Sequence
              PN WO 0192572-A/1161
              PD 06-DEC-2001
              PF 01-JUN-2001 WO 2001JP004662
              PR 01-JUN-2000 JP 00P 164798
              PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
              MATSUMURA,
              PC SHOGO MORIYA,MICHIO NISHIDA
              PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
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              /db_xref="taxon:32630"
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred.No.2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1734 GGCTCCCAACTCCTCC 1749
Db 17 GGCTCTCCACTGCTCC 2
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RESULT 534
LOCUS      BD137018
DEFINITION GFR alpha 3 and its uses.
ACCESSION BD137018
VERSION    BD137018.1 GI:23231963
KEYWORDS   JP 2002507421-A/15.
SOURCE     synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Sauvage,F.J.D., Klein,R.D., Phillips,H.S. and Rosenthal,A.
TITLE      GFR alpha 3 and its uses
JOURNAL    Patent: JP 2002507421-A 15 12-MAR-2002;
              GENENTECH INC
COMMENT     OS Artificial Sequence
              PN JP 2002507421-A/15
              PD 12-MAR-2002
              PF 19-MAR-1999 JP 2000538000
              PR 23-MAR-1998 US 60/079124,13-APR-1998 US 60/081569 PI
              FREDERIC J DE SAUVAGE,ROBERT D KLEIN,HEIDI S PHILLIPS,ARNON PI
              ROSENTHAL
              PC C12N15/09,A61K39/395,A61K45/00,A61P1/02,A61P1/10,A61P11/06, PC
              A61P17/02,
              PC A61P25/02,A61P25/06,A61P27/02,C07K14/71,C07K16/28,C07K19/00,
              PC C12N1/19,
              PC C12N1/21,C12N5/10,C12Q1/42,G01N33/68,C12N15/00,C12N5/00 CC
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Query Match 8.1%; Score 11.2; DB 1; Length 17;

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Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1739 CCAACTCTCCCTATC 1754
Db 2 CCCAGTCTCCCTACC 17

RESULT 535
BD198908
LOCUS
DEFINITION Method and reagent for treating diseases or conditions concerning
ACCESSION BD198908
VERSION BD198908.1 GI:33008678
KEYWORDS JP 2002509721-A/1934.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
Patent: JP 2002509721-A 1934 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/1934
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES
source
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1685 TCTCTCCAGCGTGGT 1700
Db 16 TCTCATTAAGCGTGGT 1

RESULT 537
BD200826/c
LOCUS
DEFINITION Method and reagent for treating diseases or conditions concerning
ACCESSION BD200826
VERSION BD200826.1 GI:33010596
KEYWORDS JP 2002509721-A/3852.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
Patent: JP 2002509721-A 3852 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/3852
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES
source
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1665 TCACGCTGGAACCT 1680
Db 1 TCACGCTGGAACCT 16

RESULT 536
BD199121/c
LOCUS
DEFINITION Method and reagent for treating diseases or conditions concerning
ACCESSION BD199121
VERSION BD199121.1 GI:33008891
KEYWORDS JP 2002509721-A/2147.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
Patent: JP 2002509721-A 2147 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/2147
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.

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TITLE
JOURNAL
COMMENT
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
Patent: JP 2003509721-A 2147 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/2147
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES
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Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1685 TCTCTCCAGCGTGGT 1700
Db 16 TCTCATTAAGCGTGGT 1

RESULT 537
BD200826/c
LOCUS
DEFINITION Method and reagent for treating diseases or conditions concerning
ACCESSION BD200826
VERSION BD200826.1 GI:33010596
KEYWORDS JP 2002509721-A/3852.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
Patent: JP 2002509721-A 3852 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/3852
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
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/organism='Homo sapiens (human)'.

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        /organism="Homo sapiens"
        /mol_type="genomic RNA"
        /db_xref="taxon:9606"

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  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1704 AGTTGGGTTAGGAGTA 1719
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Db 17 AGCGGGTTACAGTA 2

RESULT 538
BD223385 17 bp DNA linear PAT 17-JUL-2003
LOCUS BD223385 Nucleic acid encoding rat agouti related protein.
ACCESSION BD223385
VERSION BD223385.1 GI:33033155
KEYWORDS JP 2002512786-A/5.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Der, L.H.T.V., Guan, X., Yu, H. and Trivedi, P.G.
TITLE Nucleic acid encoding rat agouti related protein
JOURNAL Patent: JP 2002512786-A 5 08-MAY-2002;
MERCK AND CO INC
COMMENT OS Unidentified
PN JP 2002512786-A/5
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545978
PR 29-APR-1998 US 60/083549
PI LEONARDUS H T VAN DER PLOEG, XIOMING GUAN, HONG YU, PRASHANT G
PT TRIVEDI
PC C12Q1/68, C07K5/00, C07K14/47, C12N1/15, C12N1/19, C12N1/21, C12N5/
PC 10, C12N15/09,
PC C12P21/02
CC PCR primer
FH Key
FT source
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      /organism="Unidentified".

FEATURES
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        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match
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  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1656 GCACACGGCTCACAGC 1671
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Db 1 GCACATGGGTCACAGC 16

RESULT 539
AR106914/C 18 bp DNA linear PAT 14-FEB-2001
LOCUS AR106914 Sequence 75 from patent US 6107092.
ACCESSION AR106914
VERSION AR106914.1 GI:12821444
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cowsett, L.M., Bennett, C.Frank, and O'Malley, B.W.
TITLE Antisense modulation of SRA expression
JOURNAL Patent: US 6107092-A 75 22-AUG-2000;

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Query Match
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  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCACAGCTG 1673
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Db 16 ACCAGGCTTCCAGCAG 1

RESULT 540
AR381288/C 20 bp DNA linear PAT 18-DEC-2003
LOCUS AR381288 Sequence 19 from patent US 6607915.
ACCESSION AR381288
VERSION AR381288.1 GI:40089107
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P. and Wanciewicz, E.
TITLE Antisense inhibition of E2A-Pbx1 expression
JOURNAL Patent: US 6607915-A 19 19-AUG-2003;
JOURNAL Location/Qualifiers
FEATURES
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        /mol_type="genomic DNA"

Query Match
  Best Local Similarity 8.1%; Score 11.2; DB 1; Length 20;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAACTCTGGT 1693
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Db 16 CAGCTGTCAGCTGCT 1

RESULT 541
AX623106 11 bp DNA linear PAT 21-FEB-2003
LOCUS AX623106 Sequence 147 from Patent WO02053774.
ACCESSION AX623106
VERSION AX623106.1 GI:28451047
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn, D., Conradt, M. and Hofmann, K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 147 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
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        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 7.9%; Score 11; DB 1; Length 11;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1681 GGTGTCTCTC 1691
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Db 1 GGTGTCTCTC 11

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RESULT 542
AX630527
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7568 from Patent WO02053774.
ACCESSION  AX630527
VERSION     AX630527.1 GI:28458565
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 7568 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Query Match      7.9%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1681 GGTGTCCTCTC 1691
Db      1 GGTGTCCTCTC 11

RESULT 543
AL5061/c
LOCUS      15 bp      DNA      linear      PAT 07-FEB-1994
DEFINITION oligonucleotide.
ACCESSION  AL5061
VERSION     AL5061.1 GI:492828
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Roskam,W. and Ferrara,P.
TITLE      Non-amidated derivatives of somatotroline and process for the
           preparation by genetic engineering
JOURNAL    Patent: EP 0206863-A 2 30-DEC-1986;
           SANOFI S.A.
FEATURES   Location/Qualifiers
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Query Match      7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1666 CACAGCTGGAA 1676
Db      13 CACAGCTGGAA 3

RESULT 544
BD251646/c
LOCUS      15 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Selection of animal based on character imprinted by parent.
ACCESSION  BD251646
VERSION     BD251646.1 GI:33061416
KEYWORDS   JP 2002535963-A/166.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
REFERENCE  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

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REFERENCE 1 (bases 1 to 15)
AUTHORS    Andersson,L., Georges,M., Spincemaille,G. and Nezer,C.D.A.
TITLE      Selection of animal based on character imprinted by parent
JOURNAL    Patent: JP 2002535963-A 166 29-OCT-2002;
           UNIVERSITY OF L'EGE,MELICA HB,SEGHERS GENTEC NV
COMMENT    OS Sus scrofa (pig)
           PN JP 2002535963-A/166
           PD 29-OCT-2002
           PF 16-DEC-1999 JP 2000589390
           PI 16-DEC-1998 EP 98204291.3
           PI LEIF ANDERSSON,MICHEL GEORGES,GEERT SPINCEMAILLE, PI CARINE
           DANIELLE ANDREE NEZER
           PC C12N15/09,A01K67/027,C12N5/06,C12Q1/68,C12N15/00,C12N5/00 CC
           /note='Polymorphism Insulin-IGF2'
           FH Key Location/Qualifiers
           FT source 1..15
           FT /organism='Sus scrofa (pig)'.
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Query Match      7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1631 GGATGGGCTT 1641
Db      12 GGATGGGCTT 2

RESULT 545
AR180150
LOCUS      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 218 from patent US 6333152.
ACCESSION  AR180150
VERSION     AR180150.1 GI:20222183
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE      Gene expression profiles in normal and cancer cells
JOURNAL    Patent: US 6333152-A 218 25-DEC-2001;
           Location/Qualifiers
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Query Match      7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1672 TGGAACTCTGG 1682
Db      3 TGGAACTCTGG 13

RESULT 546
AR180787
LOCUS      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 855 from patent US 6333152.
ACCESSION  AR180787
VERSION     AR180787.1 GI:20222820
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE      Gene expression profiles in normal and cancer cells

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JOURNAL Patent: US 633152-A 855 25-DEC-2001;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 TGAACCTGG 1682
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Db 3 TGAACCTGG 13

RESULT 547
AX028347/C
LOCUS AX028347 15 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 166 from Patent WO0036143.
ACCESSION AX028347
VERSION AX028347.1 GI:10189560
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
JOURNAL Georges, M., Spincemaille, G. and Andersson, L.
SELECTING animals for parentally imprinted traits
PATENT: WO 0036143-A 166 22-JUN-2000;
SEGHERSGENTEC N V (BE) ; GEORGES MICHEL (BE) ; UNIV LIEGE (BE) ;
SPINCEMAILLE GEERT (BE) ; MELICA HB (SE) ; ANDERSSON LEIF (SE)
FEATURES Location/Qualifiers
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/db_xref="taxon:9823"
/note="Polymorphism Insulin-IGF2"

Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1631 GGATGGGCTT 1641
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Db 12 GGATGGGCTT 2

RESULT 548
AR008042
LOCUS AR008042 16 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5753431.
ACCESSION AR008042
VERSION AR008042.1 GI:3967151
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Chiang, J. Young-Ling.
TITLE Cholesterol 7.alpha.-hydroxylase gene regulatory elements and
transcription factors
JOURNAL Patent: US 5753431-A 2 19-MAY-1998;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 7.9%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1740 CAACTCCTCCC 1750
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Db 1 CAACTCCTCCC 11

RESULT 549
AR029494
LOCUS AR029494 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5859334.
ACCESSION AR029494
VERSION AR029494.1 GI:5941467
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Brugliera, F. and Holton, T. Albert.
TITLE Generic sequences encoding glycosyltransferase enzymes and uses
therefor
JOURNAL Patent: US 5859334-A 6 12-JAN-1999;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 7.9%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1683 TGTCTCCTCCA 1693
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Db 2 TGTCTCCTCCA 12

RESULT 550
AR110507
LOCUS AR110507 16 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 16 from patent US 6114598.
ACCESSION AR110507
VERSION AR110507.1 GI:12826783
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kucherlapati, R., Jakobovits, A., Kalpholz, S., Brenner, D. G. and
Capon, D. J.
TITLE Generation of xenogeneic antibodies
JOURNAL Patent: US 6114598-A 16 05-SEP-2000;
FEATURES Location/Qualifiers
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QY 1669 AGCTGGAACCC 1679
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Db 1 AGCTGGAACCC 11

RESULT 551
AR137060
LOCUS AR137060 16 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 16 from patent US 6162963.
ACCESSION AR137060
VERSION AR137060.1 GI:14478310
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
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AUTHORS Kucherlapati,R., Jakobovits,A., Klapholz,S., Brenner,D.G. and Capon,D.J.
 TITLE Generation of Xenogenetic antibodies
 JOURNAL Patent: US 6162963-A 16 19-DEC-2000;
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 Qy 1669 AGCTGGAACCC 1679
 Db 1 AGCTGGAACCC 11

RESULT 552
 LOCUS 126587
 DEFINITION Sequence 2 from patent US 5558999.
 ACCESSION 126587
 VERSION 126587.1 GI:1606457
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Chiang,J.Y.L.
 TITLE Cholesterol 7.alpha.-hydroxylase gene regulatory elements and methods for using them
 JOURNAL Patent: US 5558999-A 2 24-SEP-1996;
 FEATURES Location/Qualifiers
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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1740 CAACTCTCTCC 1750
 Db 1 CAACTCTCTCC 11

RESULT 553
 AX349231/c
 LOCUS AX349231
 DEFINITION Sequence 15 from Patent WO202810.
 ACCESSION AX349231
 VERSION AX349231.1 GI:18615263
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Bickel,R., Ehrlich,R., Ellinger,T., Ermantraut,E., Kaiser,T., Schulz,T. and Wagner,G.
 TITLE Method for qualitative and/or quantitative detecting of molecular interactions on probe arrays
 JOURNAL Patent: WO 0202810-A 15 10-JAN-2002;
 FEATURES Clondlag Chip Technologies GmbH (DE)
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 1. .16
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Oligonukleotidsonde"

Query Match 7.9%; Score 11; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1753 TCCTAAGGCC 1763
 Db 13 TCCTAAGGCC 3

RESULT 554
 A64216
 LOCUS A64216
 DEFINITION Sequence 4 from Patent WO9727332.
 ACCESSION A64216
 VERSION A64216.1 GI:377647
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1
 AUTHORS Stuyver,L., Louvagie,J. and Rosau,R.
 TITLE METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE TRANSCRIPTASE GENE
 JOURNAL Patent: WO 9727332-A 4 31-JUL-1997;
 COMMENT INNOGENETICS NV (BE)
 FEATURES Other publication AU 1444397 19970820.
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 1. .14
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"
 Query Match 7.8%; Score 10.8; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1718 TACGAGATGGAGA 1731
 Db 1 TACAGAGATGGA 14

RESULT 555
 A8858/c
 LOCUS A8858
 DEFINITION Sequence 1006 from Patent WO9833904.
 ACCESSION A8858
 VERSION A8858.1 GI:6737428
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Brysch,W. and Schlingensiepen,K.
 TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 JOURNAL Patent: WO 9833904-A 1006 06-AUG-1998;
 FEATURES BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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 /organism="unidentified"
 /mol_type="unassigned DNA"
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 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1726 TGGAGATTGGCTCC 1739
 Db 14 TGGAGATAGACTCC 1

RESULT 556
 AR029990
 LOCUS AR029990
 DEFINITION Sequence 179 from patent US 5861244.
 linear 14 bp DNA
 PAT 29-SEP-1999

Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1726 TGGAGATTGGCTCC 1739
Db 14 TGGAGATAGACTCC 1

RESULT 561
A42347
LOCUS A42347 15 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 7 from Patent WO9501363.
ACCESSION A42347
VERSION A42347.1 GI:2297823
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Uhlmann,E. and Meier,C.
TITLE METHYLPHOSPHONIC ACID ESTER, PROCESS FOR PREPARING THE SAME AND ITS
JOURNAL US
COMMENT Patent: WO 9501363-A 7 12-JAN-1995;
HOECHST AG (DE)
Other publication FI 956341 960219
Other publication CA 2165971 950112
Other publication NO 955352 960214
Other publication AU 7073594 950124
Other publication DE 4321946 950112.
Other publication Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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/note="C-HA-RAS"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCCCTG 1681
Db 1 CAGCTGCAACCCAG 14

RESULT 562
A44378
LOCUS A44378 15 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 8 from Patent EP0653439.
ACCESSION A44378
VERSION A44378.1 GI:2299207
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Peyman,A.D., Uhlmann,E.D., Mag,M., Kretschmar,G.D., Helsing,M.D.
JOURNAL and Winkler,I.D.
COMMENT Stabilized oligonucleotids and the use thereof
Patent: EP 0653439-A 8 17-MAY-1995;
HOECHST AG (DE)
Other publication JP 7194385 950801
Other publication CA 2135591 950513
Other publication AU 7779994 950518
Other publication DE 4338704 950518.
Other publication Location/Qualifiers
FEATURES
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/note="C-HA-RAS"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCCCTG 1681
Db 1 CAGCTGCAACCCAG 14

RESULT 563
A47165
LOCUS A47165 15 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 8 from Patent EP0680969.
ACCESSION A47165
VERSION A47165.1 GI:2301207
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Seela,F.P. and Lampe,S.D.
JOURNAL Modified oligonucleotides, their preparation and their use
COMMENT Patent: EP 0680969-A 8 08-NOV-1995;
HOECHST AG (DE)
Other publication JP 8003186 960109
Other publication AU 1778295 951109
Other publication DE 4415370 951109.
Other publication Location/Qualifiers
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source 1..15
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/note="C-HA-RAS"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCCCTG 1681
Db 1 CAGCTGCAACCCAG 14

RESULT 564
A56641
LOCUS A56641 15 bp DNA linear PAT 03-MAR-1998
DEFINITION Sequence 8 from Patent EP0739898.
ACCESSION A56641
VERSION A56641.1 GI:3712686
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Peyman,A.D., Uhlmann,E.D., Breipohl,G.D. and Wallmeier,H.D.
TITLE Phosphonomonoester nucleic acids, methods for their preparation and
JOURNAL their use
COMMENT Patent: EP 0739898-A 8 30-OCT-1996;
HOECHST AG (DE)
Other publication CZ 9600743 961016
Other publication CN 1138588 961225
Other publication PL 313207 960916
Other publication JP 8259579 961008
Other publication NO 961006 960916
Other publication CA 2171589 960914
Other publication AU 4802896 960926
Other publication DE 19508923 960919.
Other publication Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAACCGTG 1691
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Db 1 CAGCTGCAACCCAG 14

RESULT 565
LOCUS A80362 15 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 8 from Patent EP0726274.
ACCESSION A80362
VERSION A80362.1 GI:6093089
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Peyman,A.D. and Uhlmann,E.D.
TITLE G-CAP STABILIZED OLIGONUCLEOTIDES
JOURNAL
PATENT: EP 0726274-A 8 14-AUG-1996;
HOECHST AG (DE)
FEATURES
Location/Qualifiers
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAACCGTG 1691
||||| |||||
Db 1 CAGCTGCAACCCAG 14

RESULT 566
LOCUS A88333 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 481 from Patent WO9833904.
ACCESSION A88333
VERSION A88333.1 GI:6736903
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL
PATENT: WO 9833904-A 481 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
Location/Qualifiers
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTGG 1699
||||| |||||
Db 14 CTCCTCCAGCATGG 1

RESULT 569
LOCUS AR041808 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 598 from patent US 5811300.
ACCESSION AR041808
VERSION AR041808.1 GI:5962304
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
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RESULT 567
LOCUS A89423 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1571 from Patent WO9833904.
ACCESSION A89423
VERSION A89423.1 GI:6737993
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL
PATENT: WO 9833904-A 1571 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
Location/Qualifiers
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/organism="unidentified"
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Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1753 TCCTAAAGGCCAC 1766
||||| |||||
Db 14 TCCGAAAGGTCCAC 1

RESULT 568
LOCUS A90300 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 481 from Patent EP0856579.
ACCESSION A90300
VERSION A90300.1 GI:6738814
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL
PATENT: EP 0856579-A 481 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
Location/Qualifiers
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTGG 1699
||||| |||||
Db 14 CTCCTCCAGCATGG 1

RESULT 569
LOCUS AR041808 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 598 from patent US 5811300.
ACCESSION AR041808
VERSION AR041808.1 GI:5962304
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
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TITLE      TNF- $\alpha$  ribozymes
JOURNAL    Patent: US 5811300-A 598 22-SEP-1998;
FEATURES   Location/Qualifiers
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           /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1708 GGGTTAGGAGTACG 1721
      |||||
Db 15 GGGTGAGGAGCAG 2

RESULT 570
AR041809/c
LOCUS      AR041809      15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 599 from patent US 5811300.
ACCESSION AR041809
VERSION    AR041809.1 GI:5962305
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
TITLE     TNF- $\alpha$  ribozymes
JOURNAL   Patent: US 5811300-A 599 22-SEP-1998;
FEATURES   Location/Qualifiers
           source
           1..15
           /organism="unknown"
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Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1708 GGGTTAGGAGTACG 1721
      |||||
Db 15 GGGTGAGGAGCAG 2

RESULT 571
AR073553
LOCUS      AR073553      15 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 18 from patent US 5952011.
ACCESSION AR073553
VERSION    AR073553.1 GI:10000317
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   O'Hara,P.J., Grant,F.J. and Sheppard,P.O.
TITLE     Human transglutaminases
JOURNAL   Patent: US 5952011-A 18 14-SEP-1999;
FEATURES   Location/Qualifiers
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           1..15
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1663 GCTCAGCTGGAA 1676
      |||||
Db 1 GCGCTCAGCTGGAA 14

RESULT 572
AR111765
LOCUS      AR111765      15 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 8 from patent US 6127346.
ACCESSION AR111765
VERSION    AR111765.1 GI:12828613
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Peyman,A., Uhlmann,E., Breipohl,G. and Wallmeier,H.
TITLE     Phosphonomonoester nucleic acids process for their preparation and
           their use
JOURNAL   Patent: US 6127346-A 8 03-OCT-2000;
FEATURES   Location/Qualifiers
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           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCTC 1681
      |||||
Db 1 CAGCTGCAACCCAG 14

RESULT 573
AR133622
LOCUS      AR133622      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 2047 from patent US 6194150.
ACCESSION AR133622
VERSION    AR133622.1 GI:14122527
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE     Nucleic acid based inhibition of CD40
JOURNAL   Patent: US 6194150-A 2047 27-FEB-2001;
FEATURES   Location/Qualifiers
           source
           1..15
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 CCTGGTGTCCTC 1691
      |||||
Db 2 CCTGGTCTCACCTC 15

RESULT 574
I20495
LOCUS      I20495      15 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 18 from patent US 5514579.
ACCESSION I20495
VERSION    I20495.1 GI:16C0850
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   O'Hara,P.J., Grant,F.J. and Sheppard,P.O.
TITLE     Human transglutaminases
JOURNAL   Patent: US 5514579-A 18 07-MAY-1996;
FEATURES   Location/Qualifiers
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           1..15
           /organism="unknown"
           /mol_type="unassigned DNA"

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/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1663 GCTCAGCTGGAA 1676
||| |||||
Db 1 GCGCTCAGCTGGAA 14

RESULT 575
LOCUS I33987 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5594121.
ACCESSION I33987
VERSION I33987.1 GI:1824778
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Froehler,B. and Matteucci,M.
TITLE Enhanced triple-helix and double-helix formation with oligomers
JOURNAL Patent: US 5594121-A 1 14-JAN-1997;
FEATURES Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1743 CTCCTCCCTATCCT 1756
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Db 14 CTCCTCCCTTCTCCT 1

RESULT 576
LOCUS I33988 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5594121.
ACCESSION I33988
VERSION I33988.1 GI:1824779
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Froehler,B. and Matteucci,M.
TITLE Enhanced triple-helix and double-helix formation with oligomers
JOURNAL Patent: US 5594121-A 2 14-JAN-1997;
FEATURES Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1743 CTCCTCCCTATCCT 1756
||| |||||
Db 2 CTCCTCCCTTCTCCT 15

RESULT 577
LOCUS I84720 15 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 8 from patent US 5696248.

ACCESSION I84720 GI:3022240
VERSION I84720.1
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Peyman,A., Uhlmann,E. and Carolus,C.
TITLE 3'-modified oligonucleotide derivatives
JOURNAL Patent: US 5696248-A 8 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAACCTG 1681
||| |||||
Db 1 CAGCTGCAACCCAG 14

RESULT 578
LOCUS AR179805 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 8 from patent US 6326487.
ACCESSION AR179805
VERSION AR179805.1 GI:20221360
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Peyman,A., Uhlmann,E. and Carolus,C.
TITLE 3 modified oligonucleotide derivatives
JOURNAL Patent: US 6326487-A 8 04-DEC-2001;
FEATURES Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAACCTG 1681
||| |||||
Db 1 CAGCTGCAACCCAG 14

RESULT 579
LOCUS AR193504 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 8 from patent US 6348312.
ACCESSION AR193504
VERSION AR193504.1 GI:20240096
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Peyman,A., Uhlmann,E., Mag,M., Kretschmar,G., Helsberg,M. and Winkler,I.
TITLE Stabilized oligonucleotides and their use
JOURNAL Patent: US 6348312-A 8 19-FEB-2002;
FEATURES Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
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Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTG 1681
Db 1 CAGCTGCAACCCAG 14

RESULT 580
LOCUS AR254155 15 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 7 from patent US 6479651.
ACCESSION AR254155
VERSION AR254155.1 GI:27302892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Seela,F. and Thomas,H.
TITLE Modified oligonucleotides, their preparation and their use
JOURNAL Patent: US 6479651-A 7 12-NOV-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTG 1681
Db 1 CAGCTGCAACCCAG 14

RESULT 581
LOCUS AX081337 15 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 16 from Patent WO0108707.
ACCESSION AX081337
VERSION AX081337.1 GI:13170179
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.
TITLE Conjugates and methods for the production thereof, and their use
for transporting molecules via biological membranes
JOURNAL Patent: WO 0108707-A 16 08-FEB-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
source
1..15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTG 1681
Db 1 CAGCTGCAACCCAG 14

RESULT 582
LOCUS AX283167 15 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 5 from Patent WO0179216.
ACCESSION AX283167

Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTG 1681
Db 1 CAGCTGCAACCCAG 14

RESULT 583
LOCUS AX283281 15 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 45 from Patent WO0179249.
ACCESSION AX283281
VERSION AX283281.1 GI:17044162
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
producing the same
JOURNAL Patent: WO 0179249-A 45 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Oligonukleotide"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTG 1681
Db 1 CAGCTGCAACCCAG 14

RESULT 584
LOCUS AX637264/c 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 4403 from Patent EP1260586.
ACCESSION AX637264
VERSION AX637264.1 GI:28472878
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,

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VERSION AX283167.1 GI:17044048
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
producing them
JOURNAL Patent: WO 0179216-A 5 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Oligonukleotide"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTG 1681
Db 1 CAGCTGCAACCCAG 14

RESULT 583
LOCUS AX283281 15 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 45 from Patent WO0179249.
ACCESSION AX283281
VERSION AX283281.1 GI:17044162
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
producing the same
JOURNAL Patent: WO 0179249-A 45 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz:
Oligonukleotide"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTG 1681
Db 1 CAGCTGCAACCCAG 14

RESULT 584
LOCUS AX637264/c 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 4403 from Patent EP1260586.
ACCESSION AX637264
VERSION AX637264.1 GI:28472878
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,

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Karpeisky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J., McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, D.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 4403 27-NOV-2002;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)
 source Location/Qualifiers
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 /organism="unidentified"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1708 GGGTTAGGAGTACG 1721
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Db 15 GGGTGAGGAGCAG 2

RESULT 585
AX637266/c
LOCUS AX637266 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 4405 from Patent EP1260586.
ACCESSION AX637266
VERSION AX637266.1 GI:28472880
KEYWORDS unidentified
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1
AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Drenzo, A., Karpeisky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J., McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, D.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 4405 27-NOV-2002;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)
 source Location/Qualifiers
 1. .15
 /organism="unidentified"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1708 GGGTTAGGAGTACG 1721
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Db 15 GGGTGAGGAGCAG 2

RESULT 586
AX742553/c
LOCUS AX742553 15 bp DNA linear PAT 12-MAY-2003
DEFINITION Sequence 356 from Patent EP1302550.
ACCESSION AX742553
VERSION AX742553.1 GI:30576521
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Lin, C.Y., Lin, R.W., You, C.M., Huang, H.H., Lee, B.H., Lee, H.H., Lin, Y.J., Fan, C.C., Hsu, H.C., Shih, C.W., Yeh, C.H., Kao, Y.F., Pan, C.L. and Chan, P.
TITLE Method and detector for identifying subtypes of human papilloma

viruses
JOURNAL Patent: EP 1302550-A 356 16-APR-2003;
FEATURES King Car Food Industrial Co., Ltd. (TW)
 source Location/Qualifiers
 1. .15
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Oligonucleotide for Identifying HPV 61"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1635 GGGGCTTGATGACG 1648
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Db 14 GGGGATGTAGCAG 1

RESULT 597
BD065846/c
LOCUS BD065846 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065846
VERSION BD065846.1 GI:22611449
KEYWORDS JP 2001511000-A/481.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlengersiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 481 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
 OS Unknown
 PN JP 2001511000-A/481
 PD 07-AUG-2001
 PF 30-JAN-1998 JP 1998532533
 PI 31-JAN-1997 EP 97101531.8
 PR KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
 PC C12N15/11.C07H21/04.A61K31/70
 CC An antisense oligonucleotide preparation method FH Key
 Location/Qualifiers
 FT source 1. .15
 /organism="Unknown".
FEATURES Location/Qualifiers
 source 1. .15
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1686 CTCCTCCAGCGTGG 1699
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Db 14 CTTCTCCAGCATGG 1

RESULT 588
BD066936/c
LOCUS BD066936 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066936
VERSION BD066936.1 GI:22612539
KEYWORDS JP 2001511000-A/1571.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlengersiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method

Qy	1635	GGGCTTGTAGCAG	1648
Db	14	GGGGATGTAGCAG	1

RESULT 590

AR057424 LOCUS AR057424 16 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 1628 from patent US 5837542.

ACCESSION AR057424

VERSION AR057424.1 GI:5983001

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.

TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes

JOURNAL Patent: US 5837542-A 1628 17-NOV-1998;

FEATURES Location/Qualifiers

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/organism="unknown"

/mol_type="unassigned DNA"

Query Match 7.8%; Score 10.8; DB 1; Length 16;

Best Local Similarity 85.7%; Pred. No. 3.2e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1689 CTCACGCGTGTC 1702

Db 1 CTACAGCGTGTC 14

RESULT 591

AR115182 LOCUS AR115182 16 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 1628 from patent US 6132967.

ACCESSION AR115182

VERSION AR115182.1 GI:14095504

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.

TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)

JOURNAL Patent: US 6132967-A 1628 17-OCT-2000;

FEATURES Location/Qualifiers

source 1..16

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 7.8%; Score 10.8; DB 1; Length 16;

Best Local Similarity 85.7%; Pred. No. 3.2e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1689 CTCACGCGTGTC 1702

Db 1 CTACAGCGTGTC 14

RESULT 592

BD233053 LOCUS BD233053 16 bp DNA linear PAT 17-JUL-2003

DEFINITION Method of detecting mutation selected by drug in HIV protease gene.

ACCESSION BD233053

VERSION BD233053.1 GI:23042823

KEYWORDS JP 2002518065-A/149.

SOURCE Aids-associated retrovirus

ORGANISM Aids-associated retrovirus

Viruses; Retrovird viruses; Retroviridae.
1 (bases 1 to 16)
Stuyver, L.
Method of detecting mutation selected by drug in HIV protease gene
Patent: JP 2002518065-A 149 25-JUN-2002;
INNOGENETICS NV
OS Aids-associated retrovirus
PN JP 2002518065-A/149
PD 25-JUN-2002
PR 22-JUN-1999 JP 2000556068
PF 24-JUN-1998 EP 98870143.9
PI LIEVEN STUYVER
PC C12N15/09, C12Q1/68, C12Q1/70, C12N15/00
CC Method of detecting mutation selected by drug in HIV protease
gene
FH Key Location/Qualifiers
FT source 1..16
FT Location/Qualifiers
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source
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/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"
Query Match 7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1721 GGAGTGGAGATTG 1734
|||||
Db 3 GGAGTTGGAGGTTG 16
RESULT 593
E39140
LOCUS Improved PCR method for primer elongation pre-amplification.
DEFINITION E39140 16 bp DNA linear PAT 18-JUN-2001
ACCESSION E39140
VERSION E39140.1 GI:13017702
KEYWORDS JP 1999318498-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Urufuganku, D. and Joseph, R.
TITLE Improved PCR method for primer elongation pre-amplification
JOURNAL Patent: JP 1999318498-A 6 24-NOV-1999;
COMMENT OS Artificial Sequence
PN JP 1999318498-A/6
PD 24-NOV-1999
PF 26-MAR-1999 JP 1999084967
PR 26-MAR-1998 DE 19813317:0
PI URUFUGANKU DIETOMATYA, JOSEPH RUSSHOFU
PC C12Q1/68, C12N15/09, C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..16
FT Location/Qualifiers
FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1713 AGGAGTACGAGAT 1726
|||||
Db 2 AGCAGTAAGGAGAT 15

RESULT 594
I50741/c
LOCUS Sequence 23 from patent US 5643724.
DEFINITION I50741 16 bp DNA linear PAT 07-OCT-1997
ACCESSION I50741
VERSION I50741.1 GI:2472444
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Fildes, N. Jane, and Reynolds, R. Lynne.
TITLE Methods and reagents for Glycophorin A typing
JOURNAL Patent: US 5643724-A 23 01-JUL-1997;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1672 TGGAACCTCGGTGT 1685
|||||
Db 15 TGGAGAGCTTGTGT 2
RESULT 595
AR203385
LOCUS Sequence 6 from patent US 6365375.
DEFINITION AR203385 16 bp DNA linear PAT 20-JUN-2002
ACCESSION AR203385
VERSION AR203385.1 GI:21499760
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Dietmaier, W. and Ruschoff, J.
TITLE Method of primer-extension preamplification PCR
JOURNAL Patent: US 6365375-A 6 02-APR-2002;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1713 AGGAGTACGAGAT 1726
|||||
Db 2 AGCAGTAAGGAGAT 15
RESULT 596
AR328401
LOCUS Sequence 5803 from patent US 6566127.
DEFINITION AR328401 16 bp RNA linear PAT 17-AUG-2003
ACCESSION AR328401
VERSION AR328401.1 GI:33714209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco, P., McSwiggen, J. A., Stinchcomb, D. T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 5803 20-MAY-2003;
FEATURES Location/Qualifiers

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source      1..16
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
Best Local Similarity  7.8%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1746 CTCCTTATCCTTAA 1759
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Db 1 CTCCTTATCGAAA 14

RESULT 597
AR328478
LOCUS      AR328478          16 bp      RNA          linear      PAT 17-AUG-2003
DEFINITION Sequence 5880 from patent US 6566127.
ACCESSION  AR328478
VERSION     AR328478.1 GI:33714286
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 5880 20-MAY-2003;
FEATURES    Location/Qualifiers
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Query Match
Best Local Similarity  7.8%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1738 CCCACTCTCTCCT 1751
    |||||
Db 1 CTCACCTCTGCCT 14

RESULT 598
AR328510/c
LOCUS      AR328510          16 bp      RNA          linear      PAT 17-AUG-2003
DEFINITION Sequence 5912 from patent US 6566127.
ACCESSION  AR328510
VERSION     AR328510.1 GI:33714318
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 5912 20-MAY-2003;
FEATURES    Location/Qualifiers
            source
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            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
Best Local Similarity  7.8%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1692 CAGCGTGGTGAG 1705
    |||||
Db 14 CAGCGTGGTCGAG 14

RESULT 599
AX007607
LOCUS      AX007607          16 bp      DNA          linear      PAT 06-SEP-2000
DEFINITION Sequence 149 from Patent WO9967428.
ACCESSION  AX007607
VERSION     AX007607.1 GI:9995304
KEYWORDS    Aids-associated retrovirus
SOURCE      Aids-associated retrovirus
ORGANISM    Viruses; Retrovirdae; Retroviridae.
REFERENCE 1
AUTHORS     Stuyver,L.
TITLE       Method for detection of drug-selected mutations in the hiv protease
           gene
JOURNAL    Patent: WO 9967428-A 149 29-DEC-1999;
           INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES    Location/Qualifiers
            source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:11966"

Query Match
Best Local Similarity  7.8%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTG 1734
    |||||
Db 3 GGAGTTGGAGGTTC 16

RESULT 600
AX011283
LOCUS      AX011283          16 bp      DNA          linear      PAT 06-SEP-2000
DEFINITION Sequence 6 from Patent EP0957177.
ACCESSION  AX011283
VERSION     AX011283.1 GI:5997834
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE 1
AUTHORS     Dietmaier,W.D. and Rueschoff,J.P.
TITLE       Improved method for primer extension preamplification-pcr
JOURNAL    Patent: EP 0957177-A 6 17-NOV-1999;
           ROCHE DIAGNOSTICS GMBH (DE)
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity  7.8%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1713 AGGAGTACGAGAT 1726
    |||||
Db 2 AGCAGTAGGAGAT 15

RESULT 601
AX384636
LOCUS      AX384636          16 bp      DNA          linear      PAT 19-MAR-2002
DEFINITION Sequence 8 from Patent EP1182206.
ACCESSION  AX384636
VERSION     AX384636.1 GI:19577831
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE 1
AUTHORS     Peymann,A., Uhlmann,E., Mag,M., Kretschmar,G., Helsberg,M. and
           Winkler,I.

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TITLE      Stabilized oligonucleotids and the use thereof
JOURNAL    Patent: EP 1182206-A 8 27-FEB-2002;
           HOECHST AKTIENGESELLSCHAFT (DE)
FEATURES   Location/Qualifiers
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Antisense Oligonucleotide"

Query Match      7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1668 CAGCTGGAACCTG 1681
       1 CAGCTGCACCCAG 14
Db

RESULT 602
AX419931/c
LOCUS      AX419931
DEFINITION Sequence 268 from Patent WO0198537.
ACCESSION  AX419931
VERSION     AX419931.1 GI:21524298
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE       Nucleic acid accessible hybridization sites
JOURNAL     Patent: WO 0198537-A 268 27-DEC-2001;
            THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES    Location/Qualifiers
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"

Query Match      7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1685 TCTCTCCAGCGTG 1698
       16 TCTCTCCATCATG 3
Db

RESULT 603
AX521635/c
LOCUS      AX521635
DEFINITION Sequence 15 from Patent WO0227031.
ACCESSION  AX521635
VERSION     AX521635.1 GI:23572675
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Busa,W.B.
TITLE       Methods and reagents for live-cell gene expression quantification
JOURNAL     Patent: WO 0227031-A 15 04-APR-2002;
            Cellomics, Inc. (US)
FEATURES    Location/Qualifiers
            source
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                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="synthetic oligonucleotide"

Query Match      7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;

QY      1661 AGGCTCACAGCTGG 1674
       16 AGGCTCAGATCTGG 3
Db

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1661 AGGCTCACAGCTGG 1674
       16 AGGCTCAGATCTGG 3
Db

RESULT 604
AX634479
LOCUS      AX634479
DEFINITION Sequence 1618 from Patent EPI260586.
ACCESSION  AX634479
VERSION     AX634479.1 GI:28470093
KEYWORDS    unidentified
SOURCE      unidentified
            unclassified.
REFERENCE   1
AUTHORS     Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
            Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
            McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE       Method and reagent for inhibiting the expression of disease related
            genes
JOURNAL     Patent: EP 1260586-A 1618 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
            source
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                /organism="unidentified"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32644"

Query Match      7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1689 CTCACAGCTGGTGG 1702
       1 CTCACAGCTGGTGG 14
Db

RESULT 605
AR106948/c
LOCUS      AR106948
DEFINITION Sequence 109 from patent US 6107092.
ACCESSION  AR106948
VERSION     AR106948.1 GI:12821478
KEYWORDS    Unknown.
SOURCE      Unknown.
            unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Cowser,L.M., Bennett,C.Frank. and O'Malley,B.W.
TITLE       Antisense modulation of SRA expression
JOURNAL     Patent: US 6107092-A 109 22-AUG-2000;
            Location/Qualifiers
            source
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                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 18;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1658 ACCAGGCTCACAGC 1671
       15 ACCAGGCTTCAGC 2
Db

RESULT 606
AX532451/c
LOCUS      AX532451

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DEFINITION Sequence 1960 from Patent EP1239051.
ACCESSION AX532451
VERSION AX532451.1 GI:25256676
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1960 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 7.6%; Score 10.6; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1733 TGGCTCCCACTCTCC 1749
Db 17 TGGACCCCATCTCCAC 1
RESULT 607
AX532452/C
LOCUS
DEFINITION Sequence 1961 from Patent EP1239051.
ACCESSION AX532452
VERSION AX532452.1 GI:25256678
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1961 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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/db_xref="taxon:9606"
Query Match 7.6%; Score 10.6; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1732 TTGGTCCCACTCTCC 1748
Db 17 TTGGACCCCATCTCCAC 1
RESULT 608
AR382702
LOCUS
DEFINITION Sequence 56 from patent US 6610533.
ACCESSION AR382702
VERSION AR382702.1 GI:40091489
KEYWORDS Unknown.
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Inouye,M., Wang,N. and Yamanaka,K.
TITLE Cold-shock regulatory elements, constructs thereof, and methods of use

JOURNAL Patent: US 6610533-A 56 26-AUG-2003;
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source
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 7.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 2.7e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1754 CCTAAAGGCCCA 1765
Db 2 CCGAAGGCCCA 13
RESULT 609
A09968
LOCUS
DEFINITION Probe 33.6.
ACCESSION A09968
VERSION A09968.1 GI:485097
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Vijg,J. and Uitterlinden,A.G.
TITLE A method for the simultaneous determination of DNA sequence variations at a large number of sites, and a kit therefor
JOURNAL Patent: EP 0349024-A 3 03-JAN-1990;
NEDERLANDSE ORGANISATIE VOOR TOEGEPAST-NATUURWETENSCHAPPELIJK ONDERZOEK TWO
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 7.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1686 CTCCTCCAGCGT 1697
Db 14 CTCCTCCAGCCT 3
RESULT 610
A40553/C
LOCUS
DEFINITION Sequence 90 from Patent WO9425578.
ACCESSION A40553
VERSION A40553.1 GI:2296588
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE EFFECTS OF TRANSFORMING GROWTH FACTOR-g(b) (TGF-g(b))
JOURNAL Patent: WO 9425578-A 90 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 7.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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QY 1644 AGCAGAGGCCAA 1655
Db 14 AGCAGAGGCCGA 3

RESULT 611
A89078/c
LOCUS 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1226 from Patent WO9833904.
ACCESSION A89078
VERSION A89078.1 GI:6737648
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1226 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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Query Match 7.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCCAA 1655
Db 14 AGCAGAGGCCGA 3

RESULT 612
A89078/c
LOCUS 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 90 from patent US 6455689.
ACCESSION AR232833
VERSION AR232833.1 GI:27275171
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 90 24-SEP-2002;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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Query Match 7.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCCAA 1655
Db 14 AGCAGAGGCCGA 3

RESULT 613
AR403509/c
LOCUS 14 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1849 from patent US 6623962.
ACCESSION AR403509
VERSION AR403509.1 GI:40150959
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 1849 23-SEP-2003;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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Query Match 7.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAGAA 1650
Db 13 CTTGAGAGCGAA 2

RESULT 614
AX030128/c
LOCUS 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 90 from Patent EP1008649.
ACCESSION AX030128
VERSION AX030128.1 GI:10190345
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 90 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
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        Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match 7.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCCAA 1655
Db 14 AGCAGAGGCCGA 3

RESULT 615
AX316449/c
LOCUS 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 90 from Patent EP1160319.
ACCESSION AX316449
VERSION AX316449.1 GI:17899622
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 90 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
    source
        Location/Qualifiers
            1..14

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Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAC 1678
Db 3 ACAGCTGGAC 14

RESULT 619
A07567/c
LOCUS A07567 15 bp DNA linear PAT 28-JUN-1993
DEFINITION p11196 DNA sequence, J-region.
ACCESSION A07567
VERSION A07567.1 GI:413080
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kaluza,B. and Lenz,H.
TITLE Diagnostic method using chimeric antibodies
JOURNAL Patent: EP 0378175-A 18 JUL-1990;
BOEHRINGER MANNHEIM GMBH
FEATURES
    source
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
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        /transl_table=11
        /product="K gene, J-region rearranged"
        /protein_id="CAA00680.1"
        /db_xref="GI:4526619"
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        /translation="GTKLE"

Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1689 CTCACGCTGGT 1700
Db 15 CTCACGCTGGT 4

RESULT 620
A07569
LOCUS A07569 15 bp DNA linear PAT 28-JUN-1993
DEFINITION p11196 DNA sequence, J-region, Reverse complement.
ACCESSION A07569
VERSION A07569.1 GI:411488
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Kaluza,B. and Lenz,H.
TITLE Diagnostic method using chimeric antibodies
JOURNAL Patent: EP 0378175-A 20 JUL-1990;
BOEHRINGER MANNHEIM GMBH
FEATURES
    source
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"

Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1689 CTCACGCTGGT 1700
Db 1 CTCACGCTGGT 12

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 621
A07567/c
LOCUS A07567 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 339 from patent US 5869253.
ACCESSION A07567
VERSION A07567.1 GI:5949178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 339 09-FEB-1999;
FEATURES
    source
        1..15
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1695 CGTGTGGAGT 1706
Db 15 CGTGTGGAGT 4

RESULT 622
A07569/c
LOCUS A07569 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 339 from patent US 6132966.
ACCESSION A07569
VERSION A07569.1 GI:14093717
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 339 17-OCT-2000;
FEATURES
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        /mol_type="unassigned DNA"

Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1695 CGTGTGGAGT 1706
Db 15 CGTGTGGAGT 4

RESULT 623
A07569/c
LOCUS A07569 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1270 from patent US 6194150.
ACCESSION A07569
VERSION A07569.1 GI:14121750
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 1270 27-FEB-2001;
FEATURES
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source      1. .15
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Query Match
Best Local Similarity 7.5%; Score 10.4; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1636 GGGCTGTAGCA 1647
    |||||
Db 3 GGGCTGTATCA 14

RESULT 624
LOCUS AR143397/c 15 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 42 from patent US 6204252.
ACCESSION AR143397
VERSION AR143397.1 GI:15104683
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Murphy, C., Storey, J., Beltz, G.A. and Coughlin, R.T.
TITLE Characterization of granulocytic ehrlichia and methods of use.
JOURNAL Patent: US 6204252-A 42 20-MAR-2001;
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.5%; Score 10.4; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 GTAGCAGAGGC 1653
    |||||
Db 15 GTAGAGAGGC 4

RESULT 625
E05479
LOCUS PCR primer. 15 bp DNA linear PAT 29-SEP-1997
DEFINITION
ACCESSION E05479
VERSION E05479.1 GI:2173668
KEYWORDS
SOURCE JP 1993244982-A/7.
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 15)
AUTHORS Nakatani, T., Gomi, H., Jiyon, W. and Noguchi, H.
TITLE ANTHROPOMORPHISM B-B10
JOURNAL Patent: JP 1993244982-A 7 24-SEP-1993;
SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD, BIOTEST AG,
INOTERAPII LAB
OS Artificial Gene
OC Artificial sequence; Genes.
PN JP 1993244982-A/7
PD 24-SEP-1993
PF 06-DEC-1991 JP 1991323319
PI NAKATANI TOMOSUKE, GOMI HIDEYUKI, JIYON WAIDENESU, PI
NOGUCHI HIROSHI
PC C12P21/08, A61K39/395//C12N5/10, C12N15/13, G01N33/577; CC
strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
LOCATION/Qualifiers
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/mol_type="genomic DNA"

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            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.5%; Score 10.4; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1689 CTCGAGCTGGT 1700
    |||||
Db 1 CTCGAGCTGGT 12

RESULT 626
LOCUS I15197/c 15 bp DNA linear PAT 02-APR-1996
DEFINITION Sequence 14 from patent US 5460949.
ACCESSION I15197
VERSION I15197.1 GI:1250105
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Saunders, C.A., Wolf, F.R. and Mukharji, I.
TITLE Method and composition for increasing the accumulation of squalene
and specific sterols in yeast
JOURNAL Patent: US 5460949-A 14 24-OCT-1995;
FEATURES
Location/Qualifiers
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source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.5%; Score 10.4; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAAC 1677
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Db 12 CACAGCTGGATC 1

RESULT 627
I57802/c
LOCUS I57802 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 339 from patent US 5610054.
ACCESSION I57802
VERSION I57802.1 GI:2482866
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Draper, K.G.
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL Patent: US 5610054-A 339 11-MAR-1997;
FEATURES
Location/Qualifiers
1. .15
source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.5%; Score 10.4; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1695 CGTGGTGGAGT 1706
    |||||
Db 15 CGTAGTGGAGT 4

RESULT 628
LOCUS I61657/c 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 211 from patent US 5658780.
ACCESSION I61657

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AX636078/c
LOCUS AX636078 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3217 from Patent EP1260586.
ACCESSION AX636078
VERSION AX636078.1 GI:28471692
KEYWORDS unidentifed
SOURCE unidentifed
ORGANISM unclassified.

REFERENCE
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelsky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweeder,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Wolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 3217 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LOCUS 1639 CTTGTAGCGGAA 1650
DB 12 CTTGTAGCGGAA 1

RESULT 634
LOCUS BD207306/c
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD207306
VERSION BD207306.1 GI:33017076
KEYWORDS JP 2002512791-A/896.
SOURCE unidentifed
ORGANISM unclassified.

REFERENCE
1 (bases 1 to 15)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 896 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/896
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO.
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
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CC hepatitis C virus infection.
PH Key Location/Qualifiers
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FT /organism='Hepatitis virus (hepatitis C FT

FEATURES
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Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LOCUS 1688 CTTCCAGCGTGG 1699
DB 1 CTTCCAGCGTGG 12

RESULT 636
LOCUS S45933/c
DEFINITION COL2A1-procollagen II [human, Genomic Mutant, 15 nt].
ACCESSION S45933
VERSION S45933.1 GI:1679995
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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/mol_type="genomic RNA"
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Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LOCUS 1695 CTTGCTGGAGT 706
DB 15 CGTAGTGGAGT 4

RESULT 635
LOCUS BD208694
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD208694
VERSION BD208694.1 GI:33018464
KEYWORDS JP 2002512791-A/2284.
SOURCE unidentifed
ORGANISM unclassified.

REFERENCE
1 (bases 1 to 15)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 2284 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2284
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO.
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
PH Key Location/Qualifiers
FT source 1..15
FT /organism='Hepatitis virus (hepatitis C FT

FEATURES
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/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LOCUS 1688 CTTCCAGCGTGG 1699
DB 1 CTTCCAGCGTGG 12

RESULT 636
LOCUS S45933/c
DEFINITION COL2A1-procollagen II [human, Genomic Mutant, 15 nt].
ACCESSION S45933
VERSION S45933.1 GI:1679995
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 15)
 Ahmad,N.N., Ala-Kokko,L., Knowlton,R.G., Jimenez,S.A., Weaver,E.J.,
 Maguire,J.I., Tasman,W. and Prockop,D.J.
 Stop codon in the procollagen II gene (COL2A1) in a family with the
 Stickler syndrome (arthro-ophthalmopathy)
 Proc. Natl. Acad. Sci. U.S.A. 88 (15), 6624-6627 (1991)
 91319736
 MEDLINE
 PUBMED 1677770

REMARK
 GenBank staff at the National Library of Medicine created this
 entry [NCBI gibseq 45933] from the original journal article.
 This sequence comes from fig 3.
 On Nov 21, 1996 this sequence version replaced gi:1619744.

COMMENT
 On Nov 21, 1996 this sequence version replaced gi:1619744.

FEATURES
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 /gene="COL2A1"
 /note="procollagen II"

Query Match 7.5%; Score 10.4; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.4e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1684 GTCTCTCCAGC 1695
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 Db 15 GTCTCTCAAGC 4

RESULT 637
 128863/c
 LOCUS 128863 16 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 8 from patent US 5574142.
 ACCESSION 128863
 VERSION 128863.1 GI:1819650
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 1 (bases 1 to 16)
 Meyer,R.B., Jx., Gall,A.A. and Reed,M.W.
 Peptide linkers for improved oligonucleotide delivery
 JOURNAL Patent: US 5574142-A 8 12-NOV-1996;
 FEATURES
 Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 7.5%; Score 10.4; DB 1; Length 16;
 Best Local Similarity 91.7%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1719 ACGGAGTGGAG 1730
 |||||
 Db 12 ACGAAGTGGAG 1

RESULT 638
 AR328508
 LOCUS AR328508 16 bp RNA linear PAT 17-AUG-2003
 DEFINITION Sequence 5910 from patent US 6566127.
 ACCESSION AR328508
 VERSION AR328508.1 GI:33714316
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 1 (bases 1 to 16)
 Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
 Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6566127-A 5910 20-MAY-2003;
 FEATURES
 Location/Qualifiers
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 /mol_type="unassigned RNA"

Query Match 7.5%; Score 10.4; DB 1; Length 16;
 Best Local Similarity 91.7%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1648 GAAGGCAAGCAC 1659
 |||||
 Db 1 GAAGGCAAGCGC 12

RESULT 639
 AR329723/c
 LOCUS AR329723 16 bp RNA linear PAT 17-AUG-2003
 DEFINITION Sequence 7125 from patent US 6566127.
 ACCESSION AR329723
 VERSION AR329723.1 GI:33715531
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 1 (bases 1 to 16)
 Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
 Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6566127-A 7125 20-MAY-2003;
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 Location/Qualifiers
 1..16
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 /mol_type="unassigned RNA"

Query Match 7.5%; Score 10.4; DB 1; Length 16;
 Best Local Similarity 91.7%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1650 AGGCAAGCACCA 1661
 |||||
 Db 14 AGGCAAGAACCA 3

RESULT 640
 AX349227
 LOCUS AX349227 16 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 11 from Patent WO0202810.
 ACCESSION AX349227
 VERSION AX349227.1 GI:18615259
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE
 1
 Bickel,R., Ehricht,R., Ellinger,T., Ermantraut,E., Kaiser,T.,
 Schulz,I. and Wegner,G.
 Method for qualitative and/or quantitative detecting of molecular
 interactions on probe arrays
 JOURNAL Patent: WO 0202810-A 11 10-JAN-2002;
 FEATURES
 Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Oligonukleotidsonde"

Query Match 7.5%; Score 10.4; DB 1; Length 16;
 Best Local Similarity 91.7%; Pred. No. 3.8e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1636 GGGCTTGTAGCA 1647

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Db          2 GGGCTTTAGCA 13
|||||
RESULT 641
AX103735/c
LOCUS      18 bp      DNA      linear      PAT 30-APR-2001
DEFINITION
Sequence 52 from Patent WO0125458.
ACCESSION  AX103735
VERSION     AX103735.1 GI:13919945
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Olivier,J., Deslandes,L. and Marco,Y.
AUTHORS    Novel class of proteins and uses thereof for plant resistance to
TITLE      various pathogenic agents
JOURNAL    Patent: WO 0125458-A' 52 12-APR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR) ;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match      7.5%; Score 10.4; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 4.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGACATGCGAG 1730
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Db 17 ACGGACATGCGAG 6

RESULT 642
A70767
LOCUS      20 bp      DNA      linear      PAT 07-MAY-1999
DEFINITION
Sequence 88 from Patent WO9813490.
ACCESSION  A70767
VERSION     A70767.1 GI:4774770
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE
1 (bases 1 to 20)
AUTHORS    Ophoff,R.A., Terwindt,G.M., Ferrari,M.D. and Frants,R.R.
TITLE      A gene related to migraine in man
JOURNAL    Patent: WO 9813490-A 88 02-APR-1998;
OPHOFF ROEL ANDRE (NL)
FEATURES
source
1..20
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match      7.5%; Score 10.4; DB 1; Length 20;
Best Local Similarity 70.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGAACCTGGTG 1684
|||||
Db 1 TGACTTCGCCACCTGGTG 20

RESULT 643
A79251
LOCUS      20 bp      DNA      linear      PAT 20-OCT-1999
DEFINITION
Sequence 88 from Patent EP0834561.
ACCESSION  A79251
VERSION     A79251.1 GI:6092296

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KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE
1 (bases 1 to 20)
AUTHORS    A GENE RELATED TO MIGRAINE IN MAN
TITLE      Patent: EP 0834561-A 88 08-APR-1998;
JOURNAL    UNIV LEIDEN (NL)
FEATURES
source
1..20
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match      7.5%; Score 10.4; DB 1; Length 20;
Best Local Similarity 70.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGAACCTGGTG 1684
|||||
Db 1 TGACTTCGCCACCTGGTG 20

RESULT 644
BD003481
LOCUS      20 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION
A gene related to migraine in man.
ACCESSION  BD003481
VERSION     BD003481.1 GI:18631442
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 20)
AUTHORS    Frantz,R.R.I.B., Ferrari,M.D., Teruvinato,H.M. and Opuhofu,R.A.
TITLE      A gene related to migraine in man
JOURNAL    Patent: JP 2001500743-A 50 23-JAN-2001;
RYUKUS UNIVERSITY TO RAIDEN
COMMENT      OS Homo sapiens (human)
PN JP 2001500743-A/50
PD 23-JAN-2001
PF 26-SEP-1997 JP 1998515527
PR 27-SEP-1996 EP 96202707.4
PI RENE ROBERT ISAAC ERIK FRANTZ,MICHEL DOMINIQUE FERRARI, PI
HISERA MARRY TEFUVINTO,RURU ANDRE OPUHOFU
PC C12N15/09,A01K67/027,C07K14/435,C07K16/18,C12N1/15,C12N1/19,
PC C12N1/21,
PC C12N5/10,C12Q1/02,C12Q1/68,C12N15/00,C12N5/00 CC
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FT primer bind
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match      7.5%; Score 10.4; DB 1; Length 20;
Best Local Similarity 70.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGAACCTGGTG 1684
|||||
Db 1 TGACTTCGCCACCTGGTG 20

RESULT 645
A20991/c
LOCUS      15 bp      DNA      linear      PAT 29-SEP-1994
DEFINITION
N-terminal coding sequence.
ACCESSION  A20991
VERSION     A20991.1 GI:641297

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ACCESSION	AR041361				
VERSION	AR041361.1	GI:5961857			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified..				
AUTHORS	1 (bases 1 to 15)				
TITLE	Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.				
JOURNAL	TNF- α . ribozymes				
FEATURES	Patent: US 5811300-A 151 22-SEP-1998;				
source	Location/Qualifiers				
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	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	7.3%; Score 10.2; DB 1; Length 15;				
Best Local Similarity	80.0%; Pred. No. 3.8e+02;				
Matches	12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Qy	1664 CTCACGCTGGACC 1678				
Db	1 CTGACATCTGGAATC 15				
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RESULT 651					
LOCUS	AR041957	15 bp DNA linear	PAT 29-SEP-1999		
DEFINITION	Sequence 747 from patent US 5811300.				
ACCESSION	AR041957				
VERSION	AR041957.1	GI:5962453			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 15)				
TITLE	Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.				
JOURNAL	TNF- α . ribozymes				
FEATURES	Patent: US 5811300-A 747 22-SEP-1998;				
source	Location/Qualifiers				
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	/mol_type="unassigned DNA"				
Query Match	7.3%; Score 10.2; DB 1; Length 15;				
Best Local Similarity	80.0%; Pred. No. 3.8e+02;				
Matches	12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Qy	1676 ACCCTGGTGTCCTCCT 1690				
Db	1 ACCTTGTGTGCTCCT 15				
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RESULT 652					
LOCUS	AR056148	15 bp DNA linear	PAT 29-SEP-1999		
DEFINITION	Sequence 352 from patent US 5837542.				
ACCESSION	AR056148				
VERSION	AR056148.1	GI:5981725			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 15)				
TITLE	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and				
JOURNAL	Draper,K.G.				
FEATURES	Intercellular adhesion molecule-1 (ICAM-1) ribozymes				
source	Patent: US 5837542-A 352 17-NOV-1998;				
	Location/Qualifiers				
	1..15				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	7.3%; Score 10.2; DB 1; Length 15;				

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SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Llieven,S., Joost,L. and Rudi.R.
TITLE      Method for detection of drug-induced mutations in the reverse
           transcriptase gene
JOURNAL     Patent: US 6087093-A 61 11-JUL-2000;
FEATURES   Location/Qualifiers
           source
             1..15
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CCACGCTGGTGAAG 1705
Db 15 CCATCCTTGTGAAG 1

RESULT 656
AR113906 LOCUS AR113906 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 352 from patent US 6132967.
ACCESSION AR113906
VERSION AR113906.1 GI:14094228
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
           Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
           intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 352 17-OCT-2000;
FEATURES Location/Qualifiers
           source
             1..15
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CCACGCTGGTGAAG 1705
Db 15 CCATCCTTGTGAAG 1

RESULT 656
AR113906 LOCUS AR113906 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 352 from patent US 6132967.
ACCESSION AR113906
VERSION AR113906.1 GI:14094228
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
           Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
           intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 352 17-OCT-2000;
FEATURES Location/Qualifiers
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             /organism="unknown"
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Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCACTC 1745
Db 1 ATAGGCTCAACAC 15

RESULT 657
AR113978 LOCUS AR113978 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 424 from patent US 6132967.
ACCESSION AR113978
VERSION AR113978.1 GI:14094300
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
           Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
           intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 424 17-OCT-2000;
FEATURES Location/Qualifiers
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             /organism="unknown"
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Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCACTC 1745
Db 1 ATAGGCTCAACAC 15

RESULT 657
AR113978 LOCUS AR113978 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 424 from patent US 6132967.
ACCESSION AR113978
VERSION AR113978.1 GI:14094300
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
           Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
           intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 424 17-OCT-2000;
FEATURES Location/Qualifiers
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Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1650 AGGCAAGCACCAGGC 1664
Db 15 AGGCAGGAACAGGC 1

RESULT 658
AR114083 LOCUS AR114083 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 529 from patent US 6132967.
ACCESSION AR114083
VERSION AR114083.1 GI:14094405
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
           Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
           intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 529 17-OCT-2000;
FEATURES Location/Qualifiers
           source
             1..15
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1650 AGGCAAGCACCAGGC 1664
Db 15 AGGCAGGAACAGGC 1

RESULT 659
AR131838 LOCUS AR131838 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 263 from patent US 6194150.
ACCESSION AR131838
VERSION AR131838.1 GI:14120741
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 263 27-FEB-2001;
FEATURES Location/Qualifiers
           source
             1..15
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1650 AGGCAAGCACCAGGC 1664
Db 15 AGGCAGGAACAGGC 1

RESULT 659
AR131838 LOCUS AR131838 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 263 from patent US 6194150.
ACCESSION AR131838
VERSION AR131838.1 GI:14120741
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 263 27-FEB-2001;
FEATURES Location/Qualifiers
           source
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             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1715 GAGTACGGAGATGGA 1729
Db 15 GAGAAAGGAGAGGGA 1

RESULT 660
AR132776 LOCUS AR132776 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1201 from patent US 6194150.
ACCESSION AR132776
VERSION AR132776.1 GI:14121681
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KEYWORDS      .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      Unclassified.
AUTHORS        1 (bases 1 to 15)
TITLE          Stinchcomb,D.T., Jarvis,T. and McSwiggan,J.
JOURNAL        Nucleic acid based inhibition of CD40
FEATURES       Location/Qualifiers
               source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred.No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCAAGCA 1658
Db 15 AGCAGCAGAGCA 1

RESULT 661
LOCUS          BD233013/C
DEFINITION     Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION      BD233013
VERSION        BD233013.1 GI:33042783
KEYWORDS       JP 2002518065-A/109.
SOURCE         Aids-associated retrovirus
ORGANISM       Viruses; Retroid viruses; Retroviridae.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Stuyver,L.
TITLE          Method of detecting mutation selected by drug in HIV protease gene
JOURNAL        Patent: JP 2002518065-A 109 25-JUN-2002;
COMMENT        INNOGENETICS NV
               OS Aids-associated retrovirus
               PN JP 2002518065-A/109
               PD 25-JUN-2002
               PP 22-JUN-1999 JP 2000556068
               PR 24-JUN-1998 EP 98870143.9
               PI LIEVEN STUYVER
               PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
               CC Method of detecting mutation selected by drug in HIV protease
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               CH Key gene Location/Qualifiers
               FT source 1..15
               FT Location/Qualifiers
               1..15
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               /mol_type="genomic DNA"
               /db_xref="taxon:11966"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred.No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1742 ACTCTCCCTATCCT 1756
Db 15 AATCCCCCTATCAT 1

RESULT 662
LOCUS          BD233078
DEFINITION     Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION      BD233078
VERSION        BD233078.1 GI:33042848
KEYWORDS       JP 2002518065-A/174.
SOURCE         Aids-associated retrovirus
ORGANISM       Aids-associated retrovirus
REFERENCE      1 (bases 1 to 15)
AUTHORS        Stuyver,L.
TITLE          Method of detecting mutation selected by drug in HIV protease gene
JOURNAL        Patent: JP 2002518065-A 174 25-JUN-2002;
COMMENT        INNOGENETICS NV
               OS Aids-associated retrovirus
               PN JP 2002518065-A/393
               PD 25-JUN-2002
               PP 22-JUN-1999 JP 2000556068
               PR 24-JUN-1998 EP 98870143.9
               PI LIEVEN STUYVER
               PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
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               CH Key gene Location/Qualifiers
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               /mol_type="genomic DNA"
               /db_xref="taxon:11966"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred.No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGG 1735
Db 1 GGAGTTGGAGTTTG 15

RESULT 663
LOCUS          BD233297
DEFINITION     Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION      BD233297
VERSION        BD233297.1 GI:33043067
KEYWORDS       JP 2002518065-A/393.
SOURCE         Aids-associated retrovirus
ORGANISM       Viruses; Retroid viruses; Retroviridae.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Stuyver,L.
TITLE          Method of detecting mutation selected by drug in HIV protease gene
JOURNAL        Patent: JP 2002518065-A 393 25-JUN-2002;
COMMENT        INNOGENETICS NV
               OS Aids-associated retrovirus
               PN JP 2002518065-A/393
               PD 25-JUN-2002
               PP 22-JUN-1999 JP 2000556068
               PR 24-JUN-1998 EP 98870143.9
               PI LIEVEN STUYVER
               PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
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               CH Key gene Location/Qualifiers
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               /mol_type="genomic DNA"
               /db_xref="taxon:11966"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred.No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGG 1735
Db 1 GGAGTTGGAGTTTG 15

RESULT 663
LOCUS          BD233297
DEFINITION     Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION      BD233297
VERSION        BD233297.1 GI:33043067
KEYWORDS       JP 2002518065-A/393.
SOURCE         Aids-associated retrovirus
ORGANISM       Viruses; Retroid viruses; Retroviridae.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Stuyver,L.
TITLE          Method of detecting mutation selected by drug in HIV protease gene
JOURNAL        Patent: JP 2002518065-A 393 25-JUN-2002;
COMMENT        INNOGENETICS NV
               OS Aids-associated retrovirus
               PN JP 2002518065-A/393
               PD 25-JUN-2002
               PP 22-JUN-1999 JP 2000556068
               PR 24-JUN-1998 EP 98870143.9
               PI LIEVEN STUYVER
               PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
               CC Method of detecting mutation selected by drug in HIV protease
               CQ
               CH Key gene Location/Qualifiers
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               /mol_type="genomic DNA"
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Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred.No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGTGTCTC 1688
Db 1 GAACTCTGTGTACTC 15

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RESULT 664
BD233300      15 bp      DNA      linear      PAT 17-JUL-2003
LOCUS          Method of detecting mutation selected by drug in HIV protease gene.
DEFINITION
ACCESSION      BD233300
VERSION         BD233300.1 GI:33043070
KEYWORDS        Aids-associated retrovirus
SOURCE           Aids-associated retrovirus
ORGANISM         Viruses; Retrovirdae; Retroviridae.
REFERENCE
1 (bases 1 to 15)
AUTHORS         Stuyver,L.
TITLE           Method of detecting mutation selected by drug in HIV protease gene
JOURNAL         Patent: JP 2002518065-A 396 25-JUN-2002;
INNOGENETICS NV
COMMENT
OS      Aids-associated retrovirus
PN      JP 2002518065-A/396
PD      25-JUN-2002
PF      22-JUN-1999 JP 2000556068
PI      24-JUN-1998 EP 98870143.9
PT      LIEVEN STUYVER
PC      C12N15/09, C12Q1/68, C12Q1/70, C12N15/00
CC      Method of detecting mutation selected by drug in HIV protease
CC      gene
FH      Key
FT      source
FT      Location/Qualifiers
FEATURES
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1..15
Location/Qualifiers
/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCTC 1688
|||||
DB 1 GAACCTGTTGACTC 15

RESULT 665
BD233419/c
LOCUS          15 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION      BD233419
VERSION         BD233419.1 GI:33043189
KEYWORDS        Aids-associated retrovirus
SOURCE           Aids-associated retrovirus
ORGANISM         Viruses; Retrovirdae; Retroviridae.
REFERENCE
1 (bases 1 to 15)
AUTHORS         Stuyver,L.
TITLE           Method of detecting mutation selected by drug in HIV protease gene
JOURNAL         Patent: JP 2002518065-A 515 25-JUN-2002;
INNOGENETICS NV
COMMENT
OS      Aids-associated retrovirus
PN      JP 2002518065-A/515
PD      25-JUN-2002
PF      22-JUN-1999 JP 2000556068
PI      24-JUN-1998 EP 98870143.9
PT      LIEVEN STUYVER
PC      C12N15/09, C12Q1/68, C12Q1/70, C12N15/00
CC      Method of detecting mutation selected by drug in HIV protease
CC      gene
FH      Key
FT      source
FT      Location/Qualifiers
FEATURES
source
1..15
Location/Qualifiers
/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCTC 1688
|||||
DB 1 GAACCTGTTGACTC 15

RESULT 666
BD233419/c
LOCUS          15 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION      Sequence 12 from patent US 5580969.
ACCESSION      I30549
VERSION         I30549.1 GI:1821340
KEYWORDS        .
SOURCE           Unknown.
ORGANISM         Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS         Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.-H.
TITLE           Antisense oligonucleotides directed against human ICAM-1 RNA
JOURNAL         Patent: US 5580969-A 12 03-DEC-1996;
FEATURES
source
1..15
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCCTCC 1749
|||||
DB 15 GCTCAGATTCCTCC 1

RESULT 667
I30549/c
LOCUS          15 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION      Sequence 12 from patent US 5580969.
ACCESSION      I30549
VERSION         I30549.1 GI:1821340
KEYWORDS        .
SOURCE           Unknown.
ORGANISM         Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS         Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.-H.
TITLE           Antisense oligonucleotides directed against human ICAM-1 RNA
JOURNAL         Patent: US 5580969-A 12 03-DEC-1996;
FEATURES
source
1..15
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAACC 1678
|||||
DB 15 CTCACAGTTCGAACC 1

RESULT 668
I39340/c
LOCUS          15 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION      Sequence 378 from patent US 5616488.

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/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCTC 1688
|||||
DB 15 GAACCTGTTGACTC 1

RESULT 666
I05468/c
LOCUS          15 bp      DNA      linear      PAT 02-DEC-1994
DEFINITION      Sequence 3 from Patent EP 0266190.
ACCESSION      I05468
VERSION         I05468.1 GI:591022
KEYWORDS        .
SOURCE           Unknown.
ORGANISM         Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS         Foster,D.C., Murray,M.J. and Berkner,K.L.
TITLE           Expression of protein C
JOURNAL         Patent: EP 0266190-A2 3 04-MAY-1988;
FEATURES
source
1..15
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCCTCC 1749
|||||
DB 15 GCTCAGATTCCTCC 1

RESULT 667
I30549/c
LOCUS          15 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION      Sequence 12 from patent US 5580969.
ACCESSION      I30549
VERSION         I30549.1 GI:1821340
KEYWORDS        .
SOURCE           Unknown.
ORGANISM         Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS         Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.-H.
TITLE           Antisense oligonucleotides directed against human ICAM-1 RNA
JOURNAL         Patent: US 5580969-A 12 03-DEC-1996;
FEATURES
source
1..15
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAACC 1678
|||||
DB 15 CTCACAGTTCGAACC 1

RESULT 668
I39340/c
LOCUS          15 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION      Sequence 378 from patent US 5616488.

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[illegible]

REFERENCE 1 (bases 1 to 15)
AUTHORS Lieven,S., Joost,L. and Rudi,R.
TITLE Method for detection of drug-induced mutations in the reverse transcriptase gene
JOURNAL Patent: US 6311389-A 61 18-DEC-2001;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1691 CCAGCGTGTGAAG 1705
Db 15 CCATCCTGTGGAAG 1

RESULT 674
LOCUS AR279380 15 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 24 from patent US 6514699.
ACCESSION AR279380
VERSION AR279380.1 GI:29714132
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS O'Neill,R.A.; Chen,J.-K.; Chiesa,C. and Fry,G.
TITLE Multiplex polynucleotide capture methods and compositions
JOURNAL Patent: US 6514699-A 24 04-FEB-2003;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1636 GGGCTTGAGCAGAA 1650
Db 15 GCGATAGTAGCAGAA 1

RESULT 675
LOCUS AX007567/c 15 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 109 from Patent WO9967428.
ACCESSION AX007567
VERSION AX007567.1 GI:9995264
KEYWORDS
SOURCE Aids-associated retrovirus
ORGANISM Aids-associated retrovirus
Viruses; Retroid viruses; Retroviridae.
REFERENCE 1
AUTHORS Stuyver,L.
TITLE Method for detection of drug-selected mutations in the hiv protease gene
JOURNAL Patent: WO 9967428-A 109 29-DEC-1999;
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES Location/Qualifiers
source 1..15
/organism="Aids-associated retrovirus"
/mol_type="unassigned DNA"
/db_xref="taxon:11966"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1674 GAACCTCGTGTCTC 1688
Db 1 GAACCTCGTGTCTC 15

RESULT 678
LOCUS AX007854 15 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 396 from Patent WO9967428.
ACCESSION AX007854
VERSION AX007854.1 GI:9995551

Qy 1742 ACTCTCCCTATCTCT 1756
Db 15 AATCCCCCTATCAT 1

RESULT 676
LOCUS AX007632 15 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 174 from Patent WO9967428.
ACCESSION AX007632
VERSION AX007632.1 GI:9995329
KEYWORDS
SOURCE Aids-associated retrovirus
ORGANISM Aids-associated retrovirus
Viruses; Retroid viruses; Retroviridae.
REFERENCE 1
AUTHORS Stuyver,L.
TITLE Method for detection of drug-selected mutations in the hiv protease gene
JOURNAL Patent: WO 9967428-A 174 29-DEC-1999;
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES Location/Qualifiers
source 1..15
/organism="Aids-associated retrovirus"
/mol_type="unassigned DNA"
/db_xref="taxon:11966"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1721 GGAGTGGAGATTGG 1735
Db 1 GGAGTGGAGATTGG 15

RESULT 677
LOCUS AX007851 15 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 393 from Patent WO9967428.
ACCESSION AX007851
VERSION AX007851.1 GI:9995548
KEYWORDS
SOURCE Aids-associated retrovirus
ORGANISM Aids-associated retrovirus
Viruses; Retroid viruses; Retroviridae.
REFERENCE 1
AUTHORS Stuyver,L.
TITLE Method for detection of drug-selected mutations in the hiv protease gene
JOURNAL Patent: WO 9967428-A 393 29-DEC-1999;
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES Location/Qualifiers
source 1..15
/organism="Aids-associated retrovirus"
/mol_type="unassigned DNA"
/db_xref="taxon:11966"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1674 GAACCTCGTGTCTC 1688
Db 1 GAACCTCGTGTCTC 15

RESULT 678
LOCUS AX007854 15 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 396 from Patent WO9967428.
ACCESSION AX007854
VERSION AX007854.1 GI:9995551

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KEYWORDS
SOURCE      Aids-associated retrovirus
ORGANISM    Aids-associated retrovirus
            Viruses; Retrovird viruses; Retroviridae.
REFERENCE   1
AUTHORS     Stuyver,L.
TITLE       Method for detection of drug-selected mutations in the hiv protease
            Gene
JOURNAL     Patent: WO 9967428-A 396 29-DEC-1999;
            INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES
source      Location/Qualifiers
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            /organism="Aids-associated retrovirus"
            /mol_type="unassigned DNA"
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Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGTGTCTC 1688
      |||||
Db 1 GAACTCTGTGTACT 15

RESULT 679
LOCUS      AX007973/c
DEFINITION Sequence 515 from Patent WO9967428.
ACCESSION  AX007973
VERSION     AX007973.1 GI:9995670
KEYWORDS   Aids-associated retrovirus
SOURCE     Aids-associated retrovirus
ORGANISM   Viruses; Retrovird viruses; Retroviridae.
REFERENCE   1
AUTHORS     Stuyver,L.
TITLE       Method for detection of drug-selected mutations in the hiv protease
            Gene
JOURNAL     Patent: WO 9967428-A 515 29-DEC-1999;
            INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES
source      Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:11966"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGTGTCTC 1688
      |||||
Db 15 GAACTCTGTGTACT 1

RESULT 680
LOCUS      AX456739
DEFINITION Sequence 211 from Patent WO0218407.
ACCESSION  AX456739
VERSION     AX456739.1 GI:121715626
KEYWORDS   Rattus norvegicus (Norway rat)
SOURCE     Rattus norvegicus
ORGANISM   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
AUTHORS     Kurreck,J. and Erdmann,V.A.
TITLE       Antisense oligonucleotides against vrl
JOURNAL     Patent: WO 0218407-A 211 07-MAR-2002;
            Gruenthal GmbH (DE)

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FEATURES
source      Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:10116"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
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Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1689 CTCACGCGTGGTGA 1703
      |||||
Db 1 CTCACGCGAGGTGA 15

RESULT 681
LOCUS      AX572218/c
DEFINITION Sequence 258 from Patent WO02055741.
ACCESSION  AX572218
VERSION     AX572218.1 GI:26004308
KEYWORDS   Human immunodeficiency virus
SOURCE     Human immunodeficiency virus
ORGANISM   Viruses; Retrovird viruses; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE   1
AUTHORS     de Smet,K. and Stuyver,L.
TITLE       Method for detection of drug-induced mutations in the hiv reverse
            transcriptase gene
JOURNAL     Patent: WO 02055741-A 258 18-JUL-2002;
            INNOGENETICS N.V. (BE)
FEATURES
source      Location/Qualifiers
            1..15
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            /mol_type="unassigned DNA"
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Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CCAGCGTGGTGAAG 1705
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Db 15 CCATCTTGTGGAG 1

RESULT 682
LOCUS      AX572222/c
DEFINITION Sequence 262 from Patent WO02055741.
ACCESSION  AX572222
VERSION     AX572222.1 GI:26004312
KEYWORDS   Human immunodeficiency virus
SOURCE     Human immunodeficiency virus
ORGANISM   Viruses; Retrovird viruses; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE   1
AUTHORS     de Smet,K. and Stuyver,L.
TITLE       Method for detection of drug-induced mutations in the hiv reverse
            transcriptase gene
JOURNAL     Patent: WO 02055741-A 262 18-JUL-2002;
            INNOGENETICS N.V. (BE)
FEATURES
source      Location/Qualifiers
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Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CCAGCGTGGTGAAG 1705
      |||||
Db 15 CCATCTTGTGGAG 1

RESULT 682
LOCUS      AX572222/c
DEFINITION Sequence 262 from Patent WO02055741.
ACCESSION  AX572222
VERSION     AX572222.1 GI:26004312
KEYWORDS   Human immunodeficiency virus
SOURCE     Human immunodeficiency virus
ORGANISM   Viruses; Retrovird viruses; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE   1
AUTHORS     de Smet,K. and Stuyver,L.
TITLE       Method for detection of drug-induced mutations in the hiv reverse
            transcriptase gene
JOURNAL     Patent: WO 02055741-A 262 18-JUL-2002;
            INNOGENETICS N.V. (BE)
FEATURES
source      Location/Qualifiers
            1..15
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            /mol_type="unassigned DNA"
            /db_xref="taxon:12721"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1690 TCCAGCGTGTGGAA 1704
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Db 15 TCCATCCTGTGGAA 1

RESULT 683
AX587077/c
LOCUS AX587077 15 bp DNA linear PAT 10-JAN-2003
DEFINITION Sequence 99 from Patent WO02072883.
ACCESSION AX587077
VERSION AX587077.1 GI:27655952
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE Nucleotide carrier for diagnosing and treating oral diseases
JOURNAL
FEATURES
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1. 15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Bacteria"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1653 CAAGCACCAGGCTCA 1667
|||||
Db 15 CGAGAACCAAGCTCA 1

RESULT 684
AX633179
LOCUS AX633179 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 318 from Patent EP1260586.
ACCESSION AX633179
VERSION AX633179.1 GI:28468793
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL
Patent: EP 1260586-A 318 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATGGCTCCCAACTC 1745
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Db 1 ATAGGCTCAACAC 15

RESULT 685

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AX633279/c
LOCUS AX633279 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 418 from Patent EP1260586.
ACCESSION AX633279
VERSION AX633279.1 GI:28468893
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL
Patent: EP 1260586-A 418 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
source
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1650 AGGCAAGCACCAGGC 1664
|||||
Db 15 AGGCAGGAACAGGC 1

RESULT 686
AX633526/c
LOCUS AX633526 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 665 from Patent EP1260586.
ACCESSION AX633526
VERSION AX633526.1 GI:28469140
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL
Patent: EP 1260586-A 665 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1650 AGGCAAGCACCAGGC 1664
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Db 15 AGGCAGGAACAGGC 1

RESULT 687
AX635641/c
LOCUS AX635641 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 2780 from Patent EP1260586.

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ACCESSION AX635641
VERSION AX635641.1 GI:28471255
SOURCE .
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 2780 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1711 TTAGGAGTAGCGGAGA 1725
|||||
Db 15 TTATGAGTAGGGACA 1
RESULT 688
AX636135
LOCUS AX636135 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3274 from Patent EP1260586.
ACCESSION AX636135
VERSION AX636135.1 GI:28471749
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 3274 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1680 TGGTGTCCTCTCCAG 1694
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Db 1 TGGTGTCCTCTCTCG 15
RESULT 689
AX636741/c
LOCUS AX636741 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3880 from Patent EP1260586.
ACCESSION AX636741
VERSION AX636741.1 GI:28472355
KEYWORDS .

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SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 3880 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1639 CTTGTAGCAGAGCC 1653
|||||
Db 15 CTGTTAGGAGAGCGC 1
RESULT 690
AX636781
LOCUS AX636781 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3920 from Patent EP1260586.
ACCESSION AX636781
VERSION AX636781.1 GI:28472395
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 3920 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
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/db_xref="taxon:32644"
Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1664 CTCACAGCTGGAGCC 1678
|||||
Db 1 CTGACATCTGGAATC 15
RESULT 691
AX637368
LOCUS AX637368 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 4507 from Patent EP1260586.
ACCESSION AX637368
VERSION AX637368.1 GI:28472982
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified

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REFERENCE
AUTHORS
1 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
  Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
  McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
  Svedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
  Wolf,T.
TITLE
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL
Patent: EP 1260586-A 4507 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

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Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1676 ACCCTGGTGTCTCTCT 1690
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Db 1 ACCTTGTTCCTCTCT 15

RESULT 692
BD007196/c
LOCUS
BD007196 15 bp DNA linear PAT 31-JAN-2002
DEFINITION
Method and composition for capturing multiple polynucleotide.
ACCESSION
BD007196
VERSION
BD007196.1 GI:18635567
KEYWORDS
JP 2001503973-A/24.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
O'Neill,R.A., Chen,J.C., Chiesa,C. and Fry,G.
TITLE
Method and composition for capturing multiple polynucleotide
JOURNAL
Patent: JP 2001503973-A 24 27-MAR-2001;
THE PERKIN ELMAR CORP
COMMENT
OS Unidentified
PN JP 2001503973-A/24
PD 27-MAR-2001
PF 02-OCT-1997 JP 1998516839
PR 04-OCT-1996 US 60/027832,12-JUN-1997 US 08/873437 PI
ROGER A O'NEILL,JAR CAIN CHEN,CLAUDIA CHIESA,GEORGE FRY PC
C1201/68,C12N15/09,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
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FT source /organism='Unidentified'.
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/db_xref="taxon:32644"

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Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1636 GGCCTTGTAGCAGAA 1650
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Db 15 GCGATAGTAGCAGAA 1

RESULT 693
AX687848
LOCUS
AX687848 17 bp DNA linear PAT 31-MAR-2003
DEFINITION
Sequence 580 from Patent EP1281758.
ACCESSION
AX687848
VERSION
AX687848.1 GI:29410544

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KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL
Patent: EP 1281758-A 580 05-FEB-2003;
Aeomica, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGCTG 1673
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Db 3 CCAGGCTCCAGCTG 17

RESULT 694
AX532453/c
LOCUS
AX532453 17 bp DNA linear PAT 22-NOV-2002
DEFINITION
Sequence 1962 from Patent EP1239051.
ACCESSION
AX532453
VERSION
AX532453.1 GI:25256680
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shannon,M.
TITLE
Human posh-like protein 1
JOURNAL
Patent: EP 1239051-A 1962 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
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Query Match
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Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1732 TTGGCTCCCACTCC 1746
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Db 16 TTGGACCCCATCTCC 2

RESULT 695
AX687851
LOCUS
AX687851 17 bp DNA linear PAT 31-MAR-2003
DEFINITION
Sequence 583 from Patent EP1281758.
ACCESSION
AX687851
VERSION
AX687851.1 GI:29410549
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL
Patent: EP 1281758-A 583 05-FEB-2003;

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    /db_xref="taxon:9606"

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  1 CAGGCATCCAGCTGG 15

Db
  179747
  Sequence 43 from patent US 5707863.
  10 bp DNA linear PAT 10-JUN-1998
  179747
  Accession
  Version 179747.1 GI:3208037
  Keywords
  Source
  ORGANISM
    Unknown.
    Unclassified.
  REFERENCE
    1 (bases 1 to 10)
    Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
    Tumor suppressor gene merlin
    Patent: US 5707863-A 43 13-JAN-1998;
  FEATURES
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Db
  179747/c
  LOCUS
  DEFINITION
  Sequence 434 from Patent WO0185941.
  10 bp DNA linear PAT 30-NOV-2001
  Accession
  AX301720
  Version
  AX301720.1 GI:17382803
  Keywords
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
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    Versteeg,R. and Caron,H.N.
    Myc targets
    Patent: WO 0185941-A 434 15-NOV-2001;
    Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
  FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

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QY 1717 GTACGGAGAT 1726
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  1 GTACGGAGAT 10

Db
  1717/c
  LOCUS
  DEFINITION
  Human activated Th1 and Th2 cell expression genes.
  10 bp DNA linear PAT 17-JAN-2003
  Accession
  BD161179
  Version
  BD161179.1 GI:27866937
  Keywords
  JP 2002186482-A/1.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
 AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
 TITLE Human activated Th1 and Th2 cell expression genes
 JOURNAL Patent: JP 2002186482-A 1 02-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002186482-A/1
 PD 02-JUL-2002
 PF 19-DEC-2000 JP 2000385816

PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
 C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
 activated Th1 and Th2 cell expression genes FH Key
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Query Match 7.2%; Score 10; DB 1; Length 10;
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Qy 1654 AAGCACCAGG 1663
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 Db 10 AAGCACCAGG 1

RESULT 701

BD161279/c
 LOCUS BD161279 10 bp DNA linear PAT 17-JAN-2003

DEFINITION Human activated Th1 and Th2 cell expression genes.

ACCESSION BD161279

VERSION BD161279.1 GI:27867037

KEYWORDS JP 2002186482-A/101.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)

AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.

TITLE Human activated Th1 and Th2 cell expression genes

JOURNAL Patent: JP 2002186482-A 101 02-JUL-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT OS Homo sapiens (human)

PN JP 2002186482-A/101

PD 02-JUL-2002

PF 19-DEC-2000 JP 2000385816

PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC

C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human

activated Th1 and Th2 cell expression genes FH Key

Location/Qualifiers

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/organism='Homo sapiens (human)'.
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Query Match 7.2%; Score 10; DB 1; Length 10;
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 Db 10 AAGCACCAGG 1

RESULT 702

AX471317/c

LOCUS AX471317 11 bp DNA linear PAT 09-AUG-2002

DEFINITION Sequence 894 from Patent WO02053773.

ACCESSION AX471317

VERSION AX471317.1 GI:22206442

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Hofmann,K., Conradt,M. and Petersohn,D.

AUTHORS Method for determining skin stress or skin ageing in vitro

JOURNAL Patent: WO 02053773-A 894 11-JUL-2002;

HENKEL KGAA (DE)

Location/Qualifiers

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/organism="Homo sapiens"

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/db_xref="taxon:9606"

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Qy 1671 CTGGAACCCCT 1680
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 Db 11 CTGGAACCCCT 2

RESULT 703

AX471659

LOCUS AX471659 11 bp DNA linear PAT 09-AUG-2002

DEFINITION Sequence 1236 from Patent WO02053773.

ACCESSION AX471659

VERSION AX471659.1 GI:22206784

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Hofmann,K., Conradt,M. and Petersohn,D.

AUTHORS Method for determining skin stress or skin ageing in vitro

JOURNAL Patent: WO 02053773-A 1236 11-JUL-2002;

HENKEL KGAA (DE)

Location/Qualifiers

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/organism="Homo sapiens"

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Query Match 7.2%; Score 10; DB 1; Length 11;
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 Db 2 AGAGGCAAG 11

RESULT 704

AX471723/c

LOCUS AX471723 11 bp DNA linear PAT 09-AUG-2002

DEFINITION Sequence 1300 from Patent WO02053773.

ACCESSION AX471723

VERSION AX471723.1 GI:22206848

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1300 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 7.2%; Score 10; DB 1; Length 11;
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QY 1693 AGCGTGTGG 1702
Db 10 AGCGTGTGG 1

RESULT 705
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LOCUS AX622975 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 16 from Patent WO02053774.
ACCESSION AX622975
VERSION AX622975.1 GI:28450916
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 16 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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QY 1693 AGCGTGTGG 1702
Db 10 AGCGTGTGG 1

RESULT 706
AX624360/c
LOCUS AX624360 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1401 from Patent WO02053774.
ACCESSION AX624360
VERSION AX624360.1 GI:28452301
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1401 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1669 AGCTGGAACC 1678
Db 11 AGCTGGAACC 2

RESULT 707
AX625117
LOCUS AX625117 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2158 from Patent WO02053774.
ACCESSION AX625117
VERSION AX625117.1 GI:28453058
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2158 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GAAGGCAAGC 1657
Db 2 GAAGGCAAGC 11

RESULT 708
AX625409
LOCUS AX625409 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2450 from Patent WO02053774.
ACCESSION AX625409
VERSION AX625409.1 GI:28453350
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2450 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1647 AGAAGGCAAG 1656
Db 2 AGAAGGCAAG 11

RESULT 709
AX625899
LOCUS AX625899 11 bp DNA linear PAT 21-FEB-2003

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DEFINITION Sequence 2940 from Patent WO02053774.
ACCESSION AX625899
VERSION AX625899.1 GI:28453937
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2940 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1721 GGAGATGGAG 1730
Db 2 GGAGATGGAG 11
RESULT 710
AX626201/c
LOCUS AX626201 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3242 from Patent WO02053774.
ACCESSION AX626201
VERSION AX626201.1 GI:28454239
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3242 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Qy 1671 CTGGAACCTT 1680
Db 11 CTGGAACCTT 2
RESULT 711
AX626758
LOCUS AX626758 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3799 from Patent WO02053774.
ACCESSION AX626758
VERSION AX626758.1 GI:28454796
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin

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JOURNAL Patent: WO 02053774-A 3799 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1744 TCCTCCCTAT 1753
Db 2 TCCTCCCTAT 11
RESULT 712
AX627300
LOCUS AX627300 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4341 from Patent WO02053774.
ACCESSION AX627300
VERSION AX627300.1 GI:28455338
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4341 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1741 AACTCTCTCC 1750
Db 2 AACTCTCTCC 11
RESULT 713
AX627599/c
LOCUS AX627599 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4640 from Patent WO02053774.
ACCESSION AX627599
VERSION AX627599.1 GI:28455637
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4640 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1741 AACTCTCTCC 1750
Db 2 AACTCTCTCC 11

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QY 1743 CTCCTCCCTA 1752
Db 11 CTCCTCCCTA 2

RESULT 714
AX628274
LOCUS AX628274 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5315 from Patent WO02053774.
ACCESSION AX628274
VERSION AX628274.1 GI:28456312
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5315 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
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1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1678 CTTGGTGCT 1687
Db 2 CTTGGTGCT 11

RESULT 715
AX629280
LOCUS AX629280 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6321 from Patent WO02053774.
ACCESSION AX629280
VERSION AX629280.1 GI:28457318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6321 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAA 1676
Db 2 ACAGCTGGAA 11

RESULT 716
AX630396/c
LOCUS AX630396 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7437 from Patent WO02053774.
ACCESSION AX630396

VERSION AX630396.1 GI:28458434
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7437 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
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1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 AGCTGGTGG 1702
Db 10 AGCTGGTGG 1

RESULT 717
AX631781/c
LOCUS AX631781 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8823 from Patent WO02053774.
ACCESSION AX631781
VERSION AX631781.1 GI:28459888
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8823 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
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1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1669 AGCTGGACC 1678
Db 11 AGCTGGACC 2

RESULT 718
AX632538
LOCUS AX632538 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9580 from Patent WO02053774.
ACCESSION AX632538
VERSION AX632538.1 GI:28468153
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9580 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)


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source
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GAAGGCACG 1657
|||||
Db 2 GAAGGCACG 11

RESULT 719
BD187463/c
LOCUS
DEFINITION
A nucleic acid involving generation of presenilin-2 gene lacking
exon 5 type-aberrant splicing.
ACCESSION
BD187463
VERSION
JP 2003018991-A/2.
KEYWORDS
synthetic construct
SOURCE
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 11)
Toyama,M., Imaizumi,K., Ikeda,Y., Katayama,T. and Manabe,T.
TITLE
A nucleic acid involving generation of presenilin-2 gene lacking
exon 5 type-aberrant splicing
JOURNAL
Patent: JP 2003018991-A 2 21-JAN-2003;
Japan Science and Technology Corporation, Taisho Pharmaceutical Co
Ltd
COMMENT
OS Artificial Sequence
PN JP 2003018991-A/2
PD 21-JAN-2003
PF 27-JUN-2001 JP 2001195472
PI masaya toyama,kazunori imaizumi,yoko ikeda,taichi katayama PI
takayuki manabe
CC Description of Artificial Sequence: a sequence for binding CC
region.
FH Key Location/Qualifiers.
FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAG 1648
|||||
Db 11 CTTGTAGCAG 2

RESULT 720
BD189593/c
LOCUS
DEFINITION
A nucleic acid involving generation of presenilin-2 gene lacking
exon 5 type-aberrant splicing.
ACCESSION
BD189593
VERSION
BD189593.1 GI:32999332
KEYWORDS
WO 03002742-A/2.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 11)
Toyama,M., Katayama,T., Manabe,T., Kazunori, Imaizumi and Ikeda,Y.
AUTHORS
TITLE
A nucleic acid involving generation of presenilin-2 gene lacking
exon 5 type-aberrant splicing
JOURNAL
Patent: WO 03002742-A 2 09-JAN-2003;

FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAG 1648
|||||
Db 11 CTTGTAGCAG 2

RESULT 721
BD190136/c
LOCUS
DEFINITION
Pharmaceutical composition.
ACCESSION
BD190136
VERSION
BD190136.1 GI:32999875
KEYWORDS
WO 03002146-A/2.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 11)
Toyama,M., Katayama,T., Manabe,T., Kazunori, Imaizumi and Ikeda,Y.
AUTHORS
TITLE
Pharmaceutical composition
JOURNAL
Patent: WO 03002146-A 2 09-JAN-2003;
JAPAN SCIENCE AND TECHNOLOGY CORP,TAISHO PHARMACEUTICAL CO LTD,
MASAYA TOYAMA,TAIICHI KATAYAMA,TAKAYUKI MANABE,KAZUNORI
IMAIZUMI,YOKO IKEDA
COMMENT
OS Artificial Sequence
PN WO 03002146-A/2
PD 09-JAN-2003
PF 27-JUN-2002 WO 2002JP006461
PI MASAYA TOYAMA,TAIICHI KATAYAMA,TAKAYUKI MANABE,KAZUNORI PI
IMAIZUMI,YOKO IKEDA
PC A61K45/00,A61K48/00,A61P25/00,A61P25/16,A61P25/28,A61P43/00 CC
Description of Artificial Sequence: a sequence of binding CC
region
FH Key Location/Qualifiers
FT source 1. .11
/organism="Artificial Sequence".
FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAG 1648
|||||
Db 11 CTTGTAGCAG 2

RESULT 722
BD190136/c
LOCUS
DEFINITION
Pharmaceutical composition.
ACCESSION
BD190136
VERSION
BD190136.1 GI:32999875
KEYWORDS
WO 03002146-A/2.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 11)
Toyama,M., Katayama,T., Manabe,T., Kazunori, Imaizumi and Ikeda,Y.
AUTHORS
TITLE
Pharmaceutical composition
JOURNAL
Patent: WO 03002146-A 2 09-JAN-2003;
JAPAN SCIENCE AND TECHNOLOGY CORP,TAISHO PHARMACEUTICAL CO LTD,
MASAYA TOYAMA,TAIICHI KATAYAMA,TAKAYUKI MANABE,KAZUNORI
IMAIZUMI,YOKO IKEDA
COMMENT
OS Artificial Sequence
PN WO 03002146-A/2
PD 09-JAN-2003
PF 27-JUN-2002 WO 2002JP006461
PI MASAYA TOYAMA,TAIICHI KATAYAMA,TAKAYUKI MANABE,KAZUNORI PI
IMAIZUMI,YOKO IKEDA
PC A61K45/00,A61K48/00,A61P25/00,A61P25/16,A61P25/28,A61P43/00 CC
Description of Artificial Sequence: a sequence of binding CC
region
FH Key Location/Qualifiers
FT source 1. .11
/organism="Artificial Sequence".
FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAG 1648
|||||
Db 11 CTTGTAGCAG 2
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Db      11 CTTGTAGCAG 2

RESULT 722
AR030066
LOCUS      AR030066      12 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 255 from patent US 5861244.
ACCESSION AR030066
VERSION    AR030066.1 GI:5943280
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 12)
AUTHORS    Wang, C.-G. and Hepburn, A.G.
TITLE      Genetic sequence assay using DNA triple strand formation
JOURNAL
FEATURES   Location/Qualifiers
            source
            1..12
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      7.2%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1747 TCCTATCCT 1756
        |||||
        1 TCCTATCCT 10

Db

RESULT 723
AR0303946/c
LOCUS      AR0303946      12 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 11 from patent US 6544755.
ACCESSION AR0303946
VERSION    AR0303946.1 GI:31692817
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 12)
AUTHORS    Thompson, J.D. and Draper, K.G.
TITLE      Method and reagent for treatment of diseases by expression of the
JOURNAL    c-Myc gene
FEATURES   Patent: US 6544755-A 11 08-APR-2003;
            Location/Qualifiers
            source
            1..12
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      7.2%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1693 TGTCTCCTCC 1692
        |||||
        11 TGTCTCCTCC 2

Db

RESULT 724
A08720/c
LOCUS      A08720      14 bp      DNA      linear      PAT 09-AUG-1993
DEFINITION Nucleotide sequence 7 from patent number WO9010713.
ACCESSION A08720
VERSION    A08720.1 GI:411729
KEYWORDS
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 14)
AUTHORS
TITLE      METHOD FOR STABILIZING THE HYBRIDIZATION OF COMPLEMENTARY

Db      11 CTTGTAGCAG 2

POLYNUCLEOTIDE SEQUENCES
JOURNAL Patent: WO 9010713-A 7 20-SEP-1990;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      7.2%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1634 TGGGGCTTGT 1643
        |||||
        13 TGGGGCTTGT 4

Db

RESULT 725
A08721
LOCUS      A08721      14 bp      DNA      linear      PAT 09-AUG-1993
DEFINITION reverse complement.
ACCESSION A08721
VERSION    A08721.1 GI:411730
KEYWORDS
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 14)
AUTHORS
TITLE      METHOD FOR STABILIZING THE HYBRIDIZATION OF COMPLEMENTARY
JOURNAL    POLYNUCLEOTIDE SEQUENCES
FEATURES   Patent: WO 9010713-A 8 20-SEP-1990;
            Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      7.2%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1634 TGGGGCTTGT 1643
        |||||
        2 TGGGGCTTGT 11

Db

RESULT 726
E03997
LOCUS      E03997      14 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Allele-specific probe for the apolipoprotein E gene.
ACCESSION E03997
VERSION    E03997.1 GI:2172208
KEYWORDS   JP 1992320700-A/8.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Toyosato, M., Kosaka, T. and Mizuno, K.
TITLE      METHOD FOR TESTING APOLIPOPROTEIN E GENOTYPE AND PRIMER AND PROBE
JOURNAL    SUITABLE FOR ITS TESTING
            Patent: JP 1992320700-A 8 11-NOV-1992;
            NIPPON SHOJI KK
COMMENT     OS Artificial gene
            OC Artificial sequence; Genes.
            PN JP 1992320700-A/8
            PD 11-NOV-1992
            PF 17-APR-1991 JP 1991112435
            PI TOYOSATO MITSUYOSHI, KOSAKA TETSUYA, MIZUNO KOJI PC
            CI2Q1/68,C07H21/04,C12N15/10,C12N15/11,G01N33/50; CC
            strandedness: Single;
            CC topology: Linear;
            FH Key
            Location/Qualifiers

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FH      allele      replace(6,'t')
FT      /note='epsilon 7 allele'.
FT      Location/Qualifiers
FEATURES   source
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            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      7.2%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGC 1695
      |||||
Db 4 CTCCTCCAGC 13

RESULT 727
E04001/c
LOCUS      14 bp DNA linear PAT 29-SEP-1997
DEFINITION Allele-specific probe for the apolipoprotein E gene.
ACCESSION E04001
VERSION E04001.1 GI:2172212
KEYWORDS JP 1992320700-A/12.
SOURCE synthetic construct
ORGANISM synthetic sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Toyosato,M., Kosaka T. and Mizuno,K.
TITLE METHOD FOR TESTING APOLIPOPROTEIN E GENOTYPE AND PRIMER AND PROBE
JOURNAL NIPPON SHOJI KK
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
FN JP 1992320700-A/12
PD 11-NOV-1992
PF 17-APR-1991 JP 1991112435
PI TOYOSATO MITSUYOSHI, KOSAKA TETSUYA, MIZUNO KOJI PC
C1201/68.C07H21/04.C12N15/10.C12N15/11.G01N33/50; CC
strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT allele      replace(9,'a')
FT      /note='epsilon 7 allele'.
FT      Location/Qualifiers
FEATURES   source
            1..14
            /organism="synthetic construct"
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            /db_xref="taxon:32630"

Query Match      7.2%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGC 1695
      |||||
Db 11 CTCCTCCAGC 2

RESULT 728
I39737/c
LOCUS      14 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 10 from patent US 5616490.
ACCESSION I39737
VERSION I39737.1 GI:2084217
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)

AUTHORS Sullivan,S.M. and Draper,K.G.
TITLE Ribozymes targeted to TNF-.alpha. RNA
JOURNAL Patent: US 5616490-A 10 01-APR-1997;
FEATURES   Location/Qualifiers
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      7.2%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1693 AGCGTGGTGG 1702
      |||||
Db 10 AGCGTGGTGG 1

RESULT 729
AR055901/c
LOCUS      15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 105 from patent US 5837542.
ACCESSION AR055901
VERSION AR055901.1 GI:5981478
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 105 17-NOV-1998;
FEATURES   Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 GCTGGAACCC 1679
      |||||
Db 13 GCTGGAACCC 4

RESULT 730
AR055902/c
LOCUS      15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 106 from patent US 5837542.
ACCESSION AR055902
VERSION AR055902.1 GI:5981479
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 106 17-NOV-1998;
FEATURES   Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 GCTGGAACCC 1679
      |||||
Db 12 GCTGGAACCC 3

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RESULT 731
AR113659/c
LOCUS AR113659 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 105 from patent US 6132967.
ACCESSION AR113659
VERSION AR113659.1 GI:14093981
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 105 17-OCT-2000;
FEATURES
source
1. .15
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 GCTGGAACCC 1679
Db 13 GCTGGAACCC 4

RESULT 732
AR113660/c
LOCUS AR113660 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 106 from patent US 6132967.
ACCESSION AR113660
VERSION AR113660.1 GI:14093982
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 106 17-OCT-2000;
FEATURES
source
1. .15
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 GCTGGAACCC 1679
Db 13 GCTGGAACCC 4

RESULT 733
AR116338
LOCUS AR116338 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 26 from patent US 6133031.
ACCESSION AR116338
VERSION AR116338.1 GI:14096660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)

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AUTHORS Monia,B.P. and Jaarde,W.A.
TITLE Antisense inhibition of focal adhesion kinase expression
JOURNAL Patent: US 6133031-A 26 17-OCT-2000;
FEATURES
source
1. .15
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1645 GCAGAGGCCA 1634
Db 5 GCAGAGGCCA 14

RESULT 734
AX084987/c
LOCUS AX084987 15 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 164 from Patent WO0113117.
ACCESSION AX084987
VERSION AX084987.1 GI:13275135
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1
AUTHORS Herath,H.M.
TITLE Proteins, genes and their use for diagnosis and treatment of breast cancer
JOURNAL Patent: WO 0113:17-A 164 22-FEB-2001;
Oxford GlycoSciences (UK) Limited (GB)
FEATURES
source
1. .15
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32830"
/notes="Probe"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1659 CCAGGCTCAC 1668
Db 10 CCAGGCTCAC 1

RESULT 735
AX374605/c
LOCUS AX374605 15 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 26 from Patent WO0210454.
ACCESSION AX374605
VERSION AX374605.1 GI:19169502
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1
AUTHORS Choi,J.Y., Koshiy,B., Kliem,S. and Stephens,J.C.
TITLE Haplotypes of the alas2 gene
JOURNAL Patent: WO 0210454-A 26 07-FEB-2002;
Genaisance Pharmaceuticals, Inc. (US)
FEATURES
source
1. .15
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;

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Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1757 AAAGGCCACTG 1768
Db 14 RAAGGCCACTG 3
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|||||

RESULT 736
AX632978/c
LOCUS AX632978 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 117 from Patent EP1260586.
ACCESSION AX632978
VERSION AX632978.1 GI:28468592
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Wolf,T.
Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL
Patent: EP 1260586-A 117 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
LOCATION/Qualifiers
1. .15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1670 GCTGGAACCC 1679
Db 13 GCTGGAACCC 4
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RESULT 737
AX632980/c
LOCUS AX632980 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 119 from Patent EP1260586.
ACCESSION AX632980
VERSION AX632980.1 GI:28468594
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Wolf,T.
Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL
Patent: EP 1260586-A 119 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
LOCATION/Qualifiers
1. .15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1670 GCTGGAACCC 1679
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Db 12 GCTGGAACCC 3
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RESULT 738
AX763334/c
LOCUS AX763334 15 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 27 from Patent WO03039703.
ACCESSION AX763334
VERSION AX763334.1 GI:32257902
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Weizenegger,M.
Method in the form of a dry rapid test for detecting nucleic acids
Patent: WO 03039703-A 27 15-MAY-2003;
Hain Lifeschience GmbH (DE)
LOCATION/Qualifiers
1. .15
/organism="Treponema denticola"
/mol_type="unassigned DNA"
/db_xref="taxon:158"

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Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 739
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DEFINITION Sequence 26 from Patent WO03040388.
ACCESSION AX763665
VERSION AX763665.1 GI:32258032
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Weizenegger,M.
Method for detecting bacteria associated with parodontitis and
tooth decay
Patent: WO 03040388-A 26 15-MAY-2003;
Hain Lifeschience GmbH (DE)
LOCATION/Qualifiers
1. .15
/organism="Treponema denticola"
/mol_type="unassigned DNA"
/db_xref="taxon:158"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1749 CCTATCCTTAAG 1760
Db 12 CCTATCCTTAAG 1
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Search completed: August 30, 2004, 09:17:59
Job time : 3 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 09:20:29 ; Search time 1 Seconds

(without alignments)

5.663 Million cell updates/sec

Title: US-09-925-139-3

Perfect score: 139

Sequence: 1 ggatggggctgttagcagaa.....ctatccataaaggccactgg 139

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 1315 seqs, 20372 residues

Total number of hits satisfying chosen parameters: 2630

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1332 summaries

Database : rng3.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	14.4	20	1	ABT13031
4	20	14.4	20	1	ABX12200
5	20	14.4	20	1	ABX12198
6	20	14.4	20	1	ABX12217
7	20	14.4	20	1	ABX12175
8	20	14.4	20	1	ABX12219
9	20	14.4	20	1	ABX12220
10	20	14.4	20	1	ABX12199
11	20	14.4	20	1	ABX12218
12	18	12.9	18	1	AAI56642
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14	17	12.2	17	1	AAI22550
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22	15	10.8	15	1	AAI49841
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33	15	10.8	15	1	AAI49817

34	15	10.8	15	1	AAI49833	Human CETP HH ribo
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37	15	10.8	15	1	AAI49835	Human CETP HH ribo
38	14.8	10.6	20	1	ABZ03987	Human genotyping P
39	14.8	10.6	20	1	ABZ85226	Human oligonucleot
40	14.6	10.5	21	1	AAI1514	Human oligonucleot
41	14.6	10.5	21	1	AAI36969	Human dysferlin PC
42	14.4	10.4	18	1	ABZ15844	Human dysferlin ex
43	14.4	10.4	20	1	ABV73609	Cyp-C probe genera
44	14.4	10.4	20	1	ABZ31506	S. albulus plasmid
45	14.4	10.4	20	1	ABZ31506	Candida albicans G
46	14.4	10.4	20	1	ABZ31506	Capture oligonucle
47	14.2	10.2	21	1	ABZ31506	Human DISC1/DISC2
48	14.2	10.2	20	1	AAQ08080	Europium (III) tex
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50	14.2	10.2	20	1	AAQ081567	Dysprosium (III) t
51	14.2	10.2	20	1	AAQ081567	Hepatitis B virus
52	14.2	10.2	20	1	AAV07290	pi42, PCR primer u
53	14.2	10.2	20	1	AAV07290	Oligonucleotide #4
54	14.2	10.2	20	1	AAV07290	Texaphyrin oligonu
55	14.2	10.2	20	1	AAZ88439	Antisense primer f
56	14.2	10.2	20	1	AAZ88439	Exemplary texaphyr
57	14.2	10.2	20	1	AAZ88439	Human diacylglycer
58	14.2	10.2	20	1	AAZ88439	Human RECQ2 antis
59	14.2	10.2	20	1	ADB83449	Stabilising reagen
60	14.2	10.2	20	1	ADB83449	Antisense oligonu
61	14.2	10.2	20	1	ADB83449	Antisense oligo (S
62	14.2	10.2	20	1	ADB83449	Cosmid amplificati
63	14.2	10.2	20	1	ADB83449	Human VH PCR prime
64	14	10.1	20	1	AAI58421	Oct-4 transcript R
65	13.8	9.9	17	1	AAV91006	Human C-raf target
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67	13.8	9.9	17	1	ACD50855	HBV hammerhead rib
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70	13.8	9.9	17	1	ACD53478	HBV G-cleaver subs
71	13.8	9.9	18	1	AAZ28045	PCR primer for hum
72	13.8	9.9	19	1	ADE15603	Tricyclic dextroca
73	13.8	9.9	20	1	AAV26436	PCR primer "A gamm
74	13.8	9.9	20	1	AAI65593	Human uteroglobin
75	13.8	9.9	20	1	AAH78641	Probe for mechan
76	13.8	9.9	20	1	AAI19416	Human delta-6-desa
77	13.8	9.9	20	1	AAI22845	CD34 cell marker D
78	13.8	9.9	20	1	ABX78257	Human bifunctional
79	13.8	9.9	20	1	ABZ92121	Human oligonucleot
80	13.8	9.9	20	1	ABX10328	Corynebacterium bacte
81	13.8	9.9	20	1	AAI55794	Probe #1 used to i
82	13.8	9.9	20	1	ADC66381	Human collapsin re
83	13.8	9.9	21	1	AAA94234	Human testosterone
84	13.8	9.9	21	1	AAI57821	Reverse PCR primer
85	13.8	9.9	21	1	ACF36406	TRPM-2 antisense o
86	13.6	9.8	20	1	AAQ46059	Sequence of PCR pr
87	13.6	9.8	20	1	AAI42248	Primer derived fro
88	13.6	9.8	20	1	AAI66085	Plasminogen activa
89	13.6	9.8	20	1	AAV62008	L monocytogenes hl
90	13.6	9.8	20	1	AAI22801	PCR primer 82689,
91	13.6	9.8	20	1	AAZ04070	PCR primer used to
92	13.6	9.8	20	1	AAI78426	Rat GAPDH primer 3
93	13.6	9.8	20	1	AAI25929	GAPDH reverse prim
94	13.6	9.8	20	1	AAI97388	Primer used to amp
95	13.6	9.8	20	1	AAI97331	Primer used to amp
96	13.6	9.8	20	1	AAZ76046	Human biallelic ma
97	13.6	9.8	20	1	AAH38150	SNP specific lower
98	13.6	9.8	20	1	AAH20719	Human telomeric re
99	13.6	9.8	20	1	AAH80623	Oligonucleotide hy
100	13.6	9.8	20	1	ABN83384	Glycerolaldehyde-3-p
101	13.6	9.8	20	1	ABZ93876	Human oligonucleot
102	13.6	9.8	20	1	ABZ99199	Human PDB4C oligon
103	13.6	9.8	20	1	ABZ55740	Glycerolaldehyde-3-p
104	13.6	9.8	20	1	ADD81514	HBV PRT antisense
105	13.4	9.5	17	1	ACD53920	HBV zincyme substr
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107	13.4	9.6	18	1	AA050940	T-cell antigen rec	180	12.8	9.2	18	1	AAA92609	Antisense oligonuc
108	13.4	9.6	18	1	ABL88809	HIV-1 related bind	c 181	12.8	9.2	19	1	AAV01272	Chymotrypsinogen p
109	13.4	9.6	18	1	ACC83346	T7 forward PCR pri	c 182	12.8	9.2	19	1	AAV34507	BRCA1 exon 21 reve
110	13.4	9.6	18	1	ACF05396	Bacteriophage T7 f	183	12.8	9.2	19	1	AAA47015	Raf-1 PCR primer,
111	13.4	9.6	19	1	AA828293	cdk4 ribozyme bind	184	12.8	9.2	19	1	AA828293	cdk3 ribozyme bind
112	13.4	9.6	19	1	AA511763	Primer to amplify	185	12.8	9.2	19	1	AAH57904	Cell-cycle depende
113	13.4	9.6	19	1	AAH58085	Cell-cycle depende	186	12.6	9.1	13	1	ABF35838	Oligonucleotide SE
114	13.4	9.6	19	1	ABL43426	Human chromosome 1	c 187	12.6	9.1	13	1	ABF35839	Oligonucleotide SE
115	13.4	9.6	19	1	ABL43434	Human chromosome 1	188	12.6	9.1	19	1	AA084806	Spinocerebellar at
116	13.4	9.6	20	1	AAF60107	Human ATM gene exo	189	12.6	9.1	19	1	AA085482	Pathogenic filamen
117	13.4	9.6	20	1	AAF60177	Human cytohesin-2	190	12.6	9.1	19	1	AA085482	Primer/probe #4 fo
118	13.4	9.6	20	1	AAF86771	Human cytohesin-2	191	12.6	9.1	19	1	AA085488	Wheat microsatelli
119	13.4	9.6	20	1	AA052270	Human IFNGR2 antis	192	12.6	9.1	19	1	AA085488	Cyclin A1 ribozyme
120	13.2	9.5	18	1	AA160161	Collagen gene prom	193	12.6	9.1	19	1	AA085488	Cyclin A1 ribozyme
121	13.2	9.5	18	1	AA160161	Human leukocyte an	c 194	12.6	9.1	19	1	AA085488	Cyclin A1 ribozyme
122	13.2	9.5	18	1	AA110567	Smad2 antisense ol	195	12.6	9.1	19	1	AA085488	Cyclin A1 ribozyme
123	13.2	9.5	18	1	AA110567	Collagen promoter	196	12.6	9.1	19	1	AA085488	Cyclin A1 ribozyme
124	13.2	9.5	18	1	AA092575	Antisense oligonuc	197	12.4	8.9	15	1	AAQ34483	Wheat microsatelli
125	13.2	9.5	18	1	AA092575	Antisense oligo, I	198	12.4	8.9	15	1	AAQ34483	Cyclin A1 ribozyme
126	13.2	9.5	18	1	ABR83357	Mouse WP-1 antisen	199	12.4	8.9	16	1	AAQ56245	Cyclin D1 ribozyme
127	13.2	9.5	18	1	ABR83357	Human chromosome 1	c 200	12.4	8.9	16	1	AAQ56245	Cyclin D1 ribozyme
128	13.2	9.5	19	1	ABL45037	Human SRC-1 antis	201	12.4	8.9	16	1	AAQ56245	Cyclin D1 ribozyme
129	13.2	9.5	19	1	AAQ91454	Dysprosium (III) t	202	12.4	8.9	16	1	AAQ56245	Cyclin D1 ribozyme
130	13.2	9.5	19	1	AAV07302	Metallotexaphyrin-	c 203	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
131	13.2	9.5	19	1	AA066840	Human tankyrase II	204	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
132	13.2	9.5	19	1	ABX95438	Human connexin 45	c 205	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
133	13.2	9.5	19	1	AD229769	Mitogen activated	c 206	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
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136	13.2	9.5	20	1	AA080655	Primer amplifies p	c 209	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
137	13.2	9.5	20	1	AA080655	Primer #4 for ente	c 210	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
138	13.2	9.5	20	1	AA080655	Calcium ion channe	c 211	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
139	13.2	9.5	20	1	AA080655	PCR primer used to	c 212	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
140	13.2	9.5	20	1	AA080655	PI3K antisense inh	c 213	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
141	13.2	9.5	20	1	AA080655	Mouse GAPDH PCR pr	c 214	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
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143	13.2	9.5	20	1	AA080655	16S/23S rRNA spacer	c 216	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
144	13.2	9.5	20	1	AA080655	Human hepsin antis	c 217	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
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146	13.2	9.5	20	1	AA080655	Mouse C/EBP beta p	c 219	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
147	13.2	9.5	20	1	AA080655	Human oligonucleot	c 220	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
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151	13.2	9.5	20	1	AA080655	Oligonucleotide SE	c 224	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
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154	13.2	9.5	20	1	AA080655	Rabbit CERP HH rib	c 227	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
155	13.2	9.5	20	1	AA080655	HBV amberyzyme subs	c 228	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
156	13.2	9.5	20	1	AA080655	Leptin gene-specif	c 229	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
157	13.2	9.5	20	1	AA080655	Human Oct-4 specif	c 230	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
158	13.2	9.5	20	1	AA080655	Human superoxide d	c 231	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
159	12.8	9.2	17	1	AAQ91452	Dysprosium (III) t	c 232	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
160	12.8	9.2	17	1	AAQ91452	Mouse flt-1 VEGF r	c 233	12.4	8.9	17	1	AAQ56245	Cyclin D1 ribozyme
161	12.8	9.2	17	1	AAV07298	Metallotexaphyrin-	c 234	12.2	8.8	17	1	AAV91297	Human C-raf target
162	12.8	9.2	17	1	AAV91007	Human C-raf target	c 235	12.2	8.8	17	1	AAV91297	Human C-raf target
163	12.8	9.2	17	1	AAV93413	Human B-raf subutr	c 236	12.2	8.8	17	1	AAV93415	Human B-raf subutr
164	12.8	9.2	17	1	AAV93414	Human B-raf subutr	c 237	12.2	8.8	17	1	AAV93415	Human B-raf subutr
165	12.8	9.2	17	1	AAV93414	Hepatitis B virus	c 238	12.2	8.8	17	1	AAV93415	Human B-raf subutr
166	12.8	9.2	17	1	AAV93414	Human urokinase ge	c 239	12.2	8.8	17	1	AAV93415	Human B-raf subutr
167	12.8	9.2	17	1	ABK18660	Human ERG G-cleave	c 240	12.2	8.8	17	1	ABK18660	Human ERG G-cleave
168	12.8	9.2	17	1	ABK17683	Human ERG hammerhe	c 241	12.2	8.8	17	1	ABK17683	Human ERG hammerhe
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170	12.8	9.2	17	1	ABK17683	Human tumour suppr	c 243	12.2	8.8	17	1	ABK17683	Human tumour suppr
171	12.8	9.2	17	1	ABK17683	HBV inozyme subutr	c 244	12.2	8.8	17	1	ABK17683	HBV inozyme subutr
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C 253	12.2	8.8	17	1	ABT34389	Tumour suppression	C 326	11.8	8.5	15	1	AAV07304	Metalloproteinase
C 254	12.2	8.8	17	1	ABT40165	Tumour suppression	C 327	11.8	8.5	15	1	AAV54266	Primer K155 used
C 255	12.2	8.8	17	1	ACA07738	NFKB sub-unit modu	C 328	11.8	8.5	15	1	AAV55348	Soluble sc-TCR fus
C 256	12.2	8.8	17	1	ACA09103	NFKB sub-unit modu	C 329	11.8	8.5	15	1	AAV66971	Human leukocyte an
C 257	12.2	8.8	17	1	ACA09102	NFKB sub-unit modu	C 330	11.8	8.5	15	1	AAV47176	IGFBP3 oligonucleo
C 258	12.2	8.8	17	1	ADA99593	Human MD23 scannin	C 331	11.8	8.5	15	1	AAV52890	IGFBP3 oligonucleo
C 259	12.2	8.8	17	1	ADA99410	Human MD23 scannin	C 332	11.8	8.5	15	1	AAV47174	IGFBP3 oligonucleo
C 260	12.2	8.8	17	1	ABT65014	Human HER2 DNzyme	C 333	11.8	8.5	15	1	AAV52891	IGFBP3 oligonucleo
C 261	12.2	8.8	17	1	ACD55654	HBV amebzyme subs	C 334	11.8	8.5	15	1	AAV52889	IGFBP3 oligonucleo
C 262	12.2	8.8	17	1	ACD67113	Murine oligonucleo	C 335	11.8	8.5	15	1	ABV99795	Human PKF82 allel
C 263	12.2	8.8	17	1	ABT45561	Tumour suppression	C 336	11.8	8.5	15	1	AAV99376	Aldehyde dehydroge
C 264	12.2	8.8	17	1	ABT30685	Cholesterol homeos	C 337	11.8	8.5	15	1	ACD56639	HBV enzymatic nucl
C 265	12.2	8.8	17	1	AAV92642	Antisense oligonuc	C 338	11.8	8.5	15	1	ACD56644	HBV enzymatic nucl
C 266	12.2	8.8	18	1	ABT61371	Amidophosphoribos	C 339	11.8	8.5	16	1	AAQ91451	Dysprosium (III) t
C 267	12.2	8.8	18	1	AAV35472	Immunoglobulin hea	C 340	11.8	8.5	16	1	AAV07300	Metalloproteinase
C 268	12.2	8.8	18	1	AAV16095	PCR primer used in	C 341	11.8	8.5	16	1	AAV07308	Tetraphyrin oligonu
C 269	12.2	8.8	18	1	AAV08683	Primer ATP/20RT fo	C 342	11.8	8.5	16	1	AAZ97664	HIV-1 protease gen
C 270	12.2	8.8	18	1	AAV24515	Human SR-BI gene e	C 343	11.8	8.5	16	1	AAZ88440	Exemplary tetaphyr
C 271	12.2	8.8	18	1	AAV24607	Human SR-BI gene e	C 344	11.8	8.5	16	1	ABX14989	Human delta opioide
C 272	12.2	8.8	18	1	AAV38311	Human ATL regulato	C 345	11.8	8.5	16	1	ABT34281	Opioid receptor D1
C 273	12.2	8.8	18	1	AAV61311	Human ACE, AGT and	C 346	11.8	8.5	17	1	AAV69127	Human flt1 VEGF re
C 274	12.2	8.8	18	1	AAV61109	PCR primer SQ ID	C 347	11.8	8.5	17	1	AAV69126	Human flt1 VEGF re
C 275	12.2	8.8	18	1	AAV58358	Human PRO2145 reve	C 348	11.8	8.5	17	1	AAV97558	Human EGF-R target
C 276	12.2	8.8	18	1	AAV75254	Human inducible NO	C 349	11.8	8.5	17	1	AAV57626	HSV-1 thymidine ki
C 277	12.2	8.8	18	1	AAV14080	Forward PCR primer	C 350	11.8	8.5	17	1	AAV17419	Aryl hydrocarbon n
C 278	12.2	8.8	18	1	AAV25354	Antisense oligonuc	C 351	11.8	8.5	17	1	AAV18520	Human TIE-2 substr
C 279	12.2	8.8	18	1	AAV59542	Otoferlin exon PCR	C 352	11.8	8.5	17	1	AAV22628	Integrin subunit b
C 280	12.2	8.8	18	1	AAV79532	Caspase-4 protease	C 353	11.8	8.5	17	1	AAV93558	Human B-raf subtr
C 281	12.2	8.8	18	1	ABZ80661	Magnaporthe grisea	C 354	11.8	8.5	17	1	AAV91355	Human C-raf target
C 282	12.2	8.8	18	1	ABV98053	Human multidrug re	C 355	11.8	8.5	17	1	AAV92633	Human A-raf subtr
C 283	12.2	8.8	18	1	ABX10592	PCR primer, ZC22,1	C 356	11.8	8.5	17	1	AAV15355	HSV-1 thymidine ki
C 284	12.2	8.8	18	1	ACD44968	Human SR-BI gene P	C 357	11.8	8.5	17	1	AAV79845	Hepatitis B virus
C 285	12.2	8.8	18	1	ABC24242	Human NOV1b revers	C 358	11.8	8.5	17	1	AAV01906	Hammerhead ribozym
C 286	12.2	8.8	18	1	ABC98350	ACLP06 polymorphis	C 359	11.8	8.5	17	1	AAV67340	Alzheimer's diseas
C 287	12.2	8.8	18	1	ABE78579	Human CERP DNA rel	C 360	11.8	8.5	17	1	AAV67310	Alzheimer's diseas
C 288	12.2	8.8	21	1	AAI66686	Endogenous caroten	C 361	11.8	8.5	17	1	ABV81112	LDLR mutation corr
C 289	12.2	8.6	12	1	ABH93471	Oligonucleotide pr	C 362	11.8	8.5	17	1	ABV7557	Beta globin mutati
C 290	12.2	8.6	12	1	ABH80452	Oligonucleotide pr	C 363	11.8	8.5	17	1	ABV7558	Beta globin mutati
C 291	12.2	8.6	12	1	ABH12177	Oligonucleotide SE	C 364	11.8	8.5	17	1	ABV7561	Beta globin mutati
C 292	12.2	8.6	13	1	ABC63273	Oligonucleotide SE	C 365	11.8	8.5	17	1	ABV81113	LDLR mutation corr
C 293	12.2	8.6	13	1	ABF24345	Oligonucleotide SE	C 366	11.8	8.5	17	1	ABV7562	Beta globin mutati
C 294	12.2	8.6	13	1	ABH00388	Oligonucleotide SE	C 367	11.8	8.5	17	1	AAH24589	Human endometrium
C 295	12.2	8.6	13	1	ABH00389	Oligonucleotide SE	C 368	11.8	8.5	17	1	ABN02361	Human endometrium
C 296	12.2	8.6	13	1	ABH47625	Oligonucleotide SE	C 369	11.8	8.5	17	1	ABN02360	Human endometrium
C 297	12.2	8.6	13	1	ABF95704	Oligonucleotide SE	C 370	11.8	8.5	17	1	ABN00533	Human endometrium
C 298	12.2	8.6	13	1	ABC84321	Oligonucleotide SE	C 371	11.8	8.5	17	1	ABN00534	Human endometrium
C 299	12.2	8.6	13	1	ABC05018	Oligonucleotide SE	C 372	11.8	8.5	17	1	ABN07838	Human endometrium
C 300	12.2	8.6	13	1	ABC05019	Oligonucleotide SE	C 373	11.8	8.5	17	1	ABN02359	Human endometrium
C 301	12.2	8.6	13	1	ABC63272	Oligonucleotide SE	C 374	11.8	8.5	17	1	ABN07837	Human endometrium
C 302	12.2	8.6	13	1	ABF24344	Oligonucleotide SE	C 375	11.8	8.5	17	1	ABV79508	Human HTPL scannin
C 303	12.2	8.6	13	1	ABC84320	Oligonucleotide SE	C 376	11.8	8.5	17	1	ABV79507	Human HTPL scannin
C 304	12.2	8.6	13	1	ABH47624	Oligonucleotide SE	C 377	11.8	8.5	17	1	ABV78965	Human HTPL scannin
C 305	12.2	8.6	13	1	ABF95705	Oligonucleotide SE	C 378	11.8	8.5	17	1	ABV78967	Human HTPL scannin
C 306	12.2	8.6	15	1	AAV26061	Human apolipoprote	C 379	11.8	8.5	17	1	ABV78966	Human HTPL scannin
C 307	12.2	8.6	15	1	AAV98750	Colony stimulating	C 380	11.8	8.5	17	1	ABK18405	Human ERG hammerhe
C 308	12.2	8.6	15	1	ABL52231	Human PKG2 allele	C 381	11.8	8.5	17	1	ABV90894	Human POSHL1 scann
C 309	12.2	8.6	16	1	AAV44022	Human cytochrome P	C 382	11.8	8.5	17	1	ABV91047	Human POSHL1 scann
C 310	12.2	8.6	17	1	AAV02799	Hammerhead ribozym	C 383	11.8	8.5	17	1	ACC52599	Human tumour suppr
C 311	12.2	8.6	17	1	ABV90232	Human POSHL1 scann	C 384	11.8	8.5	17	1	ABT40179	Tumour suppression
C 312	12.2	8.6	17	1	ABV90236	Human POSHL1 scann	C 385	11.8	8.5	17	1	ABT40171	Tumour suppression
C 313	12.2	8.6	17	1	ABV90234	Human POSHL1 scann	C 386	11.8	8.5	17	1	ABT36364	Tumour suppression
C 314	12.2	8.6	17	1	ABV90235	Human POSHL1 scann	C 387	11.8	8.5	17	1	ABT38111	Tumour suppression
C 315	12.2	8.6	17	1	ABV90233	Human POSHL1 scann	C 388	11.8	8.5	17	1	ACA07737	NFKB sub-unit modu
C 316	12.2	8.6	17	1	ABV90237	Human POSHL1 scann	C 389	11.8	8.5	17	1	ADA99592	Human MD23 scannin
C 317	12.2	8.6	17	1	ABV90233	Murine oligonucleo	C 390	11.8	8.5	17	1	ADA99303	Human MD23 scannin
C 318	12.2	8.6	18	1	AAV28111	PCR primer for M.	C 391	11.8	8.5	17	1	ADA9591	Human MD23 scannin
C 319	12.2	8.6	18	1	AAV82250	Influenza virus PA	C 392	11.8	8.5	17	1	ADA99302	Human MD23 scannin
C 320	12.2	8.6	18	1	AAV46979	Bcl-Xl mRNA specif	C 393	11.8	8.5	17	1	ADA99301	Human MD23 scannin
C 321	12.2	8.6	18	1	ABZ10839	Haematopoietic cel	C 394	11.8	8.5	17	1	ABZ64947	Human MD23 scannin
C 322	11.8	8.5	15	1	AAQ050548	Human chromosome 6	C 395	11.8	8.5	17	1	ABZ65447	Human HER2 DNzyme
C 323	11.8	8.5	15	1	AAV89133	Lutetium texaphyri	C 396	11.8	8.5	17	1	ABZ64946	Human HER2 DNzyme
C 324	11.8	8.5	15	1	AAV65005	Human chromosome 6	C 397	11.8	8.5	17	1	ABZ64946	Human HER2 DNzyme
C 325	11.8	8.5	15	1	AAV98897	Probe 41w19 for HI	C 398	11.8	8.5	17	1	ABZ64792	Human HER2 DNzyme

C 399	11.8	8.5	17	1	AB264791	Human HER2 DNAzyme	472	11.4	8.2	13	1	ABC62590	Oligonucleotide SE
C 400	11.8	8.5	17	1	ACD62967	HCV minus strand D	473	11.4	8.2	13	1	ABF42171	Oligonucleotide SE
C 401	11.8	8.5	17	1	ACD52213	HBV inzyme substr	474	11.4	8.2	13	1	ABH33146	Oligonucleotide SE
C 402	11.8	8.5	17	1	ACD59647	HBV DNAzyme substr	475	11.4	8.2	13	1	ABF15452	Oligonucleotide SE
C 403	11.8	8.5	17	1	ACD62966	HCV minus strand D	476	11.4	8.2	13	1	ABF62159	Oligonucleotide SE
C 404	11.8	8.5	17	1	ACC65896	Murine oligonucleo	477	11.4	8.2	13	1	ABC49591	Oligonucleotide SE
C 405	11.8	8.5	17	1	ACC67445	Murine oligonucleo	478	11.4	8.2	13	1	ABC25065	Oligonucleotide SE
C 406	11.8	8.5	17	1	ACC63689	Murine oligonucleo	479	11.4	8.2	13	1	ABC08446	Oligonucleotide SE
C 407	11.8	8.5	17	1	ACC63888	Murine oligonucleo	480	11.4	8.2	13	1	ABC84786	Oligonucleotide SE
C 408	11.8	8.5	17	1	ABX04768	Thymidine kinase (481	11.4	8.2	13	1	ABF10343	Oligonucleotide SE
C 409	11.8	8.5	17	1	ADC37712	Human AMLPLA scann	482	11.4	8.2	13	1	ABC62760	Oligonucleotide SE
C 410	11.8	8.5	18	1	AAQ20431	Debrisoquine polym	483	11.4	8.2	13	1	ABC38204	Oligonucleotide SE
C 411	11.8	8.5	18	1	AAQ95428	Primer B (Group 3,	484	11.4	8.2	13	1	ABF36186	Oligonucleotide SE
C 412	11.8	8.5	18	1	AAV49520	Mycobacterium sp.	485	11.4	8.2	13	1	ABF42170	Oligonucleotide SE
C 413	11.8	8.5	18	1	AAV49618	AlaDH derived olig	486	11.4	8.2	13	1	ABC26849	Oligonucleotide SE
C 414	11.8	8.5	18	1	AAV47637	Primer 1, located	487	11.4	8.2	13	1	ABC62591	Oligonucleotide SE
C 415	11.8	8.5	18	1	AAV60911	Angiogenin antisen	488	11.4	8.2	13	1	ABC65199	Oligonucleotide SE
C 416	11.8	8.5	18	1	AAV60919	Angiogenin sense o	489	11.4	8.2	13	1	ABC08447	Oligonucleotide SE
C 417	11.8	8.5	18	1	AAV86530	PCR primer rb21, u	490	11.4	8.2	13	1	ABH57117	Oligonucleotide SE
C 418	11.8	8.5	18	1	AAV74957	PCR primer used to	491	11.4	8.2	13	1	ABC84686	Oligonucleotide SE
C 419	11.8	8.5	18	1	AAZ65415	Human CD71 phospho	492	11.4	8.2	13	1	ABC93116	Oligonucleotide SE
C 420	11.8	8.5	18	1	AAZ63106	Antisense oligonuc	493	11.4	8.2	13	1	ABC25064	Oligonucleotide SE
C 421	11.8	8.5	18	1	AAZ71696	Human diallelic ma	494	11.4	8.2	13	1	ABF19170	Oligonucleotide SE
C 422	11.8	8.5	18	1	AAZ84596	Probe and primer f	495	11.4	8.2	13	1	ABF19306	Oligonucleotide SE
C 423	11.8	8.5	18	1	AA503672	PCR primer rb21, u	496	11.4	8.2	13	1	ABH33147	Oligonucleotide SE
C 424	11.8	8.5	18	1	ABZ72191	Gene 216 SSCP sequ	497	11.4	8.2	13	1	ABF19307	Oligonucleotide SE
C 425	11.8	8.5	18	1	ABJ88792	HIV-1 related bind	498	11.4	8.2	13	1	ABF42169	Oligonucleotide SE
C 426	11.8	8.5	18	1	ABJ88789	HIV-1 related bind	499	11.4	8.2	13	1	ABC93115	Oligonucleotide SE
C 427	11.8	8.5	18	1	ABA97088	Human cathepsin B	500	11.4	8.2	13	1	ABC33224	Oligonucleotide SE
C 428	11.8	8.5	18	1	ABJ44660	Human chromosome 1	501	11.4	8.2	13	1	ABC93113	Oligonucleotide SE
C 429	11.8	8.5	18	1	ABK94528	Human BRCA1 gene r	502	11.4	8.2	13	1	ABC84687	Oligonucleotide SE
C 430	11.8	8.5	18	1	AB597959	Human urokinase ge	503	11.4	8.2	13	1	ABC38205	Oligonucleotide SE
C 431	11.8	8.5	18	1	AB598011	Human urokinase ge	504	11.4	8.2	13	1	ABF36187	Oligonucleotide SE
C 432	11.8	8.5	18	1	ABJ30541	Human HLA genotypi	505	11.4	8.2	13	1	ABH57116	Oligonucleotide SE
C 433	11.8	8.5	18	1	ABZ76994	Bovine DGAT PCR pr	506	11.4	8.2	13	1	ABH62557	Oligonucleotide SE
C 434	11.8	8.5	18	1	ABX75044	Human gene 216 pol	507	11.4	8.2	14	1	AAQ74479	Primer based on pl
C 435	11.8	8.5	18	1	ABZ58715	Human HAM cDNA fra	508	11.4	8.2	15	1	AAQ98901	Probe 41w32 for HI
C 436	11.8	8.5	18	1	ADC59461	Human precutin PCR	509	11.4	8.2	15	1	AAQ04287	G. oxydans T100 L-
C 437	11.8	8.5	18	1	ADJ13404	HLA class I allele	510	11.4	8.2	15	1	AAQ80594	M.tuberculosis 16S
C 438	11.8	8.5	20	1	AAH78641	Probe for mechanic	511	11.4	8.2	15	1	AAZ62841	Substrate for HH r
C 439	11.6	8.3	13	1	ABH66153	Oligonucleotide SE	512	11.4	8.2	15	1	AAZ47175	IGFp3 oligonucleo
C 440	11.6	8.3	13	1	ABH66152	Oligonucleotide SE	513	11.4	8.2	15	1	AAZ51493	IGF-I oligonucleot
C 441	11.6	8.3	15	1	AAZ44834	H. annuus slidi hom	514	11.4	8.2	15	1	AAZ53421	IGF-I oligonucleot
C 442	11.6	8.3	15	1	ABN81456	Human HPA1P allele	515	11.4	8.2	15	1	AAZ53420	IGF-I oligonucleot
C 443	11.6	8.3	15	1	ABJ36320	Human lysosomal ac	516	11.4	8.2	15	1	AAZ53669	IGF-I oligonucleot
C 444	11.4	8.2	13	1	AAAO6017	CFTR gene analysis	517	11.4	8.2	15	1	AAZ51495	IGF-I oligonucleot
C 445	11.4	8.2	13	1	ABC25889	Oligonucleotide SE	518	11.4	8.2	15	1	AAZ53670	IGF-I oligonucleot
C 446	11.4	8.2	13	1	ABC26848	Oligonucleotide SE	519	11.4	8.2	15	1	AAZ53671	IGF-I oligonucleot
C 447	11.4	8.2	13	1	ABF15453	Oligonucleotide SE	520	11.4	8.2	15	1	AAZ53419	IGF-I oligonucleot
C 448	11.4	8.2	13	1	ABC93112	Oligonucleotide SE	521	11.4	8.2	15	1	AAZ45302	Human KGNB1 gene a
C 449	11.4	8.2	13	1	ABC93117	Oligonucleotide SE	522	11.4	8.2	15	1	AAZ45302	Human GNRH2 gene p
C 450	11.4	8.2	13	1	ABC70351	Oligonucleotide SE	523	11.4	8.2	15	1	AAZ25425	Human PBR1 allele
C 451	11.4	8.2	13	1	ABC84787	Oligonucleotide SE	524	11.4	8.2	15	1	ABJ52104	Human AKR1B1 gene
C 452	11.4	8.2	13	1	ABF19171	Oligonucleotide SE	525	11.4	8.2	15	1	ABJ01115	ASO probe #1, used
C 453	11.4	8.2	13	1	ABC47949	Oligonucleotide SE	526	11.4	8.2	15	1	ABK12736	SCYA20 allele spec
C 454	11.4	8.2	13	1	ABC49590	Oligonucleotide SE	527	11.4	8.2	15	1	ABK81430	Human PRKFB2 allel
C 455	11.4	8.2	13	1	ABF10345	Oligonucleotide SE	528	11.4	8.2	15	1	ABV99783	RDG1 gene allele-s
C 456	11.4	8.2	13	1	ABF16692	Oligonucleotide SE	529	11.4	8.2	15	1	ABK96301	Human APOA4 allele
C 457	11.4	8.2	13	1	ABF16693	Oligonucleotide SE	530	11.4	8.2	15	1	ABJ16721	Hepatitis C virus
C 458	11.4	8.2	13	1	ABF47948	Oligonucleotide SE	531	11.4	8.2	15	1	ABX00692	Hepatitis B virus
C 459	11.4	8.2	13	1	ABC23225	Oligonucleotide SE	532	11.4	8.2	15	1	ABK29978	Human GNRH2 gene p
C 460	11.4	8.2	13	1	ABC62761	Oligonucleotide SE	533	11.4	8.2	15	1	AAQ35520	B allele probe SN2
C 461	11.4	8.2	13	1	ABC65198	Oligonucleotide SE	534	11.4	8.2	16	1	AAQ29804	Hypervariable regi
C 462	11.4	8.2	13	1	ABF62158	Oligonucleotide SE	535	11.4	8.2	16	1	AAQ40622	LDLR mutation corr
C 463	11.4	8.2	13	1	ABF16693	Oligonucleotide SE	536	11.4	8.2	17	1	ABA81112	LDLR mutation corr
C 464	11.4	8.2	13	1	ABF16692	Oligonucleotide SE	537	11.4	8.2	17	1	ABA81113	Primer for human s
C 465	11.4	8.2	13	1	ABH42168	Oligonucleotide SE	538	11.4	8.2	17	1	AAZ70103	Human flt1 VEGF re
C 466	11.4	8.2	13	1	ABH62596	Oligonucleotide SE	539	11.4	8.2	17	1	AAZ70102	Human flt1 VEGF re
C 467	11.4	8.2	13	1	ABC93114	Oligonucleotide SE	540	11.4	8.2	17	1	AAZ62178	Granule bound star
C 468	11.4	8.2	13	1	ABC70350	Oligonucleotide SE	541	11.4	8.2	17	1	AAV97519	Human EGF-R target
C 469	11.4	8.2	13	1	ABC25888	Oligonucleotide SE	542	11.4	8.2	17	1	AAJ18625	Human TIE-2 subutr
C 470	11.4	8.2	13	1	ABF10342	Oligonucleotide SE	543	11.4	8.2	17	1	AAJ18625	Human TIE-2 subutr
C 471	11.4	8.2	13	1	ABF10344	Oligonucleotide SE	544	11.4	8.2	17	1	AAJ18519	Human TIE-2 subutr

C 545	11.4	8.2	17	1	RAV92465	Human A-Raf substr	C 618	11.2	8.1	17	1	ABZ65014	Human HER2 DNAzyme
C 546	11.4	8.2	17	1	RAV92632	Human A-Raf substr	C 619	11.2	8.1	17	1	ADA99592	Human MD23 scannin
C 547	11.4	8.2	17	1	AAV72307	Human blood bacter	C 620	11.2	8.1	17	1	AAQ29810	C allele probe VP1
C 548	11.4	8.2	17	1	AAA60267	Mouse HPC2 cDNA ex	C 621	11.2	8.1	17	1	AAQ29815	C allele probe VP4
C 549	11.4	8.2	17	1	AAF02259	Hammerhead ribozym	C 622	11.2	8.1	17	1	AAQ29814	C allele probe VP4
C 550	11.4	8.2	17	1	ABL46650	Human GRID NCH rib	C 623	11.2	8.1	17	1	AAQ29789	C allele probe VP1
C 551	11.4	8.2	17	1	ABL46649	Human GRID NCH rib	C 624	11.2	8.1	17	1	AAQ29812	C allele probe VP2
C 552	11.4	8.2	17	1	ABL46463	Human GRID hammerh	C 625	11.2	8.1	17	1	AAQ29788	C allele probe VP1
C 553	11.4	8.2	17	1	ABL46651	Human GRID NCH rib	C 626	11.2	8.1	17	1	AAQ29811	C allele probe VP1
C 554	11.4	8.2	17	1	ABL92148	Long human Tumour	C 627	11.2	8.1	17	1	AAQ66711	Primer to amplify
C 555	11.4	8.2	17	1	ABN07835	Human GDMLP-1 17-m	C 628	11.2	8.1	17	1	AAT53734	Rat ICAM hammerhea
C 556	11.4	8.2	17	1	ABN07836	Human GDMLP-1 17-m	C 629	11.2	8.1	17	1	AAT53501	Rat ICAM hammerhea
C 557	11.4	8.2	17	1	RAA99002	Mouse prostate can	C 630	11.2	8.1	17	1	AAT60652	Antisense oligonuc
C 558	11.4	8.2	17	1	ABV78964	Human HTPL scannin	C 631	11.2	8.1	17	1	AAT70570	Haemoglobin G gamm
C 559	11.4	8.2	17	1	ABV79490	Human HTPL scannin	C 632	11.2	8.1	17	1	AAAX68727	Human flk-1 VEGF r
C 560	11.4	8.2	17	1	ABV79494	Human HTPL scannin	C 633	11.2	8.1	17	1	AAAX72948	Mouse flk-1 VEGF r
C 561	11.4	8.2	17	1	ABV79491	Human HTPL scannin	C 634	11.2	8.1	17	1	AAAX73306	Mouse flk-1 VEGF r
C 562	11.4	8.2	17	1	ABV79492	Human HTPL scannin	C 635	11.2	8.1	17	1	AAAX73324	Mouse flk-1 VEGF r
C 563	11.4	8.2	17	1	ABV79493	Human HTPL scannin	C 636	11.2	8.1	17	1	AAAX69487	Human flk1 VEGF re
C 564	11.4	8.2	17	1	ABV78968	Human HTPL scannin	C 637	11.2	8.1	17	1	AAAX73305	Mouse flk-1 VEGF r
C 565	11.4	8.2	17	1	ABV78963	Human HTPL scannin	C 638	11.2	8.1	17	1	AAT95345	Treatment of human
C 566	11.4	8.2	17	1	ABV78969	Human HTPL scannin	C 639	11.2	8.1	17	1	AAV14126	Probe HBPr42 for p
C 567	11.4	8.2	17	1	ABV91046	Human POSHL1 scann	C 640	11.2	8.1	17	1	AAAX62812	Delta-9 desaturase
C 568	11.4	8.2	17	1	ABV90586	Human POSHL1 scann	C 641	11.2	8.1	17	1	AAV44920	Promoter molecule
C 569	11.4	8.2	17	1	ABV90585	Human POSHL1 scann	C 642	11.2	8.1	17	1	AAV97520	Human EGF-R target
C 570	11.4	8.2	17	1	ABV91045	Human POSHL1 scann	C 643	11.2	8.1	17	1	AAV97591	Human EGF-R target
C 571	11.4	8.2	17	1	ABV90583	Human POSHL1 scann	C 644	11.2	8.1	17	1	AAV49878	Myo-D E-box muscle
C 572	11.4	8.2	17	1	ABV90587	Human POSHL1 scann	C 645	11.2	8.1	17	1	AAV43831	Artificial promote
C 573	11.4	8.2	17	1	ABV90584	Human POSHL1 scann	C 646	11.2	8.1	17	1	AAV44681	Bromoctrityphan-sp
C 574	11.4	8.2	17	1	ABL31671	Human HLA genotypi	C 647	11.2	8.1	17	1	AAV42344	E box nucleotide s
C 575	11.4	8.2	17	1	ABL31564	Human HLA genotypi	C 648	11.2	8.1	17	1	AAV80328	Phage lambda PCR p
C 576	11.4	8.2	17	1	ABX72073	Human tumour endot	C 649	11.2	8.1	17	1	AAA20626	Integrin alpha 6 s
C 577	11.4	8.2	17	1	ABZ69604	Human telomerase c	C 650	11.2	8.1	17	1	AAA18708	Human TIE-2 substr
C 578	11.4	8.2	17	1	ABT35614	Tumour suppression	C 651	11.2	8.1	17	1	AAA18921	Human TIE-2 substr
C 579	11.4	8.2	17	1	ABT36109	Tumour suppression	C 652	11.2	8.1	17	1	AAV91363	Human C-raf target
C 580	11.4	8.2	17	1	ABT38378	Tumour suppression	C 653	11.2	8.1	17	1	AAV92631	Human A-Raf substr
C 581	11.4	8.2	17	1	ACA08206	NFKB sub-unit modu	C 654	11.2	8.1	17	1	AAV91075	Human C-raf target
C 582	11.4	8.2	17	1	ACA08207	NFKB sub-unit modu	C 655	11.2	8.1	17	1	AAAX88523	Conus radiatus con
C 583	11.4	8.2	17	1	ACA07619	NFKB sub-unit modu	C 656	11.2	8.1	17	1	AAAX32865	HBV pre-S gene pro
C 584	11.4	8.2	17	1	ACA08196	NFKB sub-unit modu	C 657	11.2	8.1	17	1	AAAX76849	PCR primer for T66
C 585	11.4	8.2	17	1	ADB03602	Human MD27 scannin	C 658	11.2	8.1	17	1	AAAX77880	HLH protein DNA bi
C 586	11.4	8.2	17	1	ADA99413	Human MD23 scannin	C 659	11.2	8.1	17	1	AAZ23521	MyoD E box DNA mot
C 587	11.4	8.2	17	1	ADA99414	Human MD23 scannin	C 660	11.2	8.1	17	1	AAZ24146	HLH protein E box
C 588	11.4	8.2	17	1	ADA99411	Human MD23 scannin	C 661	11.2	8.1	17	1	AAZ29110	Antisense primer s
C 589	11.4	8.2	17	1	ADB03600	Human MD27 scannin	C 662	11.2	8.1	17	1	AAZ288531	MyoD E-box muscle-
C 590	11.4	8.2	17	1	ADB03601	Human MD27 scannin	C 663	11.2	8.1	17	1	AAZ47108	Rat AGRP mRNA PCR
C 591	11.4	8.2	17	1	ADB03603	Human MD27 scannin	C 664	11.2	8.1	17	1	AAA24961	Oestrogen receptor
C 592	11.4	8.2	17	1	ADA99412	Human MD23 scannin	C 665	11.2	8.1	17	1	AAF02991	Hammerhead ribozym
C 593	11.4	8.2	17	1	ADB03599	Human MD27 scannin	C 666	11.2	8.1	17	1	AAF01814	Hammerhead ribozym
C 594	11.4	8.2	17	1	ABZ65291	Human HER2 DNAzyme	C 667	11.2	8.1	17	1	ABK00575	Human NOGO Hammerh
C 595	11.4	8.2	17	1	ABZ65290	Human HER2 DNAzyme	C 668	11.2	8.1	17	1	ABK03212	Human CD20 Inozyme
C 596	11.4	8.2	17	1	ACD63408	HCV minus strand D	C 669	11.2	8.1	17	1	ABK03213	Human CD20 Inozyme
C 597	11.4	8.2	17	1	ACD55657	HBV ambezyme subs	C 670	11.2	8.1	17	1	ABK02836	Human CD20 Hammerh
C 598	11.4	8.2	17	1	ACD59262	HCV DNAzyme substr	C 671	11.2	8.1	17	1	ABK01446	Human NOGO Inozyme
C 599	11.4	8.2	17	1	ACD59261	HCV DNAzyme substr	C 672	11.2	8.1	17	1	ABK02837	Human CD20 Hammerh
C 600	11.4	8.2	17	1	ACC66380	Murine oligonucleo	C 673	11.2	8.1	17	1	ABA78857	APC mutation corre
C 601	11.4	8.2	17	1	ACC66764	Murine oligonucleo	C 674	11.2	8.1	17	1	ABA78858	APC mutation corre
C 602	11.4	8.2	17	1	ADB98907	LRP5 mutagenic PCR	C 675	11.2	8.1	17	1	AAH24608	Human endometrium
C 603	11.4	8.2	17	1	ADB42129	Tumour suppression	C 676	11.2	8.1	17	1	AAF16612	Gastric acid produ
C 604	11.4	8.2	17	1	ADB39940	Tumour suppression	C 677	11.2	8.1	17	1	ABL46487	Human GRID hammerh
C 605	11.4	8.2	17	1	ADB39941	Tumour suppression	C 678	11.2	8.1	17	1	ABL46970	Human GRID zinzyme
C 606	11.4	8.2	17	1	ADC37717	Human AMLP1a scann	C 679	11.2	8.1	17	1	ABL46776	Human GRID NCH rib
C 607	11.4	8.2	17	1	ADB44320	Tumour suppression	C 680	11.2	8.1	17	1	ABL46486	Human GRID hammerh
C 608	11.4	8.2	20	1	AA766085	Plasminogen activa	C 681	11.2	8.1	17	1	ABL92165	Long human Tumour
C 609	11.2	8.1	16	1	AAQ29795	A allele probe VP5	C 682	11.2	8.1	17	1	ABN10216	Human GDMLP-1 17-m
C 610	11.2	8.1	16	1	AAQ29793	A allele probe VP5	C 683	11.2	8.1	17	1	ABN00537	Human GDMLP-1 17-m
C 611	11.2	8.1	16	1	AAQ52859	Cytomegalovirus ta	C 684	11.2	8.1	17	1	ABN01271	Human GDMLP-1 17-m
C 612	11.2	8.1	16	1	AAA74719	Mycobacterium BCG	C 685	11.2	8.1	17	1	ABN01293	Human GDMLP-1 17-m
C 613	11.2	8.1	16	1	AAAS56873	Validation ribozym	C 686	11.2	8.1	17	1	ABN01293	Human GDMLP-1 17-m
C 614	11.2	8.1	16	1	AAI68609	ICAM-1 triple heli	C 687	11.2	8.1	17	1	ABN09665	Human GDMLP-1 17-m
C 615	11.2	8.1	16	1	ABZ34019	HTV-1 reverse tran	C 688	11.2	8.1	17	1	ABN01294	Human GDMLP-1 17-m
C 616	11.2	8.1	16	1	ADE14208	Optineurin promote	C 689	11.2	8.1	17	1	ABN10217	Human GDMLP-1 17-m
C 617	11.2	8.1	17	1	ADA99593	Human MD23 scannin	C 690	11.2	8.1	17	1	ABN01273	Human GDMLP-1 17-m
												ABN07992	Human GDMLP-1 17-m

691	11.2	8.1	17	1	ABN07993	Human GDMPLP-1 17-m	764	11.2	8.1	17	1	ACD58497	HCV DNazyme substr
c 692	11.2	8.1	17	1	ABN09667	Human GDMPLP-1 17-m	765	11.2	8.1	17	1	ACD53921	HBV zinyzme substr
693	11.2	8.1	17	1	ABN07840	Human GDMPLP-1 17-m	c 766	11.2	8.1	17	1	ACD55653	HBV amberzyme subs
694	11.2	8.1	17	1	ABQ63738	Human KTM1a porti	767	11.2	8.1	17	1	ACD51378	HBV hammerhead rib
695	11.2	8.1	17	1	ABQ63739	Human KTM1a porti	768	11.2	8.1	17	1	ACD57917	HCV DNazyme substr
696	11.2	8.1	17	1	ABK13146	Oligonucleotide us	769	11.2	8.1	17	1	ACD51053	HBV hammerhead rib
697	11.2	8.1	17	1	ABD42386	A. ochraceus il al	770	11.2	8.1	17	1	ACD64268	HCV minus strand D
698	11.2	8.1	17	1	ABK27291	Reduced linolenic	c 771	11.2	8.1	17	1	ACD64752	HCV minus strand D
c 699	11.2	8.1	17	1	ABK27292	Reduced linolenic	c 772	11.2	8.1	17	1	ACC67762	Murine oligonucleo
700	11.2	8.1	17	1	ABV79505	Human HTPL scannin	c 773	11.2	8.1	17	1	ACC64522	Murine oligonucleo
701	11.2	8.1	17	1	ABV79023	Human HTPL scannin	c 774	11.2	8.1	17	1	ACC66061	Murine oligonucleo
702	11.2	8.1	17	1	ABV79024	Human HTPL scannin	775	11.2	8.1	17	1	ACC67106	Murine oligonucleo
703	11.2	8.1	17	1	ABK19420	Human ERG Amberzym	c 776	11.2	8.1	17	1	ACC67588	Murine oligonucleo
704	11.2	8.1	17	1	ABK19419	Human ERG Amberzym	777	11.2	8.1	17	1	ACC65714	Murine oligonucleo
705	11.2	8.1	17	1	ABV90072	Human POSHL1 scann	c 778	11.2	8.1	17	1	ACC64616	Murine oligonucleo
706	11.2	8.1	17	1	ABV91247	Human POSHL1 scann	c 779	11.2	8.1	17	1	ACC64238	Murine oligonucleo
707	11.2	8.1	17	1	ABV90073	Human POSHL1 scann	780	11.2	8.1	17	1	ACC83620	Escherichia coli d
708	11.2	8.1	17	1	ABV90892	Human POSHL1 scann	c 781	11.2	8.1	17	1	ADB40118	Tumour suppression
709	11.2	8.1	17	1	ABV91245	Human POSHL1 scann	782	11.2	8.1	17	1	ADB40655	Tumour suppression
c 710	11.2	8.1	17	1	ABV91051	Human POSHL1 scann	783	11.2	8.1	17	1	ADB40250	Tumour suppression
c 711	11.2	8.1	17	1	ABV91071	Human POSHL1 scann	784	11.2	8.1	17	1	ADB39772	Tumour suppression
712	11.2	8.1	17	1	ABV91248	Human POSHL1 scann	c 785	11.2	8.1	17	1	ADC04842	Tumour suppression
713	11.2	8.1	17	1	ABV90896	Human POSHL1 scann	786	11.2	8.1	17	1	ADC04230	Human Na/H exchang
714	11.2	8.1	17	1	ABV90900	Human POSHL1 scann	787	11.2	8.1	17	1	ADC04229	Human Na/H exchang
c 715	11.2	8.1	17	1	ABV91072	Human POSHL1 scann	c 788	11.2	8.1	17	1	ADC04843	Human Na/H exchang
716	11.2	8.1	17	1	ABV91244	Human POSHL1 scann	c 789	11.2	8.1	17	1	ADB45742	Tumour suppression
717	11.2	8.1	17	1	ABV91246	Human POSHL1 scann	790	11.2	8.1	17	1	ADB45372	Tumour suppression
718	11.2	8.1	17	1	ABV91249	Human POSHL1 scann	c 791	11.2	8.1	17	1	ADB44858	Tumour suppression
719	11.2	8.1	17	1	ABV90898	Human POSHL1 scann	c 792	11.2	8.1	17	1	ADB48000	Human NOVX reverse
720	11.2	8.1	17	1	ABL30789	Human HLA genotypi	c 793	11.2	8.1	18	1	AAA92575	Antisense oligonuc
c 721	11.2	8.1	17	1	ABL31672	Human HLA genotypi	c 794	11.2	8.1	19	1	AC58274	Human PRO212 rever
722	11.2	8.1	17	1	ABK56128	Human CLC1 gene e	c 795	11.2	8.1	20	1	ADB66783	Human E2A-Pbx1 ant
723	11.2	8.1	17	1	ABK56803	Human CLC1 gene e	796	11	7.9	11	1	ABV69782	Human skin EST 756
c 724	11.2	8.1	17	1	ACA61316	Human cytochrome p	797	11	7.9	11	1	ABV62361	Human skin EST 147
725	11.2	8.1	17	1	ACC52643	Human tumour suppr	798	11	7.9	12	1	AB108693	Oligonucleotide pr
726	11.2	8.1	17	1	ACC52645	Human tumour suppr	c 799	11	7.9	12	1	AB158915	Oligonucleotide pr
727	11.2	8.1	17	1	ACC52645	Human tumour suppr	800	11	7.9	12	1	AB101113	Oligonucleotide pr
728	11.2	8.1	17	1	ACC51350	Human tumour suppr	801	11	7.9	12	1	AB153626	Oligonucleotide pr
729	11.2	8.1	17	1	ACC52642	Human tumour suppr	c 802	11	7.9	12	1	AB165852	Oligonucleotide pr
c 730	11.2	8.1	17	1	ACC51413	Human tumour suppr	c 803	11	7.9	12	1	AB133606	Oligonucleotide pr
731	11.2	8.1	17	1	ABX72090	Human tumour endot	c 804	11	7.9	12	1	AB181002	Oligonucleotide pr
732	11.2	8.1	17	1	ABT40040	Tumour suppression	805	11	7.9	12	1	AB168036	Oligonucleotide pr
c 733	11.2	8.1	17	1	ABT34526	Tumour suppression	806	11	7.9	12	1	AB159814	Oligonucleotide pr
c 734	11.2	8.1	17	1	ABT37658	Tumour suppression	c 807	11	7.9	12	1	AB177791	Oligonucleotide pr
c 735	11.2	8.1	17	1	ABT38730	Tumour suppression	808	11	7.9	12	1	ABH98049	Oligonucleotide pr
c 736	11.2	8.1	17	1	ABT37668	Tumour suppression	809	11	7.9	12	1	ABH74564	Oligonucleotide pr
737	11.2	8.1	17	1	ABT37550	Tumour suppression	810	11	7.9	12	1	AB140118	Oligonucleotide pr
c 738	11.2	8.1	17	1	ABT40013	NFKB sub-unit modu	811	11	7.9	13	1	ABC37623	Oligonucleotide SE
c 739	11.2	8.1	17	1	ACA09101	NFKB sub-unit modu	812	11	7.9	13	1	ABF98563	Oligonucleotide SE
740	11.2	8.1	17	1	ACA06383	NFKB sub-unit modu	813	11	7.9	13	1	ABH01585	Oligonucleotide SE
c 741	11.2	8.1	17	1	ACA09104	NFKB sub-unit modu	c 814	11	7.9	13	1	ABH30529	Oligonucleotide SE
742	11.2	8.1	17	1	ACA06384	NFKB sub-unit modu	815	11	7.9	13	1	ABC21702	Oligonucleotide SE
c 743	11.2	8.1	17	1	ADB04487	Human MDZ3 scannin	816	11	7.9	13	1	ABH22016	Oligonucleotide SE
c 744	11.2	8.1	17	1	ADA99556	Human MDZ3 scannin	c 817	11	7.9	13	1	ABF22699	Oligonucleotide SE
c 745	11.2	8.1	17	1	ADB04488	Human MDZ3 scannin	c 818	11	7.9	13	1	ABF28976	Oligonucleotide SE
c 746	11.2	8.1	17	1	ADA99485	Human MDZ3 scannin	c 819	11	7.9	13	1	ABH01584	Oligonucleotide SE
747	11.2	8.1	17	1	ADB03481	Human MDZ3 scannin	820	11	7.9	13	1	ABH08492	Oligonucleotide SE
c 748	11.2	8.1	17	1	AD399486	Human MDZ3 scannin	821	11	7.9	13	1	ABH22016	Oligonucleotide SE
749	11.2	8.1	17	1	ADB03480	Human MDZ3 scannin	c 822	11	7.9	13	1	ABH35639	Oligonucleotide SE
c 750	11.2	8.1	17	1	ADA99559	Human MDZ3 scannin	823	11	7.9	13	1	ABF86040	Oligonucleotide SE
c 751	11.2	8.1	17	1	ADA99555	Human MDZ3 scannin	c 824	11	7.9	13	1	ABF86041	Oligonucleotide SE
752	11.2	8.1	17	1	ADA99409	Human MDZ3 scannin	825	11	7.9	13	1	ABC82521	Oligonucleotide SE
c 753	11.2	8.1	17	1	AB261824	Human H-Ras DNazym	826	11	7.9	13	1	ABF35842	Oligonucleotide SE
c 754	11.2	8.1	17	1	AB264589	Human HER2 DNazyme	827	11	7.9	13	1	ABH30528	Oligonucleotide SE
c 755	11.2	8.1	17	1	AB260463	Human K-Ras DNazym	828	11	7.9	13	1	ABH31315	Oligonucleotide SE
756	11.2	8.1	17	1	AB265103	Human HER2 DNazyme	c 829	11	7.9	13	1	ABC82520	Oligonucleotide SE
757	11.2	8.1	17	1	AB265446	Human HER2 DNazyme	c 830	11	7.9	13	1	ABF15181	Oligonucleotide SE
c 758	11.2	8.1	17	1	AB260977	Human K-Ras DNazym	831	11	7.9	13	1	ABC33136	Oligonucleotide SE
c 759	11.2	8.1	17	1	ACD64172	HCV minus strand D	832	11	7.9	13	1	ABF15180	Oligonucleotide SE
760	11.2	8.1	17	1	ACD55658	HBV amberzyme subs	c 833	11	7.9	13	1	ABF35843	Oligonucleotide SE
c 761	11.2	8.1	17	1	ACD58401	HCV DNazyme substr	c 834	11	7.9	13	1	ABF46427	Oligonucleotide SE
762	11.2	8.1	17	1	ACD51379	HBV hammerhead rib	c 835	11	7.9	13	1	ABH05407	Oligonucleotide SE
763	11.2	8.1	17	1	ACD55659	HBV amberzyme subs	836	11	7.9	13	1	ABH35638	Oligonucleotide SE

C 837	11	7.9	13	1	ABC46634	Oligonucleotide SE	C 910	10.8	7.8	15	1	AAF51599	IGF-I oligonucleot
C 838	11	7.9	13	1	ABC21703	Oligonucleotide SE	C 911	10.8	7.8	15	1	AAF47177	IGFBP3 oligonucleo
C 839	11	7.9	13	1	ABC37622	Oligonucleotide SE	C 912	10.8	7.8	15	1	AAF51266	IGF-I oligonucleot
C 840	11	7.9	13	1	ABF35840	Oligonucleotide SE	C 913	10.8	7.8	15	1	AAF47173	IGFBP3 oligonucleo
C 841	11	7.9	13	1	ABH08493	Oligonucleotide SE	C 914	10.8	7.8	15	1	AAF51501	IGF-I oligonucleot
C 842	11	7.9	13	1	ABC61029	Oligonucleotide SE	C 915	10.8	7.8	15	1	AAF45992	IGFBP2 oligonucleo
C 843	11	7.9	13	1	ABH19250	Oligonucleotide SE	C 916	10.8	7.8	15	1	AAF51598	IGF-I oligonucleot
C 844	11	7.9	13	1	ABH21128	Oligonucleotide SE	C 917	10.8	7.8	15	1	AAF51268	IGF-I oligonucleot
C 845	11	7.9	13	1	ABF98562	Oligonucleotide SE	C 918	10.8	7.8	15	1	AAF51502	IGF-I oligonucleot
C 846	11	7.9	13	1	ABF84271	Oligonucleotide SE	C 919	10.8	7.8	15	1	AAF51269	IGF-I oligonucleot
C 847	11	7.9	13	1	ABF46426	Oligonucleotide SE	C 920	10.8	7.8	15	1	AAF69956	Human TNFRSF1B ge
C 848	11	7.9	13	1	ABF15421	Oligonucleotide SE	C 921	10.8	7.8	15	1	AAF69487	Human ILARalpha ge
C 849	11	7.9	13	1	ABH21129	Oligonucleotide SE	C 922	10.8	7.8	15	1	AAH49214	Anti-c-Ha-ras olig
C 850	11	7.9	13	1	ABH05406	Oligonucleotide SE	C 923	10.8	7.8	15	1	ABL01599	c-Ha-ras targeted
C 851	11	7.9	13	1	ABC33137	Oligonucleotide SE	C 924	10.8	7.8	15	1	ABA97499	c-Ha-ras targeted
C 852	11	7.9	13	1	ABF84270	Oligonucleotide SE	C 925	10.8	7.8	15	1	ABS97484	Human epoxide hydr
C 853	11	7.9	13	1	ABC61028	Oligonucleotide SE	C 926	10.8	7.8	15	1	ACL46735	c-Ha-ras antisense
C 854	11	7.9	13	1	ABF61028	Oligonucleotide SE	C 927	10.8	7.8	15	1	ACL82348	Nucleic acid cloni
C 855	11	7.9	13	1	ABF35841	Oligonucleotide SE	C 928	10.8	7.8	15	1	ADC84126	Human papillomavir
C 856	11	7.9	13	1	ABC46635	Oligonucleotide SE	C 929	10.8	7.8	16	1	AAQ29796	A allele probe VP6
C 857	11	7.9	13	1	ABF28977	Oligonucleotide SE	C 930	10.8	7.8	16	1	AAQ29791	A allele probe VP4
C 858	11	7.9	13	1	ABF15420	Oligonucleotide SE	C 931	10.8	7.8	16	1	AAQ29787	A allele probe RS2
C 859	11	7.9	13	1	ABH19251	Oligonucleotide SE	C 932	10.8	7.8	16	1	AAQ29809	C allele probe RS3
C 860	11	7.9	13	1	ABH22017	Oligonucleotide SE	C 933	10.8	7.8	16	1	AAQ29809	Rat ICAM hairpin r
C 861	11	7.9	14	1	AAV23395	Oligonucleotide pr	C 934	10.8	7.8	16	1	AAT53422	Haemoglobin G gamm
C 862	11	7.9	15	1	AAV31919	Peptide nucleic ac	C 935	10.8	7.8	16	1	AAT70568	PMR2 gene exon 11-
C 863	11	7.9	15	1	AAX31800	Transcript tag seq	C 936	10.8	7.8	16	1	AAT85750	p53 exon 7 PCR pri
C 864	11	7.9	15	1	AAX31164	Tag sequence of a	C 937	10.8	7.8	16	1	AAZ09804	HIV-1 protease gen
C 865	11	7.9	15	1	AAI67293	Human FKBP8 allele	C 938	10.8	7.8	16	1	AAZ97659	SNP containing pro
C 866	11	7.9	15	1	AAI67292	IGF-I oligonucleot	C 939	10.8	7.8	16	1	AAS06834	Human ribosomal pr
C 867	11	7.9	15	1	AAV50724	IGF-I oligonucleot	C 940	10.8	7.8	16	1	ABL46301	RNA binding peptid
C 868	11	7.9	15	1	AAV50721	IGF-I oligonucleot	C 941	10.8	7.8	16	1	AAA92609	Antisense oligonuc
C 869	11	7.9	15	1	AAV50725	IGF-I oligonucleot	C 942	10.6	7.6	15	1	ABN81420	Human HTARIP allel
C 870	11	7.9	15	1	AAV50723	IGF-I oligonucleot	C 943	10.6	7.6	15	1	ABN80551	Human P450(cytochr
C 871	11	7.9	15	1	AAS98658	Colony stimulating	C 944	10.6	7.6	17	1	ACD55655	HBV amebzyme subs
C 872	11	7.9	15	1	ABK92567	ASO primer #4 to d	C 945	10.6	7.6	17	1	ABV91247	Human POSHL1 scann
C 873	11	7.9	15	1	ABK92619	ASO primer #17 to	C 946	10.6	7.6	17	1	ABV91248	Human POSHL1 scann
C 874	11	7.9	15	1	ABK32117	Human colon cancer	C 947	10.4	7.5	12	1	AAV28522	Blackcurrant rever
C 875	11	7.9	15	1	ABK32754	Human colorectal a	C 948	10.4	7.5	12	1	ABH71060	Oligonucleotide pr
C 876	11	7.9	15	1	AAL39485	CCBP2 detecting AS	C 949	10.4	7.5	12	1	ABH84710	Oligonucleotide pr
C 877	11	7.9	16	1	AAQ89557	Rat CYP7 gene ster	C 950	10.4	7.5	12	1	ABH13903	Oligonucleotide pr
C 878	11	7.9	16	1	AAS09026	Human SAPI40 exon	C 951	10.4	7.5	12	1	ABH71789	Oligonucleotide pr
C 879	10.8	7.8	14	1	AAQ74120	Platelet derived g	C 952	10.4	7.5	12	1	ABI22425	Oligonucleotide pr
C 880	10.8	7.8	14	1	AAV98896	Probe 4lw18 for HI	C 953	10.4	7.5	12	1	ABI24271	Oligonucleotide pr
C 881	10.8	7.8	14	1	AAV55199	Multiple antisense	C 954	10.4	7.5	12	1	ABH77659	Oligonucleotide pr
C 882	10.8	7.8	14	1	AAX14792	Triple helix formi	C 955	10.4	7.5	12	1	ABI03913	Oligonucleotide pr
C 883	10.8	7.8	14	1	AAA34646	Human adenosine re	C 956	10.4	7.5	12	1	ABI16026	Oligonucleotide pr
C 884	10.8	7.8	14	1	AAF20768	Human multiple tar	C 957	10.4	7.5	12	1	ABI71584	Oligonucleotide pr
C 885	10.8	7.8	14	1	AAF21471	Human multiple tar	C 958	10.4	7.5	12	1	ABI73215	Oligonucleotide pr
C 886	10.8	7.8	14	1	ABZ96462	Human nucleic acid	C 959	10.4	7.5	12	1	ABI18149	Oligonucleotide pr
C 887	10.8	7.8	14	1	ABZ97165	Human MTA oligonuc	C 960	10.4	7.5	12	1	ABH72659	Oligonucleotide pr
C 888	10.8	7.8	15	1	AAQ22446	Probe (6) for DNA	C 961	10.4	7.5	12	1	ABI02394	Oligonucleotide pr
C 889	10.8	7.8	15	1	AAQ45774	Human prostate tra	C 962	10.4	7.5	12	1	ABI07435	Oligonucleotide pr
C 890	10.8	7.8	15	1	AAQ88720	c-Ha-ras modified	C 963	10.4	7.5	12	1	ABI13369	Oligonucleotide pr
C 891	10.8	7.8	15	1	AAT56203	Mouse TNF-a hammer	C 964	10.4	7.5	12	1	ABI16174	Oligonucleotide pr
C 892	10.8	7.8	15	1	AAQ97685	Biotinylated antic	C 965	10.4	7.5	12	1	ABI41618	Oligonucleotide pr
C 893	10.8	7.8	15	1	AAT44432	Antisense oligonuc	C 966	10.4	7.5	12	1	ABI46964	Oligonucleotide pr
C 894	10.8	7.8	15	1	AAT44237	c-Ha-ras antisense	C 967	10.4	7.5	12	1	ABI18906	Oligonucleotide pr
C 895	10.8	7.8	15	1	AAX33907	c-Ha-ras expressio	C 968	10.4	7.5	12	1	ABI08058	Oligonucleotide pr
C 896	10.8	7.8	15	1	AAT14843	Human prostatic tr	C 969	10.4	7.5	12	1	ABI46421	Oligonucleotide pr
C 897	10.8	7.8	15	1	AAX66553	Human CD40 hammerh	C 970	10.4	7.5	12	1	ABI50037	Oligonucleotide pr
C 898	10.8	7.8	15	1	AAX24191	Phosphononoester	C 971	10.4	7.5	12	1	ABI55710	Oligonucleotide pr
C 899	10.8	7.8	15	1	AAT50231	Rabbit CERP HH rib	C 972	10.4	7.5	12	1	ABI66750	Oligonucleotide pr
C 900	10.8	7.8	15	1	AAT50229	Rabbit CERP HH rib	C 973	10.4	7.5	12	1	ABI30472	Oligonucleotide pr
C 901	10.8	7.8	15	1	AAV48892	c-fos gene antisen	C 974	10.4	7.5	12	1	ABI07173	Oligonucleotide pr
C 902	10.8	7.8	15	1	AAT10279	Primer ZC4048 used	C 975	10.4	7.5	12	1	ABI13408	Oligonucleotide pr
C 903	10.8	7.8	15	1	AAV60907	Anti-c-Ha-ras olig	C 976	10.4	7.5	12	1	ABH92015	Oligonucleotide pr
C 904	10.8	7.8	15	1	AAS04348	Human DAXX DNA all	C 977	10.4	7.5	12	1	ABI18788	Oligonucleotide pr
C 905	10.8	7.8	15	1	AAS04346	Human DAXX DNA all	C 978	10.4	7.5	12	1	ABH94245	Oligonucleotide pr
C 906	10.8	7.8	15	1	AAF51267	IGF-I oligonucleot	C 979	10.4	7.5	12	1	ABH73848	Oligonucleotide pr
C 907	10.8	7.8	15	1	AAF52888	IGF-I oligonucleot	C 980	10.4	7.5	12	1	ABI03256	Oligonucleotide pr
C 908	10.8	7.8	15	1	AAF45991	IGFBP2 oligonucleo	C 981	10.4	7.5	12	1	ABI11679	Oligonucleotide pr
C 909	10.8	7.8	15	1	AAF52892	IGF-I oligonucleot	C 982	10.4	7.5	12	1	ABI66422	Oligonucleotide pr

983	10.4	7.5	12	1	AB118936	Oligonucleotide pr	1056	10.4	7.5	13	1	ABR46002	Oligonucleotide SE
c 984	10.4	7.5	12	1	AB125117	Oligonucleotide pr	1057	10.4	7.5	13	1	ABR55622	Oligonucleotide SE
c 985	10.4	7.5	12	1	AB100532	Oligonucleotide pr	c1058	10.4	7.5	13	1	ABH47623	Oligonucleotide SE
c 986	10.4	7.5	12	1	AB103600	Oligonucleotide pr	c1059	10.4	7.5	13	1	ABC69427	Oligonucleotide SE
987	10.4	7.5	12	1	AB106503	Oligonucleotide pr	c1060	10.4	7.5	13	1	ABC00339	Oligonucleotide SE
988	10.4	7.5	12	1	ABH85010	Oligonucleotide pr	c1061	10.4	7.5	13	1	ABC31788	Oligonucleotide SE
989	10.4	7.5	12	1	ABH87531	Oligonucleotide pr	c1062	10.4	7.5	13	1	ABC31801	Oligonucleotide SE
c 990	10.4	7.5	12	1	AB151466	Oligonucleotide pr	c1063	10.4	7.5	13	1	ABC31809	Oligonucleotide SE
991	10.4	7.5	12	1	AB168217	Oligonucleotide pr	c1064	10.4	7.5	13	1	ABC11715	Oligonucleotide SE
992	10.4	7.5	12	1	AB169091	Oligonucleotide pr	c1065	10.4	7.5	13	1	ABF20795	Oligonucleotide SE
993	10.4	7.5	12	1	ABH95646	Oligonucleotide pr	c1066	10.4	7.5	13	1	ABF24349	Oligonucleotide SE
c 994	10.4	7.5	12	1	AB100799	Oligonucleotide pr	c1067	10.4	7.5	13	1	ABF25383	Oligonucleotide SE
995	10.4	7.5	12	1	AB116484	Oligonucleotide pr	c1068	10.4	7.5	13	1	ABF43730	Oligonucleotide SE
996	10.4	7.5	12	1	ABH91477	Oligonucleotide pr	c1069	10.4	7.5	13	1	ABF73145	Oligonucleotide SE
c 997	10.4	7.5	12	1	AB142917	Oligonucleotide pr	c1070	10.4	7.5	13	1	ABF74436	Oligonucleotide SE
998	10.4	7.5	12	1	AB143245	Oligonucleotide pr	c1071	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
999	10.4	7.5	12	1	AB168275	Oligonucleotide pr	c1072	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1000	10.4	7.5	12	1	AB168271	Oligonucleotide pr	c1073	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1001	10.4	7.5	12	1	AB166749	Oligonucleotide pr	c1074	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1002	10.4	7.5	12	1	ABH98561	Oligonucleotide pr	c1075	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1003	10.4	7.5	12	1	ABH98748	Oligonucleotide pr	c1076	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1004	10.4	7.5	12	1	ABH76068	Oligonucleotide pr	c1077	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1005	10.4	7.5	12	1	AB106534	Oligonucleotide pr	c1078	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1006	10.4	7.5	12	1	ABH91324	Oligonucleotide pr	c1079	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1007	10.4	7.5	12	1	AB161369	Oligonucleotide pr	c1080	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1008	10.4	7.5	12	1	ABH78792	Oligonucleotide pr	c1081	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1009	10.4	7.5	12	1	AB169250	Oligonucleotide pr	c1082	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1010	10.4	7.5	12	1	AB170895	Oligonucleotide pr	c1083	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1011	10.4	7.5	12	1	AB179597	Oligonucleotide pr	c1084	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1012	10.4	7.5	12	1	ABH74230	Oligonucleotide pr	c1085	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1013	10.4	7.5	12	1	ABH74324	Oligonucleotide pr	c1086	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1014	10.4	7.5	12	1	AB125200	Oligonucleotide pr	c1087	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1015	10.4	7.5	12	1	AB127537	Oligonucleotide pr	c1088	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1016	10.4	7.5	12	1	AB105067	Oligonucleotide pr	c1089	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1017	10.4	7.5	12	1	AB113679	Oligonucleotide pr	c1090	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1018	10.4	7.5	12	1	AB174121	Oligonucleotide pr	c1091	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1019	10.4	7.5	12	1	ABH76760	Oligonucleotide pr	c1092	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1020	10.4	7.5	12	1	ABH93219	Oligonucleotide pr	c1093	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1021	10.4	7.5	12	1	AB145848	Oligonucleotide pr	c1094	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1022	10.4	7.5	12	1	AB148545	Oligonucleotide pr	c1095	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1023	10.4	7.5	12	1	AB167505	Oligonucleotide pr	c1096	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1024	10.4	7.5	12	1	AB154852	Oligonucleotide pr	c1097	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1025	10.4	7.5	12	1	AB155339	Oligonucleotide pr	c1098	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1026	10.4	7.5	12	1	AB163114	Oligonucleotide pr	c1099	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1027	10.4	7.5	12	1	AB128532	Oligonucleotide pr	c1100	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1028	10.4	7.5	12	1	AB150660	Oligonucleotide pr	c1101	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1029	10.4	7.5	12	1	AB171189	Oligonucleotide pr	c1102	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1030	10.4	7.5	12	1	AB181529	Oligonucleotide pr	c1103	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1031	10.4	7.5	12	1	ABH92917	Oligonucleotide pr	c1104	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1032	10.4	7.5	12	1	ABH96992	Oligonucleotide pr	c1105	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1033	10.4	7.5	12	1	ABH77660	Oligonucleotide pr	c1106	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1034	10.4	7.5	12	1	AB128296	Oligonucleotide pr	c1107	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1035	10.4	7.5	12	1	AB134755	Oligonucleotide pr	c1108	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1036	10.4	7.5	12	1	ABH86312	Oligonucleotide pr	c1109	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1037	10.4	7.5	12	1	AB158975	Oligonucleotide pr	c1110	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1038	10.4	7.5	12	1	AB161446	Oligonucleotide pr	c1111	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1039	10.4	7.5	12	1	ABH67931	Oligonucleotide pr	c1112	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1040	10.4	7.5	12	1	ABH69474	Oligonucleotide pr	c1113	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1041	10.4	7.5	12	1	ABH96180	Oligonucleotide pr	c1114	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1042	10.4	7.5	12	1	AB105053	Oligonucleotide pr	c1115	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1043	10.4	7.5	12	1	AB132594	Oligonucleotide pr	c1116	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1044	10.4	7.5	12	1	ABH90089	Oligonucleotide pr	c1117	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1045	10.4	7.5	12	1	ABH93470	Oligonucleotide pr	c1118	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1046	10.4	7.5	12	1	ABH78187	Oligonucleotide pr	c1119	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1047	10.4	7.5	12	1	ABH28998	Oligonucleotide pr	c1120	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1048	10.4	7.5	12	1	ABH81163	Oligonucleotide pr	c1121	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1049	10.4	7.5	12	1	ABH90846	Oligonucleotide pr	c1122	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1050	10.4	7.5	12	1	AB145398	Oligonucleotide pr	c1123	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
c1051	10.4	7.5	12	1	AB163218	Oligonucleotide pr	c1124	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1052	10.4	7.5	13	1	AA293102	5' UTR sequence use	c1125	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1053	10.4	7.5	13	1	ABC69426	Oligonucleotide SE	c1126	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1054	10.4	7.5	13	1	ABF18044	Oligonucleotide SE	c1127	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
1055	10.4	7.5	13	1	ABF25942	Oligonucleotide SE	c1128	10.4	7.5	13	1	ABH37503	Oligonucleotide SE

c1129	10.4	7.5	13	1	ABC04730	Oligonucleotide SE	1202	10.4	7.5	13	1	ABF54762	Oligonucleotide SE
1130	10.4	7.5	13	1	ABC80341	Oligonucleotide SE	1203	10.4	7.5	13	1	ABF61036	Oligonucleotide SE
1131	10.4	7.5	13	1	ABC31002	Oligonucleotide SE	c1204	10.4	7.5	13	1	ABH36660	Oligonucleotide SE
1132	10.4	7.5	13	1	ABF24348	Oligonucleotide SE	1205	10.4	7.5	13	1	ABH36661	Oligonucleotide SE
1133	10.4	7.5	13	1	ABF32776	Oligonucleotide SE	1206	10.4	7.5	13	1	ABF65198	Oligonucleotide SE
1134	10.4	7.5	13	1	ABF32776	Oligonucleotide SE	1207	10.4	7.5	13	1	ABH50619	Oligonucleotide SE
c1135	10.4	7.5	13	1	ABF39733	Oligonucleotide SE	c1208	10.4	7.5	13	1	ABF05796	Oligonucleotide SE
1136	10.4	7.5	13	1	ABF51621	Oligonucleotide SE	c1209	10.4	7.5	13	1	ABC33106	Oligonucleotide SE
c1137	10.4	7.5	13	1	ABC44245	Oligonucleotide SE	1210	10.4	7.5	13	1	ABC33107	Oligonucleotide SE
c1138	10.4	7.5	13	1	ABC46624	Oligonucleotide SE	1211	10.4	7.5	13	1	ABC40066	Oligonucleotide SE
1139	10.4	7.5	13	1	ABF38485	Oligonucleotide SE	1212	10.4	7.5	13	1	ABC66989	Oligonucleotide SE
1140	10.4	7.5	13	1	ABF41114	Oligonucleotide SE	c1213	10.4	7.5	13	1	ABH26444	Oligonucleotide SE
c1141	10.4	7.5	13	1	ABF95707	Oligonucleotide SE	c1214	10.4	7.5	13	1	ABH35974	Oligonucleotide SE
c1142	10.4	7.5	13	1	ABF95709	Oligonucleotide SE	1215	10.4	7.5	13	1	ABC42472	Oligonucleotide SE
1143	10.4	7.5	13	1	ABF73141	Oligonucleotide SE	1216	10.4	7.5	13	1	ABC52599	Oligonucleotide SE
c1144	10.4	7.5	13	1	ABH00391	Oligonucleotide SE	1217	10.4	7.5	13	1	ABC05020	Oligonucleotide SE
1145	10.4	7.5	13	1	ABF55722	Oligonucleotide SE	c1218	10.4	7.5	13	1	ABC80340	Oligonucleotide SE
1146	10.4	7.5	13	1	ABF82123	Oligonucleotide SE	1219	10.4	7.5	13	1	ABC31800	Oligonucleotide SE
1147	10.4	7.5	13	1	ABH12820	Oligonucleotide SE	1220	10.4	7.5	13	1	ABC82527	Oligonucleotide SE
1148	10.4	7.5	13	1	ABF90782	Oligonucleotide SE	1221	10.4	7.5	13	1	ABC11714	Oligonucleotide SE
1149	10.4	7.5	13	1	ABF66102	Oligonucleotide SE	c1222	10.4	7.5	13	1	ABC63275	Oligonucleotide SE
c1150	10.4	7.5	13	1	ABC05021	Oligonucleotide SE	1223	10.4	7.5	13	1	ABC14559	Oligonucleotide SE
c1151	10.4	7.5	13	1	ABC31005	Oligonucleotide SE	1224	10.4	7.5	13	1	ABC40888	Oligonucleotide SE
1152	10.4	7.5	13	1	ABC32492	Oligonucleotide SE	1225	10.4	7.5	13	1	ABF32046	Oligonucleotide SE
1153	10.4	7.5	13	1	ABC84322	Oligonucleotide SE	c1226	10.4	7.5	13	1	ABF32775	Oligonucleotide SE
1154	10.4	7.5	13	1	ABC87616	Oligonucleotide SE	c1227	10.4	7.5	13	1	ABF92685	Oligonucleotide SE
1155	10.4	7.5	13	1	ABC63274	Oligonucleotide SE	c1228	10.4	7.5	13	1	ABF54763	Oligonucleotide SE
1156	10.4	7.5	13	1	ABC16398	Oligonucleotide SE	c1229	10.4	7.5	13	1	ABF55623	Oligonucleotide SE
c1157	10.4	7.5	13	1	ABC66449	Oligonucleotide SE	c1230	10.4	7.5	13	1	ABF82122	Oligonucleotide SE
c1158	10.4	7.5	13	1	ABF20156	Oligonucleotide SE	c1231	10.4	7.5	13	1	ABH36975	Oligonucleotide SE
1159	10.4	7.5	13	1	ABF20157	Oligonucleotide SE	1232	10.4	7.5	13	1	ABH13559	Oligonucleotide SE
c1160	10.4	7.5	13	1	ABF30620	Oligonucleotide SE	c1233	10.4	7.5	13	1	ABF63800	Oligonucleotide SE
c1161	10.4	7.5	13	1	ABF32047	Oligonucleotide SE	c1234	10.4	7.5	13	1	ABC47685	Oligonucleotide SE
c1162	10.4	7.5	13	1	ABF32777	Oligonucleotide SE	1235	10.4	7.5	13	1	ABC31004	Oligonucleotide SE
c1163	10.4	7.5	13	1	ABF74437	Oligonucleotide SE	c1236	10.4	7.5	13	1	ABC57211	Oligonucleotide SE
c1164	10.4	7.5	13	1	ABH00387	Oligonucleotide SE	c1237	10.4	7.5	13	1	ABC82526	Oligonucleotide SE
1165	10.4	7.5	13	1	ABF79387	Oligonucleotide SE	c1238	10.4	7.5	13	1	ABC84323	Oligonucleotide SE
c1166	10.4	7.5	13	1	ABF58666	Oligonucleotide SE	1239	10.4	7.5	13	1	ABF16774	Oligonucleotide SE
1167	10.4	7.5	13	1	ABH35975	Oligonucleotide SE	1240	10.4	7.5	13	1	ABF18154	Oligonucleotide SE
1168	10.4	7.5	13	1	ABF87483	Oligonucleotide SE	c1241	10.4	7.5	13	1	ABF38484	Oligonucleotide SE
c1169	10.4	7.5	13	1	ABH13554	Oligonucleotide SE	1242	10.4	7.5	13	1	ABF43731	Oligonucleotide SE
c1170	10.4	7.5	13	1	ABH50618	Oligonucleotide SE	c1243	10.4	7.5	13	1	ABF51620	Oligonucleotide SE
1171	10.4	7.5	13	1	ABH61555	Oligonucleotide SE	c1244	10.4	7.5	13	1	ABF53251	Oligonucleotide SE
c1172	10.4	7.5	13	1	ABH63202	Oligonucleotide SE	c1245	10.4	7.5	13	1	ABF61037	Oligonucleotide SE
1173	10.4	7.5	13	1	ABC00338	Oligonucleotide SE	1246	10.4	7.5	13	1	ABH36974	Oligonucleotide SE
c1174	10.4	7.5	13	1	ABC77733	Oligonucleotide SE	1247	10.4	7.5	13	1	ABH33555	Oligonucleotide SE
1175	10.4	7.5	13	1	ABC04731	Oligonucleotide SE	c1248	10.4	7.5	13	1	ABC47422	Oligonucleotide SE
1176	10.4	7.5	13	1	ABC31808	Oligonucleotide SE	1249	10.4	7.5	13	1	ABC47684	Oligonucleotide SE
1177	10.4	7.5	13	1	ABC57210	Oligonucleotide SE	c1250	10.4	7.5	13	1	ABC75934	Oligonucleotide SE
c1178	10.4	7.5	13	1	ABC40890	Oligonucleotide SE	1251	10.4	7.5	13	1	ABC77732	Oligonucleotide SE
c1179	10.4	7.5	13	1	ABC40891	Oligonucleotide SE	1252	10.4	7.5	13	1	ABF05797	Oligonucleotide SE
c1180	10.4	7.5	13	1	ABF18045	Oligonucleotide SE	c1253	10.4	7.5	13	1	ABC31003	Oligonucleotide SE
1181	10.4	7.5	13	1	ABF24346	Oligonucleotide SE	1254	10.4	7.5	13	1	ABC09989	Oligonucleotide SE
c1182	10.4	7.5	13	1	ABF24347	Oligonucleotide SE	c1255	10.4	7.5	13	1	ABF16775	Oligonucleotide SE
c1183	10.4	7.5	13	1	ABF36621	Oligonucleotide SE	c1256	10.4	7.5	13	1	ABF34099	Oligonucleotide SE
1184	10.4	7.5	13	1	ABF34098	Oligonucleotide SE	c1257	10.4	7.5	13	1	ABF41115	Oligonucleotide SE
1185	10.4	7.5	13	1	ABF95706	Oligonucleotide SE	1258	10.4	7.5	13	1	ABH00386	Oligonucleotide SE
1186	10.4	7.5	13	1	ABH26445	Oligonucleotide SE	1259	10.4	7.5	13	1	ABF53250	Oligonucleotide SE
1187	10.4	7.5	13	1	ABF58667	Oligonucleotide SE	1260	10.4	7.5	13	1	ABH15231	Oligonucleotide SE
c1188	10.4	7.5	13	1	ABH37502	Oligonucleotide SE	c1261	10.4	7.5	13	1	ABF65199	Oligonucleotide SE
c1189	10.4	7.5	13	1	ABF87482	Oligonucleotide SE	1262	10.4	7.5	13	1	ABH47622	Oligonucleotide SE
c1190	10.4	7.5	13	1	ABH12821	Oligonucleotide SE	c1263	10.4	7.5	13	1	ABC19752	Oligonucleotide SE
1191	10.4	7.5	13	1	ABF66672	Oligonucleotide SE	1264	10.4	7.5	13	1	ABC75935	Oligonucleotide SE
c1192	10.4	7.5	13	1	ABF66673	Oligonucleotide SE	c1265	10.4	7.5	13	1	ABC02828	Oligonucleotide SE
c1193	10.4	7.5	13	1	ABH42002	Oligonucleotide SE	c1266	10.4	7.5	13	1	ABF11507	Oligonucleotide SE
1194	10.4	7.5	13	1	ABC77642	Oligonucleotide SE	c1267	10.4	7.5	13	1	ABC87617	Oligonucleotide SE
c1195	10.4	7.5	13	1	ABC09988	Oligonucleotide SE	1268	10.4	7.5	13	1	ABC66448	Oligonucleotide SE
c1196	10.4	7.5	13	1	ABC86051	Oligonucleotide SE	1269	10.4	7.5	13	1	ABF43820	Oligonucleotide SE
c1197	10.4	7.5	13	1	ABC40067	Oligonucleotide SE	1270	10.4	7.5	13	1	ABF63801	Oligonucleotide SE
c1198	10.4	7.5	13	1	ABC16399	Oligonucleotide SE	1271	10.4	7.5	13	1	AAI56800	Oligonucleotide SE
c1199	10.4	7.5	13	1	ABF43821	Oligonucleotide SE	c1272	10.4	7.5	14	1	AAQ78441	Oligonucleotide SE
1200	10.4	7.5	13	1	ABF95708	Oligonucleotide SE	c1273	10.4	7.5	14	1	AAV99069	Oligonucleotide SE
c1201	10.4	7.5	13	1	ABF73140	Oligonucleotide SE	1274	10.4	7.5	14	1	AAAL7659	Oligonucleotide SE

TGF-beta gene phos
Human EGF-R target
Aryl hydrocarbon n

```
1275 10.4 7.5 14 1 AAA26158 Oestrogen receptor
c1276 10.4 7.5 15 1 AB226045 HMGI related oligo
1277 10.4 7.5 15 1 AAQ43332 B-B10 V region pri
c1278 10.4 7.5 15 1 AA155017 Human B7-2 hammerh
1280 10.4 7.5 15 1 AAX65776 Rabbit CETP HH rib
1281 10.4 7.5 15 1 AAX311381 Tag sequence of a
c1282 10.4 7.5 15 1 AAV93861 Target sequence wi
c1283 10.4 7.5 15 1 AAV81796 Granulocytic Ehrli
c1284 10.4 7.5 15 1 AAZ62728 Substrate for HH r
1285 10.4 7.5 15 1 AAZ64116 Substrate for ham
c1286 10.4 7.5 15 1 AAA67020 Human leukocyte an
c1287 10.4 7.5 15 1 AAC68385 Human IRRR oligonu
c1288 10.4 7.5 15 1 AAH18851 UCP3 polymorphism
c1289 10.4 7.5 15 1 AAD05853 Human cholinergic
c1290 10.4 7.5 15 1 AAD05854 Human cholinergic
c1291 10.4 7.5 15 1 AAD05854 Human CHRN2 allel
c1292 10.4 7.5 15 1 AAF52917 IGF-I oligonucleot
c1293 10.4 7.5 15 1 AAF51492 IGF-I oligonucleot
c1294 10.4 7.5 15 1 AAF53418 IGF-I oligonucleot
c1295 10.4 7.5 15 1 AAF53418 IGF-I oligonucleot
c1296 10.4 7.5 15 1 AAF51496 IGF-I oligonucleot
c1297 10.4 7.5 15 1 AAF52916 IGF-I oligonucleot
c1298 10.4 7.5 15 1 AAF52918 IGF-I oligonucleot
c1299 10.4 7.5 15 1 AAF52915 IGF-I oligonucleot
c1300 10.4 7.5 15 1 AAF53422 IGF-I oligonucleot
c1301 10.4 7.5 15 1 AAF53672 IGF-I oligonucleot
c1302 10.4 7.5 15 1 AAF53668 IGF-I oligonucleot
c1303 10.4 7.5 15 1 AAF70093 Human TNFRSF1B ge
c1304 10.4 7.5 15 1 AAF70091 Human TNFRSF1B ge
c1305 10.4 7.5 15 1 AABX03889 T. Vincenti116S rR
c1306 10.4 7.5 15 1 AAD25233 Human CCR3 gene po
c1307 10.4 7.5 15 1 ABK85670 Human SCVB6 gene p
c1308 10.4 7.5 15 1 AAS98731 Colony stimulating
c1309 10.4 7.5 15 1 AAS96178 Human Acetylcholin
c1310 10.4 7.5 15 1 ABK16934 Pyridoxal (Pyridox
c1311 10.4 7.5 15 1 ABL52230 Human PKG2 allele
c1312 10.4 7.5 15 1 ABT05335 Human N-acetylglala
c1313 10.4 7.5 15 1 ABA96065 CYP8B1 allele-spec
c1314 10.4 7.5 15 1 ABQ72276 Human CYP2D6 allel
c1315 10.4 7.5 15 1 ABL91070 Hominidae LDL rece
c1316 10.4 7.5 15 1 ABL51958 Human SLC18A2 alle
c1317 10.4 7.5 15 1 ABL51566 Human HNF3A allele
c1318 10.4 7.5 15 1 ABL91860 Human LIP3 gene al
c1319 10.4 7.5 15 1 ABK96133 Human CYP1A2 allel
c1320 10.4 7.5 15 1 ABK32335 Human colon cancer
c1321 10.4 7.5 15 1 ABX01169 Hepatitis C virus
c1322 10.4 7.5 15 1 AAX00579 Hepatitis C virus
c1323 10.4 7.5 15 1 AAS99325 Aldehyde dehydroge
c1324 10.4 7.5 15 1 AAD47770 Human GNB3 gene po
c1325 10.4 7.5 15 1 ACD56053 HBV enzymatic nucl
c1326 10.4 7.5 16 1 AAQ68223 Sequence of 5'-hex
c1327 10.4 7.5 16 1 AAS15518 N-acetyltransferas
c1328 10.4 7.5 16 1 AAS15509 N-acetyltransferas
c1329 10.4 7.5 16 1 AAS15507 N-acetyltransferas
c1330 10.4 7.5 16 1 ABL57869 Human ABCA7 gene p
c1331 10.4 7.5 16 1 ACC43260 Nucleotide sequenc
c1332 10.4 7.5 16 1 ADE14013 Optineurin promote
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ALIGNMENTS

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RESULT 1
ABZ01804
ID ABZ01804 standard; DNA; 50 BP.
XX
AC ABZ01804;
XX
XX 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 1795.
XX
```

```
KW T7: leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; cateoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX Homo sapiens.
XX WO200257414-A2.
XX 25-JUL-2002.
XX 22-OCT-2001; 2001WO-US047856.
XX 20-OCT-2000; 2000US-0241994P.
XX 08-JUN-2001; 2001US-0296764P.
XX (BIOC-) BIOCARDIA INC.
XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quettermous T, Johnson F;
XX WPI; 2002-636525/68.
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX Claim 1; Page 382; Opp; English.
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX Sequence 50 BP; 12 A; 13 C; 7 G; 13 T; 0 U; 0 Other;
XX
XX Query Match Similarity 24.5%; Score 34; DB 1; Length 50;
XX Best Local Similarity 100.0%; Pred. No. 0.019;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1736 CTCCCAACTCTCTCTATCTCTATCTCTAAAGGCCCACTGG 1769
XX Db 1 CTCCCAACTCTCTCTATCTCTATCTCTAAAGGCCCACTGG 34
XX
XX RESULT 2
XX AA166686/c
XX ID AA166686 standard; DNA; 21 BP.
XX AC AA166686;
XX
XX 07-JAN-2002 (first entry)
XX Human CETP DNA related PCR primer.
XX
XX CETP; arteriosclerosis; cholesterol ester transfer protein; HDL;
XX high density lipoprotein; human; PCR primer; ss.
XX
XX Homo sapiens.
XX WO200171032-A1.
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-JP002327.
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XX 24-MAR-2000; 2000JP-00084264.
XX (BMLB-) BML INC.
XX Nagano M, Ito M, Sagehashi Y, Hattori H, Egashira T, Yamashita S;
PI Matsuzawa Y;
XX WPI; 2001-611516/70.
XX Determining a risk factor for arteriosclerosis comprises detecting
PT mutations in genes for cholesterol ester transfer protein.
XX Disclosure; Page 21; 59pp; Japanese.
XX The invention relates to detecting the risk factor for arteriosclerosis
CC in a subject that involves detecting mutations in the gene for
CC cholesterol ester transfer protein (CETP) related to the degree of risk
CC of arteriosclerosis. The mutant proteins alter the level of HDL in the
CC blood. The high frequency mutations can be detected for prevention and
CC treatment of arteriosclerosis. Sequences AA16655-91 represent PCR
CC primers related to the human CETP DNA, used during the course of the
CC invention
XX
XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 15.1%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1665 TCACAGCTGGACCCCTGGTGT 1685
DB 21 TCACAGCTGGACCCCTGGTGT 1
RESULT 3
ABT13031/c
ID ABT13031 standard; DNA; 20 BP.
XX AC AET13031;
XX 30-JAN-2003 (first entry)
XX Human cholesterol ester transfer protein PCR primer (SNP specific) #12.
XX Human; PCR; primer; ss; gene therapy; single nucleotide polymorphism;
KW cytochrome C oxidase subunit VIB; COX6B; high serum cholesterol; GPI-1;
KW N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;
KW glycosylphosphatidylinositol-1; SNP; low serum high density lipoprotein.
XX Homo sapiens.
OS
XX WO200272604-A2.
XX 19-SEP-2002.
XX 05-MAR-2002; 2002WO-US006728.
XX 09-MAR-2001; 2001US-00802640.
XX (SEQU-) SEQUENOM INC.
XX Braun A, Bansal A, Kieyn FW;
XX WPI; 2002-750478/81.
XX Detecting the presence or absence of an allelic variant of a polymorphic
PT region of COX6B and/or GPI-1 gene, useful for detecting a predisposition
PT to high serum cholesterol, low serum HDL and cardiovascular disease.
XX
XX Disclosure; Page 30; 199pp; English.
XX The invention comprises methods of detecting the presence or absence of

CC at least one allelic variant of a polymorphic region of a gene associated
CC with cardiovascular disease. The invention specifically relates to
CC detecting the region of a cytochrome C oxidase subunit VIB (COX6B) gene
CC that is associated with high serum cholesterol, or the region of the N-
CC acetylglucosaminyl transferase component glycosylphosphatidylinositol-1
CC (GPI-1) gene that is associated with low serum high density lipoprotein
CC (HDL). The methods of the invention are useful for detecting a
CC predisposition to high serum cholesterol, low serum HDL and
CC cardiovascular disease. The methods are also useful for elucidating
CC pathological pathways, developing diagnostic assays and new drug
CC therapies for such disorders. The present DNA sequence represents a PCR
CC primer used to amplify a human gene that is associated with high serum
CC cholesterol, low serum HDL and/or cardiovascular disease
XX
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1639 CTTGTAGCAGAGCAAGCA 1658
DB 20 CTTGTAGCAGAGCAAGCA 1
RESULT 4
ABX12200/c
ID ABX12200 standard; DNA; 20 BP.
XX AC ABX12200;
XX 16-MAY-2003 (first entry)
XX Human cholesteryl ester transfer protein, antisense oligo #21.
XX Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
KW antisense; probe; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides; all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..6
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003014306-A2.
XX 20-FEB-2003.
XX 05-AUG-2002; 2002WO-US024919.
XX 08-AUG-2001; 2001US-00925139.
XX (ISIS-) ISIS PHARM INC.
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
XX WPI; 2003-256564/25.
XX New antisense compound, useful for preparing a composition for treating
PT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease.
XX
XX Claim 3; Page 96; 114pp; English.
XX

CC The invention relates to new antisense compounds targeted to a nucleic
CC acid molecule encoding human cholesteryl ester transfer protein,
CC specifically hybridises with it and inhibits the expression of human
CC cholesteryl ester transfer protein. The compound is useful for preparing
CC a composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, antisense
CC oligonucleotide of the invention
XX
SQ Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1701 GGAAGTTGGTTAGGAGTAC 1720
DB 20 GGAAGTTGGTTAGGAGTAC 1

RESULT 5

ABX12198/c
ID ABX12198 standard; DNA; 20 BP.

XX AC ABX12198;

DT 16-MAY-2003 (first entry)

DE Human cholesteryl ester transfer protein, antisense oligo #19.

XX Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
KW antisense; probe; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH modified_base 1..20

FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides; all cytidine
FT residues are 5-methylcytidines"

FT modified_base 1..6

FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 15..20

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003014306-A2.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-US024919.

XX 08-AUG-2001; 2001US-00925139.

XX (ISIS-) ISIS PHARM INC.

XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;

XX WPI; 2003-256564/25.

XX New antisense compound, useful for preparing a composition for treating
PT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease.

PS Claim 3; Page 96; 114pp; English.

XX The invention relates to new antisense compounds targeted to a nucleic
CC acid molecule encoding human cholesteryl ester transfer protein,
CC specifically hybridises with it and inhibits the expression of human
CC cholesteryl ester transfer protein. The compound is useful for preparing
CC a composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, antisense
CC oligonucleotide of the invention

CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, antisense
CC oligonucleotide of the invention

XX Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1631 GGATGGGCTTGTAGCAGAA 1650
DB 20 GGATGGGCTTGTAGCAGAA 1

RESULT 6

ABX12217/c
ID ABX12217 standard; DNA; 20 BP.

XX AC ABX12217;

DT 16-MAY-2003 (first entry)

DE Human cholesteryl ester transfer protein, antisense oligo #38.

XX Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
KW antisense; probe; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH modified_base 1..20

FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides; all cytidine
FT residues are 5-methylcytidines"

FT modified_base 1..6

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 15..20

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003014306-A2.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-US024919.

XX 08-AUG-2001; 2001US-00925139.

XX (ISIS-) ISIS PHARM INC.

XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;

XX WPI; 2003-256564/25.

XX New antisense compound, useful for preparing a composition for treating
PT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease.

PS Claim 3; Page 97; 114pp; English.

XX The invention relates to new antisense compounds targeted to a nucleic
CC acid molecule encoding human cholesteryl ester transfer protein,
CC specifically hybridises with it and inhibits the expression of human
CC cholesteryl ester transfer protein. The compound is useful for preparing
CC a composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, antisense
CC oligonucleotide of the invention

XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1638 GCTGTAGCAGAGGCAAGC 1657
|||||
Db 20 GCTGTAGCAGAGGCAAGC 1

RESULT 7
ABX12175/c
ID ABX12175 standard; DNA: 20 BP.
XX
AC ABX12175;
DT 16-MAY-2003 (first entry)
XX Human cholesteryl ester transfer protein, reverse PCR primer.
XX Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
KW antisense; PCR; primer; ss.
XX Homo sapiens.
OS
XX WO2003014306-A2.
FN
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US024919.
PF
XX
XX 08-AUG-2001; 2001US-00925139.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
PI
XX WPI; 2003-256564/25.
DR

XX New antisense compound, useful for preparing a composition for treating
PT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease.
XX Example 13; Page 93; 114pp; English.
PS
XX The invention relates to new antisense compounds targeted to a nucleic
CC acid molecule encoding human cholesteryl ester transfer protein,
CC specifically hybridises with it and inhibits the expression of human
CC cholesteryl ester transfer protein. The compound is useful for preparing
CC a composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, PCR primer
XX
SQ Sequence 20 BP; 6 A; 10 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1695 CGTGTGGAAGTTGGTTAG 1714
|||||
Db 20 CGTGTGGAAGTTGGTTAG 1

RESULT 8
ABX12219/c
ID ABX12219 standard; DNA: 20 BP.
XX
AC ABX12219;
XX
DT 16-MAY-2003 (first entry)
XX

DE Human cholesteryl ester transfer protein, antisense oligo #40.
XX
KW Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
KW antisense; probe; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH modified_base 1..20
FT /mod_base= OTHER
FT /note= "phosphorothioate nucleotides; all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..6
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003014306-A2.
FN
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US024919.
PF
XX
XX 08-AUG-2001; 2001US-00925139.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
PI
XX WPI; 2003-256564/25.
DR
XX New antisense compound, useful for preparing a composition for treating
PT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease.
XX Claim 3; Page 97; 114pp; English.
PS

XX The invention relates to new antisense compounds targeted to a nucleic
CC acid molecule encoding human cholesteryl ester transfer protein,
CC specifically hybridises with it and inhibits the expression of human
CC cholesteryl ester transfer protein. The compound is useful for preparing
CC a composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, antisense
CC oligonucleotide of the invention
XX
SQ Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1714 GGAGTACGAGATGGAGATT 1733
|||||
Db 20 GGAGTACGAGATGGAGATT 1

RESULT 9
ABX12220/c
ID ABX12220 standard; DNA: 20 BP.
XX
AC ABX12220;
XX
DT 16-MAY-2003 (first entry)
XX
DE Human cholesteryl ester transfer protein, antisense oligo #41.
KW Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
KW antisense; probe; ss.

```

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate nucleotides; all cytidine
XX FT residues are 5-methylcytidines"
XX FT modified_base 1..6
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX FT modified_base 15..20
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PN WO2003014306-A2.
XX PD 20-FEB-2003.
XX PF 05-AUG-2002; 2002WO-US024919.
XX PR 08-AUG-2001; 2001US-00925139.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
XX DR WPI; 2003-256564/25.
XX PT New antisense compound, useful for preparing a composition for treating
XX PT abnormal lipid or cholesterol metabolism, atherosclerosis or
XX PT cardiovascular disease.
XX PS Claim 3; Page 97; 114pp; English.
XX CC The invention relates to new antisense compounds targeted to a nucleic
XX CC acid molecule encoding human cholesteryl ester transfer protein,
XX CC specifically hybridises with it and inhibits the expression of human
XX CC cholesteryl ester transfer protein. The compound is useful for preparing
XX CC a composition for treating abnormal lipid or cholesterol metabolism,
XX CC atherosclerosis or cardiovascular disease. The present sequence
XX CC represents a human cholesteryl ester transfer protein, antisense
XX CC oligonucleotide of the invention
XX SQ Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1750 CTATCCTAAAGGCCCACTGG 1769
DB 20 CTATCCTAAAGGCCCACTGG 1

RESULT 10
ABX12199/c
ID ABX12199 standard; DNA; 20 BP.
XX AC ABX12199;
XX XX
XX DT 16-MAY-2003 (first entry)
XX DE Human cholesteryl ester transfer protein, antisense oligo #20.
XX KW Human; cholesteryl ester transfer protein; lipid metabolism;
XX KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
XX KW antisense; probe; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20

```

```

FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides; all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..6
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PN WO2003014306-A2.
XX PD 20-FEB-2003.
XX PF 05-AUG-2002; 2002WO-US024919.
XX PR 08-AUG-2001; 2001US-00925139.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
XX DR WPI; 2003-256564/25.
XX PT New antisense compound, useful for preparing a composition for treating
XX PT abnormal lipid or cholesterol metabolism, atherosclerosis or
XX PT cardiovascular disease.
XX PS Claim 3; Page 96; 114pp; English.
XX CC The invention relates to new antisense compounds targeted to a nucleic
XX CC acid molecule encoding human cholesteryl ester transfer protein,
XX CC specifically hybridises with it and inhibits the expression of human
XX CC cholesteryl ester transfer protein. The compound is useful for preparing
XX CC a composition for treating abnormal lipid or cholesterol metabolism,
XX CC atherosclerosis or cardiovascular disease. The present sequence
XX CC represents a human cholesteryl ester transfer protein, antisense
XX CC oligonucleotide of the invention
XX SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1671 CTGGAACCCCTGGTGTCTCT 1690
DB 20 CTGGAACCCCTGGTGTCTCT 1

RESULT 11
ABX12218/c
ID ABX12218 standard; DNA; 20 BP.
XX AC ABX12218;
XX XX
XX DT 16-MAY-2003 (first entry)
XX DE Human cholesteryl ester transfer protein, antisense oligo #39.
XX KW Human; cholesteryl ester transfer protein; lipid metabolism;
XX KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
XX KW antisense; probe; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate nucleotides; all cytidine
XX FT residues are 5-methylcytidines"
XX FT modified_base 1..6
XX FT /mod_base= OTHER

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```
FT modified_base /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003014306-A2.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US024919.
XX
XX 08-AUG-2001; 2001US-00925139.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
XX
XX WPI; 2003-256564/25.
XX
XX New antisense compound, useful for preparing a composition for treating
XX abnormal lipid or cholesterol metabolism, atherosclerosis or
XX cardiovascular disease.
XX
XX Claim 3; Page 97; 114pp; English.
XX
XX The invention relates to new antisense compounds targeted to a nucleic
XX acid molecule encoding human cholesteryl ester transfer protein,
XX specifically hybridizes with it and inhibits the expression of human
XX cholesteryl ester transfer protein. The compound is useful for preparing
XX a composition for treating abnormal lipid or cholesterol metabolism,
XX atherosclerosis or cardiovascular disease. The present sequence
XX represents a human cholesteryl ester transfer protein, antisense
XX oligonucleotide of the invention
XX
XX Sequence 20 BP; 6 A; 10 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 14.4%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 7.4;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1693 AGCGTGGTGAAGTTGGTT 1712
XX |||||
XX 20 AGCGTGGTGAAGTTGGTT 1
XX
XX RESULT 12
XX AAT50642
XX ID AAT50642 standard; RNA; 18 BP.
XX
XX AC AAT50642;
XX
XX DT 10-MAR-1997 (first entry)
XX
XX DE Human CETP hairpin ribozyme target sequence #1669.
XX
XX Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9620279-A1.
XX
XX PD 04-JUL-1996.
XX
XX PF 11-DEC-1995; 95WO-US016000.
XX
XX PR 23-DEC-1994; 94US-00363240.
XX
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PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN ) WARNER LAMBERT CO.
XX
XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
XX
XX WPI; 1996-321852/32.
XX
XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX useful for preventing or treating initial development, progression or
XX regression of vascular diseases, esp. familial hypercholesterolaemia.
XX
XX Claim 4; Page 54; 72pp; English.
XX
XX AAT50595-T50642 represent target sequences for the human cholesterol
XX ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
XX CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
XX between plasma lipoproteins. The numbering of the targets refers to the
XX position of the cleavage site in full length CETP. The ribozyme then
XX binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
XX ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
XX blocking synthesis and/or expression of the mRNA. By inhibiting CETP, the
XX reverse cholesterol transport (RCT) pathway can be inhibited (or
XX eliminated) thereby preventing the reduction in size density of the high
XX density lipoproteins (HDL), prolonging HDL half life, and therefore
XX increasing HDL levels. The ribozymes can be used to treat conditions
XX associated with abnormal levels of CETP, specifically atherosclerosis,
XX peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
XX familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
XX complications of diabetes, transplant, atherectomy and angioplastic
XX restenosis. By inhibiting CETP, the levels of HDL and low density
XX lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
XX decrease in LDL levels, and a corresponding increase in HDL levels). The
XX ribozymes can also be used diagnostically to study genetic drift and
XX mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
XX target specific regions of the CETP gene, they have low non-specific
XX activity
XX
XX Sequence 18 BP; 4 A; 7 C; 4 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 12.9%; Score 18; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 18;
XX Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1663 GCTCACAGCTGGAAACCT 1680
XX |||||
XX 1 GCUCACAGCUGGAACCCU 18
XX
XX RESULT 13
XX AAX37644
XX ID AAX37644 standard; DNA; 22 BP.
XX
XX AC AAX37644;
XX
XX DT 08-JUL-1999 (first entry)
XX
XX DE HBV detecting primer 8.
XX
XX KW Detection; HBV; real time; PCR; reporter; fluorescent; primer; quencher;
XX fluorescence resonance energy transfer; ss.
XX
XX OS Synthetic.
XX
XX OS Hepatitis B virus.
XX
XX PN JP11103897-A.
XX
XX PD 20-APR-1999.
XX
XX PF 30-SEP-1997; 97JP-00282612.
XX
XX PR 30-SEP-1997; 97JP-00282612.
XX
XX (SRLS-) SRL KK.
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XX WPI; 1999-305860/26.
XX New primers and probes - for measurement of an Herpes B Virus (HBV) gene
XX by a real time detecting PCR.
XX Example 2; Page 8; 12pp; Japanese.
XX This invention describes a method for the measurement of an HBV gene by a
XX real time detecting PCR. The invention also describes a method for the
XX measurement of an HBV gene by a real time detecting PCR in which a
XX reporter fluorescent colour and a quencher fluorescent colour are
XX combined to an oligonucleotide, the fluorescence of said reporter
XX fluorescent colour is controlled by fluorescence resonance energy
XX transfer when reporter fluorescent colour is combined to the same probe
XX as quencher fluorescent colour. The method can measure an HBV exactly in
XX a high sensitivity
XX Sequence 22 BP; 5 A; 11 C; 1 G; 5 T; 0 U; 0 Other;
SQ Query Match 12.4%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1738 CCCAATCTCTCCCTATCCTTAA 1759
Db 1 CCCAATCTCTCCAGTCTTAA 22
RESULT 14
AAAX22550/c
ID AAX22550 standard; mRNA; 17 BP.
XX AAX22550;
AC AAX22550;
XX 21-MAY-1999 (first entry)
XX Human CPTP RNA fragment #5.
XX CPTP; cholesterol ester transfer protein; inhibitor; therapy; treatment;
XX surface plasmon resonance; vascular disease; pathogenic; atherosclerosis;
XX human; ss.
XX Homo sapiens.
XX DE19731609-A1.
XX 18-FEB-1999.
XX 23-JUL-1997; 97DE-01031609.
XX 23-JUL-1997; 97DE-01031609.
XX (BOEH) BOEHRINGER INGELHEIM PHARMA KG.
XX Budzinksi R, Krist B, Mark M, Mueller P;
XX WPI; 1999-143775/13.
XX RNA transcript of human cholesterol ester transfer protein gene - useful
XX in drug screening assays, especially for atherosclerosis.
XX Disclosure; Page 13; 24pp; German.
XX This invention describes the isolation of a transcript of the human
XX cholesterol ester transfer protein (CETP) gene having a 5' untranslated
XX region including a regulatory sequence. The invention also describes a
XX method (a) for identifying substances capable of inhibiting CETP gene
XX expression, comprising measuring the translation rate of the above
XX transcript in the presence of a test substance, (2) a test substance
XX capable of inhibiting CETP gene expression, (3) an antisense
XX oligonucleotide capable of binding to the 5' untranslated region of the
XX above transcript and (4) a method based on surface plasmon resonance for
CC measuring the binding of a substance to a nucleic acid. The test
CC substance of (2) and the oligonucleotide of (3) are useful for
CC prophylactic or therapeutic treatment of vascular diseases in which CETP
CC has a pathogenic role, especially atherosclerosis
XX Sequence 17 BP; 2 A; 8 C; 1 G; 0 T; 6 U; 0 Other;
SQ Query Match 12.2%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1715 GAGTACGGAGATGGAGA 1731
Db 17 GAGTACGGAGATGGAGA 1
RESULT 15
AAI99829
ID AAI99829 standard; DNA; 21 BP.
XX AAI99829;
AC AAI99829;
XX 28-JAN-2002 (first entry)
XX Human G protein-coupled receptor protein TGR5 PCR primer SEQ ID NO 5.
XX Human; TGR5; G protein-coupled receptor protein; cerebroprotective;
XX cardiant; immunomodulator; cytostatic; antiinflammatory; antidiabetic;
XX cancer; PCR primer; ss.
XX Homo sapiens.
XX WO200177325-A1.
XX 18-OCT-2001.
XX 12-APR-2001; 2001WO-JP003143.
XX 12-APR-2000; 2000JP-00110765.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Miwa M, Matsui H, Shintani Y;
XX WPI; 2002-010910/01.
XX Human brain-originated G protein-coupled receptor protein TGR5,
XX applicable in diagnosis and developing drugs for diseases of e.g. central
XX nervous system and digestive organs, inflammation, cancer and diabetes.
XX Example 2; Page 98; 104pp; Japanese.
XX The invention relates to a novel human G protein-coupled receptor protein
XX TGR5 and the encoding cDNA with cerebroprotective, cardiant,
XX immunomodulator, cytostatic, antiinflammatory and antidiabetic activity.
XX The protein, encoded DNA and anti-TGR5 antibody are applicable in
XX diagnosis and developing drugs for diseases of central nervous system and
XX circulatory organs, inflammation, cancer and diabetes. The present
XX sequence is that of a TGR5 PCR primer of the invention
XX Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 U; 0 Other;
SQ Query Match 12.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1732 TTGGCTCCCACTCTCTCTT 1751
Db 1 TTGGCTCCCACTCTCTCTT 20
RESULT 16
ADB66783
```

```
ID ADB66783 standard; DNA; 20 BP.
XX
AC ADB66783;
XX
XX 04-DEC-2003 (first entry)
XX
DE Human E2A-Pbx1 antisense phosphorothioate oligonucleotide ISIS No. 16123.
XX
XX Human; E2A-Pbx1; antisense; phosphorothioate;
XX pre-B-cell acute lymphocytic leukaemia; sarcomatous cancer; E2A-HLA;
KW E2A-HLF; cytostatic; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate internucleotide linkages"
XX
XX US6607915-B1.
XX
XX 19-AUG-2003.
XX
XX 25-JUL-2000; 2000US-00624945.
XX
XX 30-SEP-1999; 99US-0156836P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wanciewicz E;
XX WPI; 2003-707866/67.
XX
XX New antisense compounds targeted to nucleic acids encoding E2A-Pbx1,
XX useful for inhibiting the expression of E2A-Pbx1, and for treating or
XX diagnosing a disease associated with overexpression of E2A-Pbx1, e.g.
XX sarcomatous cancer.
XX
XX Example 2; Col 24; 20pp; English.
XX
XX The present invention relates to antisense compounds targeted to
XX polynucleotide sequences encoding human E2A-Pbx1. The antisense compounds
XX comprise antisense phosphorothioate oligonucleotides. The antisense
XX compounds are useful for inhibiting the expression of E2A-Pbx1, and for
XX treating or diagnosing a disease or condition associated with the
XX overexpression or constitutive activation of E2A-Pbx1, e.g. pre-B-cell
XX acute lymphocytic leukaemia or sarcomatous cancer. The compounds are also
XX useful as research reagents and tools, e.g. for detecting and determining
XX the role of E2-Pbx1 in various cell functions and physiological
XX processes. The present sequence represents a human E2A-Pbx1 antisense
XX phosphorothioate oligonucleotide.
XX
XX Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 11.8%; Score 16.4; DB 1; Length 20;
XX Best Local Similarity 94.4%; Pred. No. 48;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1658 ACCAGGCTCAGCTGGA 1675
XX |||||
XX 1 ACCAGGCTCAGCTGGA 18
XX
XX RESULT 17
XX AAV52705
XX ID AAV52705 standard; DNA; 22 BP.
XX
XX AC AAV52705;
XX
XX 21-DEC-1998 (first entry)
XX
```

```
DE Hepatocyte nuclear factor 1 beta gene exon 4-2 forward PCR primer.
XX
XX Hepatocyte nuclear factor 1 beta; HNF-1 beta; MODY4; human;
KW transcription factor; maturity onset diabetes of the young; TCF2;
KW diabetes; NIDDM; diagnosis; therapy; PCR; primer; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9811254-A1.
XX
XX 19-MAR-1998.
XX
XX 10-SEP-1997; 97WO-US016037.
XX
XX 10-SEP-1996; 96US-0025719P.
XX 02-OCT-1996; 96US-0028056P.
XX 30-OCT-1996; 96US-0029679P.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Bell GI, Yamagata K, Oda N, Kaisaki PJ, Furuta H, Menzel S;
XX Horikawa Y;
XX WPI; 1998-271667/24.
XX
XX Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-
XX beta - useful for detecting susceptibility for non-insulin dependent
XX diabetes, especially maturity-onset diabetes of the young.
XX Example 8; Page 146; 363pp; English.
XX
XX This is a forward PCR primer designed for use with a reverse primer (see
XX AAV52706) in the PCR amplification of the 4-2 exon of the human
XX hepatocyte nuclear factor-1 beta (HNF-1 beta) TCF2 gene (see AAV52730).
XX Mutations of the HNF-1 beta gene have been identified by amplifying (see
XX AAV5293-716) and sequencing the appropriate exon. The invention concerns
XX the identification of genes responsible for non-insulin dependent
XX diabetes mellitus (NIDDM) for use in diagnostics and therapeutics. It
XX demonstrates that the MODY4 (maturity-onset diabetes of the young) locus
XX is the HNF-1 beta gene. Analysis of mutations in the HNF-1 beta gene can
XX be diagnostic for diabetes
XX
XX Sequence 22 BP; 8 A; 9 C; 3 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 11.7%; Score 16.2; DB 1; Length 22;
XX Best Local Similarity 85.7%; Pred. No. 62;
XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 1658 ACCAGGCTCAGCTGGAACC 1678
XX |||||
XX 2 ACCAGACTCAGCGCTGAACC 22
XX
XX RESULT 18
XX ABZ57102/C
XX ID ABZ57102 standard; DNA; 24 BP.
XX
XX AC ABZ57102;
XX
XX 24-MAR-2003 (first entry)
XX
XX Human zinc finger protein 12.76 RT-PCR primer, SEQ ID NO:3.
XX
XX Human; zinc finger protein 12.76; recombinant production; gene therapy;
KW cancer; tumour; development disorder; cytostatic;
KW reverse transcription-PCR; RT-PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX CN1355206-A.
XX
XX 26-JUN-2002.
```



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Query Match      10.9%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1713 AGGAGTACGGAGATGGAGAT 1732
      ||||| ||||| ||||| |||||
DB 4 AGGAGGAGGGAGATGGACAT 23

RESULT 21
AAT49837
ID AAT49837 standard; RNA; 15 BP.
XX AC AAT49837;
XX DT 07-MAR-1997 (first entry)
XX DE Human CERP HH ribozyme target sequence #1752.
XX KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CERP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX OS Homo sapiens.
XX PN WO9620279-A1.
XX PD 04-JUL-1996.
XX PF 11-DEC-1995; 95WO-US016000.
XX PR 23-DEC-1994; 94US-00363240.
XX PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN ) WARNER LAMBERT CO.
XX PI Couture L, Stinchcomb D, Meswigen J, Bisgaier C, Pape M;
XX WPI; 1996-321852/32.
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
PT useful for preventing or treating initial development, progression or
PT regression of vascular diseases, esp. familial hypercholesterolaemia.
XX PS Claim 4; Page 32; 72pp; English.
XX AAT49608-T49863 represent target sequences for the human cholesterol
XX ester transfer protein (CERP) hammerhead (HH) ribozymes (see AAT49881-
XX T50137). CERP is a 74 kD glycoprotein that facilitates neutral lipid
XX transfer between plasma lipoproteins. The numbering of the targets refers
XX to the position of the cleavage site in full length CERP. The ribozyme
XX binds to 5 nucleotides either side of this site, provided the sequence
XX is immediately upstream. The ribozymes are able to cleave mRNA from the
XX gene encoding CERP, thereby blocking synthesis and/or expression of the
XX mRNA. By inhibiting CERP, the reverse cholesterol transport (RCT) pathway
XX can be inhibited (or eliminated) thereby preventing the reduction in size
XX density of the high density lipoproteins (HDL), prolonging HDL half life,
XX and therefore increasing HDL levels. The ribozymes can be used to treat
XX conditions associated with abnormal levels of CERP, specifically familial
XX hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
XX vascular complications of diabetes, transplant, atherectomy and
XX angioplastic restenosis. By inhibiting CERP, the levels of HDL and low
XX density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX (a decrease in LDL levels), and a corresponding increase in HDL levels).
XX The HH ribozymes can also be used diagnostically to study genetic drift
XX and mutations in diseased cells, and to detect CERP mRNA. As the HH
XX ribozymes target specific regions of the CERP gene, they have low non-
XX specific activity

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XX SQ Sequence 15 BP; 4 A; 7 C; 0 G; 0 T; 4 U; 0 Other;
Query Match      10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 65;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1745 CTTCCCTATCCTTAAA 1759
      ||:||||:|||||
DB 1 CCUCCCUAUCUAAA 15

RESULT 22
AAT49841
ID AAT49841 standard; RNA; 15 BP.
XX AC AAT49841;
XX DT 07-MAR-1997 (first entry)
XX DE Human CERP HH ribozyme target sequence #1757.
XX KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CERP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX OS Homo sapiens.
XX PN WO9620279-A1.
XX PD 04-JUL-1996.
XX PF 11-DEC-1995; 95WO-US016000.
XX PR 23-DEC-1994; 94US-00363240.
XX PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN ) WARNER LAMBERT CO.
XX PI Couture L, Stinchcomb D, Meswigen J, Bisgaier C, Pape M;
XX WPI; 1996-321852/32.
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX useful for preventing or treating initial development, progression or
XX regression of vascular diseases, esp. familial hypercholesterolaemia.
XX PS Claim 4; Page 32; 72pp; English.
XX AAT49608-T49863 represent target sequences for the human cholesterol
XX ester transfer protein (CERP) hammerhead (HH) ribozymes (see AAT49881-
XX T50137). CERP is a 74 kD glycoprotein that facilitates neutral lipid
XX transfer between plasma lipoproteins. The numbering of the targets refers
XX to the position of the cleavage site in full length CERP. The ribozyme
XX binds to 5 nucleotides either side of this site, provided the sequence
XX is immediately upstream. The ribozymes are able to cleave mRNA from the
XX gene encoding CERP, thereby blocking synthesis and/or expression of the
XX mRNA. By inhibiting CERP, the reverse cholesterol transport (RCT) pathway
XX can be inhibited (or eliminated) thereby preventing the reduction in size
XX density of the high density lipoproteins (HDL), prolonging HDL half life,
XX and therefore increasing HDL levels. The ribozymes can be used to treat
XX conditions associated with abnormal levels of CERP, specifically familial
XX hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
XX vascular complications of diabetes, transplant, atherectomy and
XX angioplastic restenosis. By inhibiting CERP, the levels of HDL and low
XX density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX (a decrease in LDL levels), and a corresponding increase in HDL levels).
XX The HH ribozymes can also be used diagnostically to study genetic drift
XX and mutations in diseased cells, and to detect CERP mRNA. As the HH
XX ribozymes target specific regions of the CERP gene, they have low non-
XX specific activity

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CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity
 XX
 SQ Sequence 15 BP; 4 A; 6 C; 2 G; 0 T; 3 U; 0 Other;
 Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 65;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1750 CTATCTTAAGGCC 1764
 Db 1 CUAUCCUAAAGGCC 15
 RESULT 23
 AAT49823
 ID AAT49823 standard; RNA; 15 BP.
 AC AAT49823;
 XX
 DT 07-MAR-1997 (first entry)
 XX
 DE Human CETP HH ribozyme target sequence #1712.
 XX
 KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9620279-A1.
 PD 04-JUL-1996.
 XX
 PF 11-DEC-1995; 95WO-US016000.
 XX
 PR 23-DEC-1994; 94US-00363240.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
 XX WPI; 1996-321852/32.
 DR
 PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 XX
 PS Claim 4; Page 32; 72pp; English.
 XX
 CC AAT49608-749863 represent target sequences for the human cholesterol
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
 CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
 CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CETP. The ribozyme
 CC binds to 5 nucleotides either side of this site, provided the sequence UH
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the
 CC gene encoding CETP, thereby blocking synthesis and/or expression of the
 CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,
 CC and therefore increasing HDL levels. The ribozymes can be used to treat
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
 CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low

CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
 CC The HH ribozymes can also be used diagnostically to study genetic drift
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity
 XX
 SQ Sequence 15 BP; 3 A; 0 C; 7 G; 0 T; 5 U; 0 Other;
 Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 65;
 Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1705 GTTGGTTAGGAGTA 1719
 Db 1 GUUGGUUAGGAGUA 15
 RESULT 24
 AAT49825
 ID AAT49825 standard; RNA; 15 BP.
 XX
 AC AAT49825;
 XX
 DT 07-MAR-1997 (first entry)
 XX
 DE Human CETP HH ribozyme target sequence #1713.
 XX
 KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9620279-A1.
 PD 04-JUL-1996.
 XX
 PF 11-DEC-1995; 95WO-US016000.
 XX
 PR 23-DEC-1994; 94US-00363240.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
 XX WPI; 1996-321852/32.
 DR
 PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 XX
 PS Claim 4; Page 32; 72pp; English.
 XX
 CC AAT49608-749863 represent target sequences for the human cholesterol
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
 CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
 CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CETP. The ribozyme
 CC binds to 5 nucleotides either side of this site, provided the sequence UH
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the
 CC gene encoding CETP, thereby blocking synthesis and/or expression of the
 CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,
 CC and therefore increasing HDL levels. The ribozymes can be used to treat
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
 CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low

CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
 CC The HH ribozymes can also be used diagnostically to study genetic drift
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity
 XX Sequence 15 BP; 3 A; 1 C; 6 G; 0 T; 5 U; 0 Other;
 SQ Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 65;
 Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1706 TTGGGTTAGGATAC 1720
 Db 1 UUGGUUAGGAGUAC 15
 RESULT 25
 AAT49811
 ID AAT49811 standard; RNA; 15 BP.
 XX AC AAT49811;
 DT 18-MAR-1997 (first entry)
 XX Human CETP HH ribozyme target sequence #1644.
 DE Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.
 XX Homo sapiens.
 OS WO9620279-A1.
 PN 04-JUL-1996.
 PD 11-DEC-1995; 95WO-US016000.
 XX 23-DEC-1994; 94US-00363240.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
 DR WPI; 1996-321852/32.
 XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 XX Claim 4; Page 32; 72pp; English.
 XX AAT49608-T49863 represent target sequences for the human cholesterol
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
 CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
 CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CETP. The ribozyme
 CC binds to 5 nucleotides either side of this site, provided the sequence UH
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the
 CC gene encoding CETP, thereby blocking synthesis and/or expression of the
 CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,

CC and therefore increasing HDL levels. The ribozymes can be used to treat
 CC conditions associated with abnormal levels of CETP, specifically familial
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
 CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
 CC The HH ribozymes can also be used diagnostically to study genetic drift
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity
 XX Sequence 15 BP; 4 A; 2 C; 6 G; 0 T; 3 U; 0 Other;
 SQ Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 65;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1637 GGCTTGATGAGAG 1651
 Db 1 GGCUGUAGGAGAG 15
 RESULT 26
 AAT49809
 ID AAT49809 standard; RNA; 15 BP.
 XX AC AAT49809;
 DT 18-MAR-1997 (first entry)
 XX Human CETP HH ribozyme target sequence #1641.
 DE Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.
 XX Homo sapiens.
 OS WO9620279-A1.
 PN 04-JUL-1996.
 PD 11-DEC-1995; 95WO-US016000.
 XX 23-DEC-1994; 94US-00363240.
 PR (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
 DR WPI; 1996-321852/32.
 XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 XX Claim 4; Page 32; 72pp; English.
 XX AAT49608-T49863 represent target sequences for the human cholesterol
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
 CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
 CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CETP. The ribozyme
 CC binds to 5 nucleotides either side of this site, provided the sequence UH
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the
 CC gene encoding CETP, thereby blocking synthesis and/or expression of the
 CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,

CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,
 CC and therefore increasing HDL levels. The ribozymes can be used to treat
 CC conditions associated with abnormal levels of CETP, specifically familial
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
 CC hyperbetalipoproteinaemia, hypopalipoprotheinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
 CC The HH ribozymes can also be used diagnostically to study genetic drift
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity

XX Sequence 15 BP; 2 A; 2 C; 7 G; 0 T; 4 U; 0 Other;

SQ Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 73.3%; Pred. No. 65;
 Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1634 TCGGGCTTCTAGCAG 1648

DB :|||||:|||||
 1 UGGGGCUUGAGCAG 15

RESULT 27

AAT49827
 ID AAT49827 standard; RNA; 15 BP.

AC AAT49827;

DT 07-MAR-1997 (first entry)

XX Human CETP HH ribozyme target sequence #1719.

XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypopalipoprotheinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.

XX Homo sapiens.

XX WO9620279-A1.

XX 04-JUL-1996.

XX 11-DEC-1995; 95WO-US016000.

XX 23-DEC-1994; 94US-00363240.

XX (RIBO-) RIBOZYME PHARM INC.

XX (WARN) WARNER LAMBERT CO.

XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;

XX WPI; 1996-321852/32.

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 XX Claim 4; Page 32; 72pp; English.

XX AAT49608-T49863 represent target sequences for the human cholesterol
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
 CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
 CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CETP. The ribozyme

CC binds to 5 nucleotides either side of this site, provided the sequence UH
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the
 CC gene encoding CETP, thereby blocking synthesis and/or expression of the
 CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,
 CC and therefore increasing HDL levels. The ribozymes can be used to treat
 CC conditions associated with abnormal levels of CETP, specifically familial
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
 CC hyperbetalipoproteinaemia, hypopalipoprotheinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
 CC The HH ribozymes can also be used diagnostically to study genetic drift
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity

XX Sequence 15 BP; 5 A; 1 C; 6 G; 0 T; 3 U; 0 Other;

SQ Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 65;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1712 TAGGAGTAGGAGAT 1726

DB :|||||:|||||
 1 UAGGAGUACGGAGAU 15

RESULT 28

AAT49829

ID AAT49829 standard; RNA; 15 BP.

AC AAT49829;

DT 07-MAR-1997 (first entry)

XX Human CETP HH ribozyme target sequence #1733.

XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypopalipoprotheinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.

XX Homo sapiens.

XX WO9620279-A1.

XX 04-JUL-1996.

XX 11-DEC-1995; 95WO-US016000.

XX 23-DEC-1994; 94US-00363240.

XX (RIBO-) RIBOZYME PHARM INC.

XX (WARN) WARNER LAMBERT CO.

XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;

XX WPI; 1996-321852/32.

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 XX Claim 4; Page 32; 72pp; English.

XX AAT49608-T49863 represent target sequences for the human cholesterol
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-

CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
 CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CETP. The ribozyme
 CC binds to 5 nucleotides either side of this site, provided the sequence UH
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the
 CC gene encoding CETP, thereby blocking synthesis and/or expression of the
 CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,
 CC and therefore increasing HDL levels. The ribozymes can be used to treat
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
 CC hyperbetaloproteinaemia, hypopalipoproteinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
 CC The HH ribozymes can also be used diagnostically to study genetic drift
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity
 CC
 CC Sequence 15 BP; 2 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 73.3%; Pred. No. 65;
 Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1726 TGGAGATTGGTCCC 1740

Db 1 UGGAGAUUGGUCCC 15

RESULT 29

AAT49815

ID AAT49815 standard; RNA; 15 BP.

AC AAT49815;

DT 07-MAR-1997 (first entry)

XX Human CETP HH ribozyme target sequence #1686.

XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.

XX Homo sapiens.

OS WO9620279-A1.

PN 04-JUL-1996.

XX 11-DEC-1995; 95WO-US016000.

XX 23-DEC-1994; 94US-00363240.

XX (RIBO-) RIBOZYME PHARM INC.

PA (WARN) WARNER LAMBERT CO.

PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;

XX WPI; 1996-321852/32.

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.

XX Claim 4; Page 32; 72pp; English.

XX AAT49608-T49863 represent target sequences for the human cholesterol
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
 CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
 CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CETP. The ribozyme
 CC binds to 5 nucleotides either side of this site, provided the sequence UH
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the
 CC gene encoding CETP, thereby blocking synthesis and/or expression of the
 CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,
 CC and therefore increasing HDL levels. The ribozymes can be used to treat
 CC conditions associated with abnormal levels of CETP, specifically familial
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
 CC hyperbetaloproteinaemia, hypopalipoproteinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
 CC The HH ribozymes can also be used diagnostically to study genetic drift
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity
 CC
 CC Sequence 15 BP; 1 A; 6 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 10.8%; Score 15; DB 1; Length 15;

Best Local Similarity 66.7%; Pred. No. 65;

Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1679 CTGGTGCTCTCTCCA 1693

Db 1 CUGGUGUCUCCUCA 15

RESULT 30

AAT49821

ID AAT49821 standard; RNA; 15 BP.

AC AAT49821;

DT 07-MAR-1997 (first entry)

XX Human CETP HH ribozyme target sequence #1707.

XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.

XX Homo sapiens.

OS WO9620279-A1.

PN 04-JUL-1996.

XX 11-DEC-1995; 95WO-US016000.

XX 23-DEC-1994; 94US-00363240.

XX (RIBO-) RIBOZYME PHARM INC.

PA (WARN) WARNER LAMBERT CO.

PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;

XX WPI; 1996-321852/32.

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or

PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 XX
 PS Claim 4; Page 32; 72pp; English.
 XX
 CC AAT49608-T49863 represent target sequences for the human cholesterol
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
 CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
 CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CETP. The ribozyme
 CC binds to 5 nucleotides either side of this site, provided the sequence UH
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the
 CC gene encoding CETP, thereby blocking synthesis and/or expression of the
 CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,
 CC and therefore increasing HDL levels. The ribozymes can be used to treat
 CC conditions associated with abnormal levels of CETP, specifically familial
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
 CC hyperbetalipoproteinaemia, hypopalipoproteinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
 CC The HH ribozymes can also be used diagnostically to study genetic drift
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity
 XX
 SQ Sequence 15 BP; 3 A; 0 C; 7 G; 0 T; 5 U; 0 Other;
 Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 65;
 Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1700 TGGAACTTGGGTAG 1714
 :|||||:|||||:
 Db 1 UGGAAGUUGGUUAG 15
 RESULT 31
 AAT49831
 ID AAT49831 standard; RNA; 15 BP.
 XX
 AC AAT49831;
 XX
 DT 07-MAR-1997 (first entry)
 XX
 DE Human CETP HH ribozyme target sequence #1738.
 XX
 KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9620279-A1.
 XX
 PD 04-JUL-1996.
 XX
 PF 11-DEC-1995; 95WO-US016000.
 XX
 PR 23-DEC-1994; 94US-00363240.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
 XX WPI; 1996-321852/32.
 DR

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 PS Claim 4; Page 32; 72pp; English.
 XX
 CC AAT49608-T49863 represent target sequences for the human cholesterol
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
 CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
 CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CETP. The ribozyme
 CC binds to 5 nucleotides either side of this site, provided the sequence UH
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the
 CC gene encoding CETP, thereby blocking synthesis and/or expression of the
 CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,
 CC and therefore increasing HDL levels. The ribozymes can be used to treat
 CC conditions associated with abnormal levels of CETP, specifically familial
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
 CC hyperbetalipoproteinaemia, hypopalipoproteinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
 CC The HH ribozymes can also be used diagnostically to study genetic drift
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity
 XX
 SQ Sequence 15 BP; 3 A; 6 C; 2 G; 0 T; 4 U; 0 Other;
 Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 73.3%; Pred. No. 65;
 Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1731 ATTGGCTCCCACTC 1745
 :|||:|||||:|:
 Db 1 AUUGGCCUCCCAACC 15
 RESULT 32
 AAT49819
 ID AAT49819 standard; RNA; 15 BP.
 XX
 AC AAT49819;
 XX
 DT 07-MAR-1997 (first entry)
 XX
 DE Human CETP HH ribozyme target sequence #1691.
 XX
 KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9620279-A1.
 XX
 PD 04-JUL-1996.
 XX
 PF 11-DEC-1995; 95WO-US016000.
 XX
 PR 23-DEC-1994; 94US-00363240.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX

QY 1698 GGTGAAGTTGG 1710
 Db 1 GGTGAGTTGG 13
 RESULT 463
 ABC16693/C
 ID ABC16693 standard; DNA; 13 BP.
 XX AC ABC16693;
 XX DT 20-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 16700 for detecting SNP TSC0003627.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 16700; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1709 GGTGAGGTTGACG 1721
 Db 13 GGTGAGGTTGCG 1
 RESULT 464
 ABF16652/C
 ID ABF16652 standard; DNA; 13 BP.
 XX AC ABF16652;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 142165 for detecting SNP TSC0035612.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.

DE Oligonucleotide SEQ ID NO 116649 for detecting SNP TSC0029189.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 116649; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1739 CCAACTCCTCCCT 1751
 Db 13 CCAACTACTCCCT 1
 RESULT 465
 ABF42168/C
 ID ABF42168 standard; DNA; 13 BP.
 XX AC ABF42168;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 142165 for detecting SNP TSC0035612.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 142165; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 2 A; 0 C; 8 G; 3 T; 0 U; 0 Other;
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1737 TCCCACTCTCTCC 1749
Db 13 TCCCACTCTCTCC 1
RESULT 466
ID ABH62596 standard; DNA; 13 BP.
XX AC ABH62596;
XX 22-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 262573 for detecting SNP TSC0001590.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 142165; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 2 A; 0 C; 8 G; 3 T; 0 U; 0 Other;
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1737 TCCCACTCTCTCC 1749
Db 13 TCCCACTCTCTCC 1
RESULT 466
ID ABH62596 standard; DNA; 13 BP.
XX AC ABH62596;
XX 22-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 262573 for detecting SNP TSC0001590.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 262573; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1703 AGTTGGGTAGG 1715
Db 1 AGTTGGGTAGG 13
RESULT 467
ID ABC93114/C standard; DNA; 13 BP.
XX AC ABC93114;
XX 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 93131 for detecting SNP TSC0023277.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 93131; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at


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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match      8.2%; Score 11.4; DB 1; Length 13;
  Best Local Similarity 92.3%; Pred. No. 3.3e+02;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 CCAACTCTCTCCC 1750
DB 13 CCCACACTCTCC 1

RESULT 468
ABC70350/c
ID ABC70350 standard; DNA; 13 BP.
XX
AC ABC70350;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 70367 for detecting SNP TSC0018290.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 70367; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match      8.2%; Score 11.4; DB 1; Length 13;
  Best Local Similarity 92.3%; Pred. No. 3.3e+02;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1739 CCAACTCTCTCCT 1751
DB 13 CCAACTCTCCT 1

RESULT 470
ABF10342
ID ABF10342 standard; DNA; 13 BP.
XX
AC ABF10342;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 110339 for detecting SNP TSC0027562.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
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OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB0000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 110339; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1701 GGAAGTTGGGTTA 1713
XX Db ||||| |||||
XX 1 GGAAGTAGGGTTA 13
XX
XX RESULT 471
XX ABF10344
XX AC ABF10344;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 110341 for detecting SNP TSC0027562.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB0000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 110339; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1701 GGAAGTTGGGTTA 1713
XX Db ||||| |||||
XX 1 GGAAGTAGGGTTA 13
XX
XX RESULT 471
XX ABF10344
XX AC ABF10344;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 110341 for detecting SNP TSC0016595.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB0000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 62607; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
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CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match

Best Local Similarity 8.2%; Score 11.4; DB 1; Length 13;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1701 GGAAGTGGGTTA 1713

Db 1 GGAAGTGGGTTA 13

RESULT 473

ABF42171

ID ABF42171 standard; DNA; 13 BP.

XX AC ABF42171;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 142168 for detecting SNP TSC0035612.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PS 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PX WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX PT designed to detect single-nucleotide polymorphisms and cytosine
 XX PT methylation status.

XX PS Claim 1; SEQ ID NO 142168; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 2 A; 8 C; 1 G; 2 T; 0 U; 0 Other;

Query Match

8.2%; Score 11.4; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 3.3e+02;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1737 TCCCAACTCCTCC 1749

Db 1 TCCCAAGCCTCC 13

RESULT 474

ABH33146/C

ID ABH33146 standard; DNA; 13 BP.

XX AC ABH33146;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 233123 for detecting SNP TSC0056884.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PX WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX PT designed to detect single-nucleotide polymorphisms and cytosine
 XX PT methylation status.

XX PS Claim 1; SEQ ID NO 233123; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match

8.2%; Score 11.4; DB 1; Length 13;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 TCCCTATCCTAAA 1759

Db 13 TACTATCCTAAA 1

RESULT 475

ABF15452/C

ID ABF15452 standard; DNA; 13 BP.

XX AC ABF15452;

PT designed to detect single-nucleotide polymorphisms and cytosine
methylation status.

XX Claim 1; SEQ ID NO 49608; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1745 CCTCCTATCCTTA 1757

Db 1 CCTCCTATCCTTA 13

RESULT 478

ABC25065/c

ID ABC25065 standard; DNA; 13 BP.

AC ABC25065;

XX 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 25082 for detecting SNP TSC0006096.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.

XX Claim 1; SEQ ID NO 25082; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1697 TGGTCGAAGTTGG 1709

Db 13 TAGTGGGAAGTTGG 1

RESULT 479

ABC08446/c

ID ABC08446 standard; DNA; 13 BP.

XX ABC08446;

XX 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 8437 for detecting SNP TSC0002329.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.

XX Claim 1; SEQ ID NO 8437; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 TCCCTATCCTTAA 1759

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Db      13  TCCATATCCTAAA 1
RESULT 480
ABC84786/c
ID  ABC84786 standard; DNA; 13 BP.
XX
AC  ABC84786;
XX
DT  21-FEB-2002 (first entry)
XX
DE  Oligonucleotide SEQ ID NO 84803 for detecting SNP TSC0021342.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
PS  WPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 110340; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
PS  Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
XX
CC  Query Match 8.2%; Score 11.4; DB 1; Length 13;
CC  Best Local Similarity 92.3%; Pred. No. 3.3e+02;
CC  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY  1701 GGAAGTGGGTTA 1713
DB  13 GGAAGTAGGGTTA 1
XX
RESULT 482
ABC82760/c
ID  ABC82760 standard; DNA; 13 BP.
XX
AC  ABC82760;
XX
DT  21-FEB-2002 (first entry)
XX
DE  Oligonucleotide SEQ ID NO 62777 for detecting SNP TSC0016623.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX

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XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX XX WPI; 2001-657177/75.
 XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 62777; 29pp + Sequence Listing; German.
 XX XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 3 A; 0 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1745 CCTCCTATCCTA 1757
 Db 13 CCCCCCTATCCTA 1
 RESULT 483
 ABC38204/C
 ID ABC38204 standard; DNA; 13 BP.
 XX AC ABC38204;
 XX DT 20-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 38221 for detecting SNP TSC0011836.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX XX WPI; 2001-657177/75.
 XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 38221; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1744 TCCTCCTATCCT 1756
 Db 13 TCCCCCTATCCT 1
 RESULT 484
 ABF36186/C
 ID ABF36186 standard; DNA; 13 BP.
 XX AC ABF36186;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 136183 for detecting SNP TSC0034006.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX XX WPI; 2001-657177/75.
 XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 136183; 29pp + Sequence Listing; German.
 XX XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX XX

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SQ Sequence 13 BP; 3 A; 0 C; 8 G; 2 T; 0 U; 0 Other;
Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 CCCAACTCTCTCC 1750
DB 13 CCTAACTCTCTCC 1

RESULT 485
ABF42170/c
ID ABF42170 standard; DNA; 13 BP.
XX AC ABF42170;
XX AC ABF42170;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 142167 for detecting SNP TSC0035612.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX AC ABF42170;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 142167 for detecting SNP TSC0035612.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 142167; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 2 A; 1 C; 8 G; 2 T; 0 U; 0 Other;
Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1737 TCCCAACTCTCTCC 1749
DB 13 TCCCAACGCTCTCC 1

RESULT 486
ABC26849
ID ABC26849 standard; DNA; 13 BP.
XX AC ABC26849;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 26866 for detecting SNP TSC0007227.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX DT 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 26866; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 1 A; 8 C; 0 G; 4 T; 0 U; 0 Other;
Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1739 CCAACTCTCTCTCC 1751
DB 1 CCATCTCTCTCTCC 13

RESULT 487
ABC62591/c
ID ABC62591 standard; DNA; 13 BP.
XX AC ABC62591;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 62608 for detecting SNP TSC0016595.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
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XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 62608; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1701 GGAAGTTGGGTGA 1713
Db 13 GGAAGTTGGGTGA 1

RESULT 489
ABC65199/c
ID ABC65199 standard; DNA; 13 BP.
AC ABC65199;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 65216 for detecting SNP TSC0017166.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX PI Olek A, Piepenbrock C, Berlin K;
XX

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DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 65216; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1701 GGAAGTTGGGTGA 1713
Db 13 GGAAGTTGGGTGA 1

RESULT 489
ABC08447
ID ABC08447 standard; DNA; 13 BP.
XX AC ABC08447;
XX 20-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 8438 for detecting SNP TSC0002329.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 8438; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC

```

Query Match	8.2%;	Score 11.4;	DB 1;	Length 13;
Best Local Similarity	92.3%;	Pred. No. 3.3e+02;		
Matches	12;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

XX Oligonucleotide SEQ ID NO 93133 for detecting SNP TSC0023277.
 DE
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 93133; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 1 A; 1 C; 9 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
 XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1738 CCCAACTCCCTCCC 1750
 XX 13 CCCAACGCTCCC 1
 XX
 XX RESULT 493
 XX ABC25064
 XX ID ABC25064 standard; DNA; 13 BP.
 XX
 XX AC ABC25064;
 XX
 XX 20-FEB-2002 (first entry)
 XX
 XX Oligonucleotide SEQ ID NO 25081 for detecting SNP TSC0006096.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX

PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 25081; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
 XX
 XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
 XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1697 TGGTGGAGCTGG 1709
 XX 1 TAGTGGAGCTGG 13
 XX
 XX RESULT 494
 XX ABF19170/G
 XX ID ABF19170 standard; DNA; 13 BP.
 XX
 XX AC ABF19170;
 XX
 XX 21-FEB-2002 (first entry)
 XX
 XX Oligonucleotide SEQ ID NO 119167 for detecting SNP TSC0029760.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX

XX PS Claim 1; SEQ ID NO 119167; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1739 CCACTCTCTCCT 1751
Db 13 CCTACTCTCTCCT 1

RESULT 495
ABF19306
ID ABF19306 standard; DNA; 13 BP.
XX AC ABF19306;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 119303 for detecting SNP TSC0029792.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PS WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PS Claim 1; SEQ ID NO 119303; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1739 CCACTCTCTCCT 1751
Db 13 CCTACTCTCTCCT 1

RESULT 495
ABF19306
ID ABF19306 standard; DNA; 13 BP.
XX AC ABF19306;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 119303 for detecting SNP TSC0029792.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PS WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PS Claim 1; SEQ ID NO 119303; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 TCCTATCTCTTAA 1759
Db 1 TACCTATCTTAA 13

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 1 A; 0 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1699 GTGGAAGTTGGT 1711
Db 1 GTGCTAGTTGGT 13

RESULT 496
ABH33147
ID ABH33147 standard; DNA; 13 BP.
XX AC ABH33147;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 233124 for detecting SNP TSC0056884.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PS WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PS Claim 1; SEQ ID NO 233124; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 TCCTATCTCTTAA 1759
Db 1 TACCTATCTTAA 13

RESULT 497
 ABF19307/c
 ID ABF19307 standard; DNA; 13 BP.
 XX
 AC ABF19307;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 119304 for detecting SNP TSC0029792.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 119304; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 5 A; 7 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1699 GTGGAAGTTGGGT 1711
 DB 13 GTGGAAGTTGGGT 1
 RESULT 498
 ABF42169
 ID ABF42169 standard; DNA; 13 BP.
 XX
 AC ABF42169;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 142166 for detecting SNP TSC0035612.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 WIPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 142166; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 8 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1737 TCCCAACTCCCTCC 1749
 DB 1 TCCCAACTCCCTCC 13
 RESULT 499
 ABC93115
 ID ABC93115 standard; DNA; 13 BP.
 XX
 AC ABC93115;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 93132 for detecting SNP TSC0023277.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 CCCAACTCCTCCC 1750
 |||||
 Db 1 CCCAACCTCCTCCC 13

RESULT 502
 ABC84687/c
 ID ABC84687 standard; DNA; 13 BP.
 AC ABC84687;
 XX
 XX
 DT 21-FEB-2002 (first entry)
 DE
 DE Oligonucleotide SEQ ID NO 84704 for detecting SNP TSC0021323.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.

PN WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 84704; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGAGA 1731
 |||||
 Db 13 ACGGAGATGGAGA 1

RESULT 503
 ABC38205
 ID ABC38205 standard; DNA; 13 BP.
 XX

AC ABC38205;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 XX Oligonucleotide SEQ ID NO 38222 for detecting SNP TSC0011836.

DE
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 38222; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 1 A; 8 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1744 TCCCTCCCTATCCT 1756
 |||||
 Db 1 TCCCTCCCTATCCT 13

RESULT 504

ABF36187

ID ABF36187 standard; DNA; 13 BP.

XX

AC ABF36187;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 136184 for detecting SNP TSC0034006.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1703 AAGTTGGGTTAGG 1715
 |||||
 Db 13 AAGTTGGGTTAGG 1

RESULT 507

AAT98901
 ID AAT98901 standard; DNA; 14 BP.

XX AC AAT98901;

XX DT 23-MAR-1998 (first entry)

XX DE Probe 41w32 for HIV RT gene wild type E40M41.

XX KW Reverse transcriptase gene; HIV; RT gene; antiviral drug susceptibility;
 KW virus susceptibility; antiviral drug resistant viral strain; retrovirus;
 KW Hepadnaviridae; HIV RT genotyping; probe; ss.

XX OS Synthetic.

XX OS Human immunodeficiency virus 1.

XX PN WO9727332-A1.

XX PD 31-JUL-1997.

XX PF 17-JAN-1997; 97WO-EP000211.

XX PR 26-JAN-1996; 96EP-00870005.

XX PR 25-JUN-1996; 96EP-00870081.

XX PA (INNO-) INNOGENETICS NV.

XX PI Stuyver L, Louwagie J, Rossau R;

XX WPI; 1997-393716/36.

XX DR Determining susceptibility to antiviral drugs of reverse transcriptase
 XX PT containing viruses - useful for genotyping HIV RT and detecting antiviral
 XX PT resistant HIV.

XX PS Claim 13; Page 36; 59pp; English.

XX CC This sequence represents a probe for a wild type HIV reverse
 XX CC transcriptase (RT) gene fragment. This sequence can be used in the method
 XX CC of the invention for determining the susceptibility to antiviral drugs of
 XX CC viruses which contain RT genes and are present in a biological sample. It
 XX CC comprises: (1) releasing, isolating or concentrating the polynucleic
 XX CC acids present in a sample; (2) amplifying the relevant part of the RT
 XX CC genes present with at least one suitable primer pair; (3) hybridising the
 XX CC polynucleic acids of step (1) or (2) with at least two RT gene probes,
 XX CC the probes being applied to known locations on a solid support, and are
 XX CC capable of simultaneously hybridising to their respective target regions
 XX CC under appropriate hybridisation and wash condition allowing the detection
 XX CC of homologous targets, or with the probes hybridising specifically with a
 XX CC sequence complementary to any of the target sequences; (4) detecting the
 XX CC hybrids formed in step (3); and (4) inferring the nucleotide sequence at
 XX CC the codons of interest (codons 38-44, 47-53, 65-72, 73-77, 148-154, 180-
 XX CC 187, 212-216, and 217-220), and/or the amino acids of the codons of
 XX CC interest and/or antiviral drug resistance spectrum, and possible the type
 XX CC of viral isolates involved from the differential hybridisation signals

CC obtained in step (4). The method is specifically used to detect antiviral
 CC drug resistant strains of viruses containing RT genes, especially HIV
 CC retroviruses and Hepadnaviridae. The method can also be used for
 CC genotyping HIV RT

XX SQ Sequence 14 BP; 6 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1717 GTACGAGATGGA 1729
 |||||
 Db 1 GTACGAGATGGA 13

RESULT 508

AAQ74479
 ID AAQ74479 standard; DNA; 15 BP.

XX AC AAQ74479;

XX DT 25-MAR-2003 (revised)

XX DT 28-APR-1995 (first entry)

XX DE Primer based on plasmid constructs pSD5MRV and pSD6RRV sequences.

XX KW L-sorbose dehydrogenase; Gluconobacter oxydans; enzyme;
 KW L-keto-L-gulononic acid; ascorbic acid; L-sorbose dehydrogenase; ss.

XX OS Synthetic.

XX PN WO9420609-A1.

XX PD 15-SEP-1994.

XX PF 08-MAR-1994; 94WO-JP000369.

XX PR 08-MAR-1993; 93GB-00004700.

XX PR 28-SEP-1993; 93JP-00241851.

XX PA (FUJI) FUJISAWA PHARM CO LTD.

XX PI Niwa M, Saito Y, Ishii Y, Yoshida M, Suzuki H;

XX WPI; 1994-303017/37.

XX PT Novel dehydrogenase enzymes - used in the production of L-keto-L-gulononic
 XX PT acid and L-ascorbic acid.

XX PS Example 9; Page 23; 47pp; Japanese.

XX CC Seven primers (AAQ74479-85) were based on sequences of the constructs
 XX CC designated pSD5MRV and pSD6RRV and used in amplification reactions.
 XX CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 15 BP; 4 A; 1 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 4e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1724 GATGGAGATTGGC 1736
 |||||
 Db 2 GATGGAGATTGGC 14

RESULT 509

AAT04287
 ID AAT04287 standard; DNA; 15 BP.

XX AC AAT04287;

```

DT 09-APR-1996 (first entry)
XX
DE G. oxydans T100 L-sorbose dehydrogenase gene primer 1.
XX
KW L-sorbose dehydrogenase; 2-keto-gulonic acid; ascorbic acid; synthesis;
KW recombinant production; expression vector; primer 1; ss.
XX
OS Synthetic.
XX
PN WO9523220-A1.
XX
PD 31-AUG-1995.
XX
PF 24-FEB-1995; 95WO-JP000285.
XX
PR 25-FEB-1994; 94JP-00028612.
XX
PA (FUJII) FUJISAWA PHARM CO LTD.
XX
PI Niwa M, Saito Y, Ishii Y, Yoshida M, Hayashi H;
XX WPI; 1995-311531/40.
XX
DR Vector containing L-sorbose and L-sorbose dehydrogenase genes - used to
PT transform microorganisms for the efficient production of 2-keto-L-gulonic
PT acid.
XX
PS Example 9; Page 21; 78pp; Japanese.
XX
AAAT04287-T04293 are primers for the G. oxydans L-sorbose dehydrogenase
CC (SNDH) gene. An expression vector contg. the G. oxydans L-sorbose
CC dehydrogenase and SNDH genes arranged in sequence from a single promoter,
CC is used to transform Gluconobacter or Acetobacter spp. hosts. The hosts
CC then express the above dehydrogenases which are used in the prodn. of
CC large quantities of 2-keto-gulonic acid, an ascorbic acid synthesis
CC intermediate
XX
SQ Sequence 15 BP; 4 A; 1 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGC 1736
DB ||||| |||||
2 GATGGAGATTGGC 14

RESULT 510
AAQ80594/C
ID AAQ80594 standard; DNA; 15 BP.
XX
XX AAQ80594;
XX AC
XX 25-MAR-2003 (revised)
DT 12-OCT-1995 (first entry)
XX
DE M.tuberculosis 16S rRNA 3'-biotinylated capture probe.
XX
KW Mycobacterium tuberculosis; 16S ribosomal RNA;
KW strand displacement amplification; simultaneous detection;
KW adaptor-mediated multiplex amplification; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 15
FT /*tag= a
FT /note= "3'-biotinylated"
XX
XX EP640691-A2.
XX PN
XX 01-MAR-1995.
XX PD

16-AUG-1994; 94EP-00112741.
24-AUG-1993; 93US-00111076.
(BECT) BECTON DICKINSON CO.
Walker GT, Nadeau JG, Spears PA, Nycz CM, Shank DD, Schram JL;
Jurgensen SR;
WPI; 1995-092337/13.
Detection of Mycobacterium by multiplex nucleic acid amplification - by
amplification of the IS6110 insertion element of M. tuberculosis, allows
detection and/or identification of the M. tuberculosis complex.
Example 3; Page 16; 23pp; English.
A Mycobacterium tuberculosis IS6110 amplification primer (AAQ80578) is
used in a PCR and the extension product is then displaced and an IS6110
adaptor primer (AAQ80579) is hybridised to it. Following extension of the
adaptor primer, the second extension product is displaced and hybridised
to a M.tuberculosis 16S rRNA gene amplification primer (AAQ80582) which
is then extended. The third extension product is displaced and hybridised
to a 16S adaptor primer (AAQ80583) for chain extension; the fourth
extension product is then displaced and is amplified simultaneously with
the second extension product using the IS6110 and 16S amplification
primers. The new method allows coamplification of genus- (i.e. 16S rRNA)
and species- (i.e. IS6110) specific target nucleic acids by strand
displacement amplification. Opt. an internal control sequence (AAQ80589)
can be added to the sample prior to initial amplification. In this case,
amplified target and control sequences were captured on microwell plates
by hybridisation to an immobilised (via biotin-streptavidin binding)
capture probe. Detector probes labelled with alkaline phosphatase were
then used in a sandwich hybridisation assay to indirectly detect the
amplification products. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 15 BP; 2 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1658 ACCAGGCTCACAG 1670
DB ||||| ||||| |||||
14 ACCAGGCTCACAG 2

RESULT 511
AAZ62841
ID AAZ62841 standard; RNA; 15 BP.
XX
XX AAZ62841;
XX AC
XX 28-MAR-2000 (first entry)
DT
DE
DE Substrate for HH ribozyme HCV-8701 which cleaves HCV RNA at nt. 8701.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
XX WO9955847-A2.
XX
PD 04-NOV-1999.
XX
XX 26-APR-1999; 99WO-US009027.
XX
XX 27-APR-1998; 98US-0083217P.
XX 18-SEP-1998; 98US-0100842P.
XX 25-FEB-1999; 99US-00257608.

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PR 23-MAR-1999; 99US-00274553.
XX (RIBO-) RIBOZYME PHARM INC.
XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
XX WPI; 2000-062023/05.
XX
XX Novel ribozymes for the treatment of diseases and conditions related to
XX hepatitis C infection.
XX Claim 1; Page 65; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
XX enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
XX the Hepatitis C virus (HCV) RNA sequence at the base position given in
XX the descriptor line. The HCV sequence was screened for optimal ribozyme
XX target sites using a computer folding algorithm and regions of the mRNA
XX which did not form secondary folding structures and contained potential
XX ribozyme cleavage sites were identified. Ribozymes were synthesised to
XX target these sites and their activities optimised by either varying the
XX length of the binding arms or by modification to prevent degradation by
XX nucleases. The ribozymes of the invention inhibit gene expression and/or
XX viral replication, and are used to treat diseases associated with
XX Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
XX hepatocellular carcinoma. The ribozymes may be used in combination with
XX interferon to treat HCV infection, other infectious diseases, autoimmune
XX diseases, and cancer
XX
XX Sequence 15 BP; 2 A; 6 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGGTG 1698
Db 3 CUCCUCCACGUG 15

RESULT 512
AAAF47175/c
ID AAFA47175 standard; DNA; 15 BP.
XX
XX AAFA47175;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGFBP3 oligonucleotide #595.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

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DR WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional), an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 7; Page 48; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAP45151 and AAP45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX Sequence 15 BP; 3 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1698 GGTGGAAGTTGGG 1710
Db 14 GGTGGAAGTTGGG 2

RESULT 513
AAFS1493
ID AAFS1493 standard; DNA; 15 BP.
XX
XX AAFS1493;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #2453.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

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PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 8; Page 76; 201pp; English.
 PS
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;
 SQ Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 4e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1666 CACAGCTGGACC 1678
 Db ||||| |||||
 3 CACAGCTGCNACC 15
 RESULT 514
 AAF53421/C
 ID AAF53421 standard; DNA; 15 BP.
 XX
 AC AAF53421;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGF-I oligonucleotide #4381.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 PN 28-DEC-2000.
 XX
 PD 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 8; Page 89; 201pp; English.
 PS

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
 SQ Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 4e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1753 TCCTAAGGCCCA 1765
 Db ||||| |||||
 13 TCCTAAGGCCCA 1
 RESULT 515
 AAF53420/C
 ID AAF53420 standard; DNA; 15 BP.
 XX
 AC AAF53420;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGF-I oligonucleotide #4380.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 PN 28-DEC-2000.
 XX
 PD 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 8; Page 89; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 5 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 8.3%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 4e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1753 TCCTAAGGCCCA 1765
 Db 14 TCCTAAGGCCCA 2
 RESULT 516
 AAF53669
 ID AAF53669 standard; DNA; 15 BP.
 XX
 AC AAF53669;
 XX
 DT 30-MAR-2001 (first entry)
 DE
 DE IGF-I oligonucleotide #4629.
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 91; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 5 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 4e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1721 GGAGATGGAGATT 1733
 Db 3 GGAGATGGAAATT 15
 RESULT 517
 AAF51495
 ID AAF51495 standard; DNA; 15 BP.
 XX
 AC AAF51495;
 XX
 DT 30-MAR-2001 (first entry)
 DE
 DE IGF-I oligonucleotide #2455.
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 76; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 5 A; 7 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 4e+02; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAACC 1678

DB 1 CACAGCTGGAACC 13

RESULT 518

AAFS3670

ID AAF53670 standard; DNA; 15 BP.

XX

AC AAF53670;

XX

DT 30-MAR-2001 (first entry)

XX

DE IGF-I oligonucleotide #4630.

XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

PN WO200078341-A1.

XX

PD 28-DEC-2000.

XX

PF 21-JUN-2000; 2000WO-AU000693.

XX

PR 21-JUN-1999; 99US-0140345P.

XX

PA (MURD-) MURDOCH CHILDRENS RES INST.

XX

PI Wright CJ, Werther GA, Edmondson SR;

XX

DR WPI; 2001-041421/05.

XX

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX

PS Example 8; Page 91; 201pp; English.

XX

CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX

SQ Sequence 15 BP; 5 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 4e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATT 1733

DB 2 GGAGATGGAGATT 14

RESULT 519

AAFS3671

ID AAF53671 standard; DNA; 15 BP.

XX

AC AAF53671;

XX

DT 30-MAR-2001 (first entry)

XX

DE IGF-I oligonucleotide #4631.

XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

PN WO200078341-A1.

XX

PD 28-DEC-2000.

XX

PF 21-JUN-2000; 2000WO-AU000693.

XX

PR 21-JUN-1999; 99US-0140345P.

XX

PA (MURD-) MURDOCH CHILDRENS RES INST.

XX

PI Wright CJ, Werther GA, Edmondson SR;

XX

DR WPI; 2001-041421/05.

XX

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX

PS Example 8; Page 91; 201pp; English.

XX

CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

SQ Sequence 15 BP; 5 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;

Best Local Similarity 92.3%; Pred. No. 4e+02; Mismatches 0; Indels 1; Gaps 0;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATT 1733
Db 1 GGAGATGGAAATT 13

RESULT 520
AAF51494
ID AAF51494 standard; DNA; 15 BP.
XX AC AAF51494;
XX 30-MAR-2001 (first entry)
XX IGF-I oligonucleotide #2454.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
XX WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX Example 8; Page 76; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX Sequence 15 BP; 5 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1666 CACAGCTGCAACC 1678
Db 1666 CACAGCTGCAACC 1678

Db 2 CACAGCTGCAACC 14

RESULT 521
AAF53419/C
ID AAF53419 standard; DNA; 15 BP.
XX AC AAF53419;
XX 30-MAR-2001 (first entry)
XX IGF-I oligonucleotide #4379.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
XX WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX Example 8; Page 89; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1753 TCCTTAAGGCCCA 1765
Db 15 TCCTTAAGGCCCA 3

RESULT 522
 ID AAL45302/c
 XX AAL45302 standard; DNA; 15 BP.
 AC AAL45302;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human KCNB1 gene allele-specific primer SEQ ID NO: 16.
 XX
 KW Human; KCNB1; single nucleotide polymorphism; SNP; gene therapy;
 KW potassium voltage-gated channel; Shab-related subfamily, member 1;
 KW isogene; arrhythmia; seizures; allele-specific oligonucleotide; PCR;
 KW primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200204675-A1.
 XX
 PD 17-JAN-2002.
 XX
 PF 05-JUL-2001; 2001WO-US021307.
 XX
 PR 05-JUL-2000; 2000US-0215883P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Choi JY, Koshy B;
 XX
 DR WPI; 2002-188469/24.
 XX
 PT Isolated polymorphic variants of potassium voltage-gated channel, Shab-
 PT related subfamily, member 1 (KCNB1) gene useful for expressing KCNB1
 PT protein isoform to screen drugs to treat KCNB1 activity-related disease.
 XX
 PS Claim 16; Page 13; 180pp; English.
 XX
 CC The present invention provides the protein, gene and cDNA sequences of
 CC the human potassium voltage-gated channel, Shab-related subfamily, member
 CC 1 (KCNB1) isogene and polymorphisms identified within these sequences.
 CC The sequences can be used to screen drugs, which involves contacting the
 CC polypeptide with a candidate agent, and to assay for binding activity as
 CC a target for drugs to treat arrhythmia and seizures. The present sequence
 CC is an allele-specific oligonucleotide primer for the gene of the
 CC invention
 XX
 SQ Sequence 15 BP; 1 A; 5 C; 7 G; 1 T; 0 U; 1 Other;
 XX
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1660 CAGGCTCAGCTGG 1674
 Db |:|||||:|||||
 15 CRGGCTCCAGCCGG 1
 XX
 RESULT 523
 ID AAD25425
 XX AAD25425 standard; DNA; 15 BP.
 AC AAD25425;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human GNRH2 gene polymorphism detecting ASO primer #12.
 XX
 KW Human; gonadotropin-releasing hormone 2; GNRH2 gene; haplotyping;
 KW genotyping; gene therapy; reproductive disorder; polymorphism;
 KW allele specific oligonucleotide; ASO; primer; ss.
 XX
 OS Homo sapiens.
 XX

PN WO200187910-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-US016353.
 XX
 PR 18-MAY-2000; 2000US-0205187P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Duda A, Kliem SE, Nandabalan K, Sausker EA;
 XX
 DR WPI; 2002-055683/07.
 XX
 PT New genetic variants of gonadotropin-releasing hormone 2 isogene, useful
 PT in studying expression and function of protein and for screening drugs to
 PT treat diseases e.g. reproduction disorders.
 XX
 PS Claim 16; Page 13; 64pp; English.
 XX
 CC The invention relates to genetic variants of human gonadotropin-
 CC releasing hormone 2 (GNRH2) gene. The invention also relates to
 CC compositions and methods for haplotyping and/or genotyping the GNRH2 gene
 CC in an individual. Polynucleotides of the invention are useful for
 CC studying the expression and function of GNRH2 and in expressing GNRH2
 CC proteins for use in screening candidate drugs to treat diseases related
 CC to GNRH2 activity. They are also used in gene therapy. The methods of the
 CC invention are useful in determining whether an individual has a haplotype
 CC or haplotype pairs. The haplotyping method is useful for improving the
 CC efficiency and reliability of several steps in the discovery and
 CC development of drugs for treating diseases associated with GNRH2
 CC activity, e.g., reproductive disorders. The present sequence is an allele
 CC specific oligonucleotide (ASO) primer used for detecting human GNRH2 gene
 CC polymorphisms
 XX
 SQ Sequence 15 BP; 2 A; 9 C; 0 G; 3 T; 0 U; 1 Other;
 XX
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1744 TCCTCCCTATCCTAA 1758
 Db |||||:|||||:
 1 TCCTCCCTACCCCA 15
 XX
 RESULT 524
 ID ABL52104/c
 XX ABL52104 standard; DNA; 15 BP.
 AC ABL52104;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Human PER1 allele specific oligonucleotide probe SEQ ID NO:29.
 XX
 KW Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
 KW polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
 KW single nucleotide polymorphism; SNP; gene; probe; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 8
 FT /*tag= a
 FT /note= "polymorphic site indicated by an ambiguity base"
 XX
 PN WO200222650-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 13-SEP-2001; 2001WO-US028780.
 XX

PR 13-SEP-2000; 2000US-0232468P.
 XX (GENA-) GENAISSANCE PHARM INC.
 PA Duda A, Klieh SE, Koshy B;
 XX WPI; 2002-393941/42.
 DR
 XX
 XX
 XX
 PT Novel isolated human period Drosophila homolog 1 polynucleotide, useful
 PT for therapeutic purposes, for studying the expression and function of the
 PT polynucleotide, and for expressing the homolog.
 XX
 XX
 PS Claim 17; Page 14; 162pp; English.
 XX
 XX
 CC The present invention describes an isolated human period (Drosophila)
 CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
 CC polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
 CC or its fragment, or a polymorphic variant of a reference sequence
 CC (ABL52078) for a PER1 cDNA or its fragment. The present invention also
 CC describes methods for genotyping and haplotyping the PER1 gene of an
 CC individual. (I) is useful in studying the expression and function of
 CC PER1, and in expressing PER1 protein for use in screening for candidate
 CC drugs to treat diseases related to PER1 activity. (I) is useful for
 CC therapeutic purposes. A recombinant non-human organism transformed or
 CC transfected with (I) can be used for studying expression of the PER1
 CC isogenes in vivo, for in vivo screening and testing of drugs targeted
 CC against PER1 protein, and for testing the efficacy of therapeutic agents
 CC and compounds for disorders associated with circadian rhythm regulation.
 CC The present sequence represents an allele specific oligonucleotide probe
 CC for human PER1, which is used in the exemplification of the present
 CC invention
 XX
 XX
 SQ Sequence 15 BP; 2 A; 3 C; 9 G; 0 T; 0 U; 1 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1734 GGCTCCCACTCCCTC 1748
 Db |||||: |||||
 15 GGCTCCCGCTCCCC 1
 RESULT 525
 ABL01115/c
 ID ABL01115 standard; DNA; 15 BP.
 XX ABL01115;
 AC
 XX
 XX 12-MAR-2002 (first entry)
 DT
 XX Human AKR1B1 gene polymorphism detection ASO probe SEQ ID NO:12.
 DE
 XX Human; aldo-keto reductase family 1 member B1; aldose reductase; ss;
 KW AKR1B1; chromosome 7q35; detection; polymorphism; ASO; probe; primer;
 KW allele-specific oligonucleotide; antidiabetic; gene therapy; diabetes.
 XX
 XX Homo sapiens.
 OS
 XX WO200179223-A2.
 PN
 XX
 XX 25-OCT-2001.
 PD
 XX
 XX 12-APR-2001; 2001WO-US011944.
 PF
 XX
 XX 12-APR-2000; 2000US-0196315P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Choi JY, Nandabalan K, Rounds E, Sanchis A;
 PI WPI; 2002-075056/10.
 XX
 XX

PT Novel polymorphic variants of aldo-keto reductase family 1, member b1
 PT gene useful in studying expression and function of the protein, useful
 PT for screening drugs to treat diseases e.g. diabetes.
 XX
 PS Claim 16; Page 14; 103pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I) comprising
 CC a sequence which is a polymorphic variant (PV) of a reference sequence
 CC for aldo-keto reductase family 1, member B1 (AKR1B1) gene or its
 CC fragment, having the 22214 base pair sequence given in ABL01105, AKR1B1
 CC has antidiabetic activity and can be used in gene therapy. AKR1B1 can be
 CC used in the treatment of diabetes. The human AKR1B1 gene is located on
 CC chromosome 7q35. ABL01107 to ABL01129 represent allele-specific
 CC oligonucleotide (ASO) probes used in the detection of polymorphisms in
 CC the human AKR1B1 gene; ABL01130 to ABL01175 represent ASO primers used in
 CC the detection of polymorphisms in the human AKR1B1 gene; and ABL01176 to
 CC ABL01221 represent preferred primers used in the detection of
 CC polymorphisms in the human AKR1B1 gene
 XX
 SQ Sequence 15 BP; 3 A; 3 C; 5 G; 3 T; 0 U; 1 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1662 GGCTCAGCTGGAA 1676
 Db |||||: |||||
 15 GGCTCACCCCTGTA 1
 RESULT 526
 ABLK12736/c
 ID ABLK12736 standard; DNA; 15 BP.
 XX
 XX ABLK12736;
 AC
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX
 XX ASO probe #1, used to detect human IFNG gene polymorphisms.
 DE
 XX Human; interferon-gamma; IFNG; polymorphic variant; isogene; ss;
 KW type I diabetes; multiple sclerosis; asthma; immune-related disorder;
 KW haplotyping; single nucleotide polymorphism; SNP; probe; ASO;
 KW allele-specific oligonucleotide.
 XX
 XX Homo sapiens.
 OS
 XX WO200216631-A1.
 PN
 XX
 XX 28-FEB-2002.
 PD
 XX
 XX 27-AUG-2001; 2001WO-US026678.
 PF
 XX
 XX 25-AUG-2000; 2000US-0227842P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Chew A, Denton RR, Finkel K, Nandabalan K;
 PI WPI; 2002-280945/32.
 DR
 XX
 XX Novel isolated human interferon, gamma polynucleotide, useful for
 PT therapeutic purposes, for studying the expression and function of the
 PT polynucleotide, and for expressing the interferon, gamma protein.
 XX
 PS Claim 16; Page 13; 58pp; English.
 XX
 CC The present invention relates to a new human interferon-gamma (IFNG)
 CC polynucleotide comprising a sequence which is a polymorphic variant for a
 CC reference sequence for the IFNG gene or its fragment. The invention is
 CC useful in studying the expression and function of IFNG and in expressing
 CC IFNG protein for use in screening for candidate drugs to treat diseases
 CC related to IFNG activity. The polynucleotide of the invention is useful

CC for therapeutic purposes. The invention is also useful for studying
 CC expression of the IFNG isogenes in vivo, for in vivo screening and
 CC testing of drugs targeted against IFNG protein, and for testing the
 CC efficacy of therapeutic agents and compounds for type I diabetes,
 CC multiple sclerosis, asthma and immune-related disorders, in a biological
 CC system. The present nucleic acid sequence represents ASO (allele-specific
 CC oligonucleotide) probe #1 that was used in the methods of the invention
 CC to detect polymorphisms in the human IFNG gene
 XX
 XX Sequence 15 BP; 0 A; 4 C; 3 G; 7 T; 0 U; 1 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;
 Matches 12; Conservative 1; Mismatches 0;
 QY 1648 GAAGGCAAGCACCAG 1662
 Db 15 GAAGCAGCAACAG 1
 RESULT 527
 ABK81430/c
 ID ABK81430 standard; DNA; 15 BP.
 XX
 AC ABK81430;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE SCYA20 allele specific oligonucleotide primer #10.
 XX
 KW Small inducible cytokine subfamily A (Cys-Cys) member 20; SCYA20;
 KW polymorphism; haplotype; psoriasis; gene expression; ASO;
 KW allele specific oligonucleotide; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200232927-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 19-OCT-2001; 2001WO-US046093.
 XX
 PR 19-OCT-2000; 2000US-0241725P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Bieglecki KM, Chew A, Russo DP, Sausker EA;
 XX
 DR WPI; 2002-435525/46.
 XX
 PT New genetic variants comprising haplotypes of the small inducible
 PT cytokine subfamily A, member 20 (SCYA20) gene, useful in improving the
 PT efficiency drug screening protocols for compounds (e.g. antipsoriatic
 PT drug) targeting SCYA20.
 XX
 PS Claim 14; Page 13; 62pp; English.
 XX
 CC The invention describes an isolated polynucleotide, which comprises genes
 CC and haplotypes of the small inducible cytokine subfamily A (Cys-Cys),
 CC member 20 (SCYA20) gene. The polynucleotide comprises polymorphic sites
 CC referred to as PSI-9 to designate the order in which they are located in
 CC the gene. The polymorphisms and haplotypes of SCYA20 gene are useful for
 CC validating whether SCYA20 is a suitable target for drugs to treat
 CC psoriasis and disorders associated with its abnormal expression or
 CC function, screening for such drugs and reducing bias in clinical trials
 CC of such drugs. Haplotype information would be useful in improving the
 CC efficiency and output of several steps in the drug discovery and
 CC development process, including target validation, identifying lead
 CC compounds, early phase clinical trials. The methods are useful in
 CC screening for compounds targeting SCYA20 to treat a specific condition or
 CC disease predicted to be associated with SCYA20 activity, e.g. psoriasis.
 CC This sequence represents an allele specific oligonucleotide (ASO) primer
 CC used to identify polymorphisms in the SCYA20 gene

XX
 SQ Sequence 15 BP; 5 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 4e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1696 GTGGTGAAGTTG 1708
 Db 13 GTGATGAAGTTG 1
 RESULT 528
 ABV99783
 ID ABV99783 standard; DNA; 15 BP.
 XX
 AC ABV99783;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE Human PFKFB2 allele specific oligonucleotide primer #9.
 XX
 KW Human; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2; PFKFB2;
 KW cytosolic; antidiabetic; gene therapy; cancer; diabetes; ss; ASO;
 KW allele specific oligonucleotide; primer; polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN WO200194363-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 07-JUN-2001; 2001WO-US018458.
 XX
 PR 07-JUN-2000; 2000US-0209935P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Duda A, Kazemi A, Koshy B;
 XX
 DR WPI; 2002-566434/60.
 XX
 PT New 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 (PFKFB2) gene
 PT variants, for improving efficiency and reliability in the development of
 PT drugs for treating diseases associated with PFKFB2 activity e.g. cancer.
 XX
 PS Claim 16; Page 13; 95pp; English.
 XX
 CC The invention relates to a novel human 6-phosphofructo-2-kinase/ fructose
 CC -2,6-bisphosphatase 2 (PFKFB2) isogene. The PFKFB2 of the invention has
 CC cytosolic and antidiabetic activity. The polynucleotides may have a use
 CC in gene therapy. The identified candidate agents targeting PFKFB2, are
 CC useful for treating cancer and diabetes. The methods of the invention are
 CC useful for improving the efficiency and reliability of several steps in
 CC the discovery and development of drugs for treating diseases associated
 CC with PFKFB2 activity. The present sequence represents a allele specific
 CC oligonucleotide (ASO) primer used in the invention to detect PFKFB2 gene
 CC polymorphisms
 XX
 SQ Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 1 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;
 Matches 12; Conservative 1; Mismatches 0;
 QY 1687 TCTCCAGCGCTGGTG 1701
 Db 1 TACTCCAGCGCTGGYG 15
 RESULT 529
 ABK96301/c
 ID ABK96301 standard; DNA; 15 BP.

XX ABX96301;
 AC
 XX 24-SEP-2002 (first entry)
 DT
 XX EDG1 gene allele-specific oligonucleotide #16.
 DE
 XX EDG1; human; haplotyping; vascular developmental disorder; PCR; primer;
 KW endothelial differentiation sphingolipid G protein-coupled receptor 1;
 KW ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200244200-A2.
 PN
 XX 06-JUN-2002.
 PD
 XX 03-DEC-2001; 2001WO-US046946.
 XX
 XX 01-DEC-2000; 2000US-0250606P.
 PF
 XX (GENA-) GENAISSANCE PHARM INC.
 PR
 XX Bieglecki KM, Kazemi A, Shah N;
 PA
 XX WPI; 2002-519581/55.
 PI
 XX
 XX
 XX Novel genetic variants of Endothelial Differentiation, Sphingolipid G
 PT Protein-Coupled Receptor 1 isogenes, useful for improving efficiency and
 PT reliability in drug development for treating vascular developmental
 PT disorders.
 PT
 XX Claim 14; Page 13; 68pp; English.
 PS
 XX The invention relates to an isolated polynucleotide (I) encoding
 XX endothelial differentiation, sphingolipid G protein-coupled receptor 1
 CC (EDG1) (II). Also described are methods for haplotyping or genotyping
 CC EDG1 gene of an individual by identifying single nucleotide polymorphisms
 CC (SNPs) of the gene. (II) is useful in screening for drugs targeting (II)
 CC that are useful for treating vascular developmental disorders. The
 CC methods are useful for improving the efficiency and reliability of
 CC several steps in the discovery and development of drugs for treating
 CC diseases associated with EDG1 activity. The haplotyping method is also
 CC used in pharmaceutical research to validate EDG1 as a candidate target
 CC for treating a specific condition or disease predicted to be associated
 CC with EDG1 activity, e.g. vascular developmental disorders, and in the
 CC design of clinical trials for treating a specific condition of disease
 CC associated with EDG1 activity. The methods are also useful for screening
 CC compounds targeting EDG1. ABX96286-ABX96332 represent EDG1 gene allele-
 CC specific oligonucleotides, primer extension oligonucleotides and related
 CC PCR primers of the invention
 XX
 XX Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 1 Other;
 SQ
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1725 ATGAGATGGCTCC 1739
 Db 15 AYCAGATGGCTCC 1
 : ||||| |||||
 RESULT 530
 AAS16721/c
 ID AAS16721 standard; DNA; 15 BP.
 XX
 AC AAS16721;
 AC
 XX 14-FEB-2002 (first entry)
 DT
 XX Human APOA4 allele specific oligonucleotide, ASO, probe #4.
 DE
 XX

Human; ss; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
 KW atherosclerosis; probe.
 XX
 OS Homo sapiens.
 XX
 XX WO200177124-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 03-APR-2001; 2001WO-US010670.
 PF
 XX 05-APR-2000; 2000US-0194362P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Bentivegna SC, Choi JY, Klieem SE, Koshy B;
 PI
 XX WPI; 2002-041281/05.
 DR
 XX New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
 PT and treat disorders associated with its abnormal expression or function
 PT such as coronary artery disease.
 PT
 XX Claim 16; Page 15; 71pp; English.
 PS
 XX The invention relates to haplotyping the human apolipoprotein A-IV
 CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or allele
 CC specific oligonucleotides, ASO) as well as methods for correlating a
 CC particular haplotype pair with a trait e.g. obesity, in a population. The
 CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
 CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is an APOA4 allele specific
 CC oligonucleotide, ASO, probe used to detect an APOA4 polymorphism
 XX
 XX Sequence 15 BP; 3 A; 1 C; 9 G; 1 T; 0 U; 1 Other;
 SQ
 Query Match 8.2%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1735 GCTCCCAACTCCTCC 1749
 Db 15 GCCCTCARTCTCTCC 1
 : ||||| |||||
 RESULT 531
 ABX00692
 ID ABX00692 standard; RNA; 15 BP.
 XX
 AC ABX00692;
 AC
 XX 23-DEC-2002 (first entry)
 DT
 XX Hepatitis C virus substrate #474 for HCV hammerhead ribozyme #474.
 DE
 XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.
 XX
 OS Hepatitis C virus.
 OS
 XX US2002082225-A1.
 PN
 XX


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PS Example; Page 13; 46pp; French.
XX
CC The sequence is that of a polynucleotide probe which may be used in the
CC detection of new hypervariable regions (HVR) in a DNA sequence. HVR
CC represent a fingerprint useful in e.g. forensic science, paternity
CC testing, animal breeding, etc. The probe may be used as part of a method
CC for the efficient detection in humans or other animals, without the use
CC of mini-satellites or primary enrichment. (Updated on 25-MAR-2003 to
CC correct EN field.)
XX
SQ Sequence 16 BP; 5 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
      Query Match      8.2%; Score 11.4; DB 1; Length 16;
      Best Local Similarity 92.3%; Pred. No. 4.4e+02;
      Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCA 1667
DB 1 AGACACAGGCTCA 13

RESULT 536
ABA81112/c
ID ABA81112 standard; DNA; 17 BP.
XX
AC ABA81112;
XX
DT 24-JAN-2002 (first entry)
XX
DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3958.
XX
KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytosolic; antickling; antianaemic; haemostatic;
KW antileptic; ss.
XX
OS Homo sapiens.
XX
PN WO200173002-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009761.
XX
PR 27-MAR-2000; 2000US-0192176P.
PR 27-MAR-2000; 2000US-0192179P.
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
XX
PA (UYDE ) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC;
XX
DR WPI; 2001-639230/73.
XX
PT Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.
XX
PS Claim 7; Page 257; 294pp; English.
XX
CC The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A

```

```

CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6.
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention
XX
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
      Query Match      8.2%; Score 11.4; DB 1; Length 17;
      Best Local Similarity 92.3%; Pred. No. 4.7e+02;
      Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCT 1680
DB 14 CAGCTGGAACCT 2

RESULT 537
ABA81113
ID ABA81113 standard; DNA; 17 BP.
XX
AC ABA81113;
XX
DT 24-JAN-2002 (first entry)
XX
DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3959.
XX
KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytosolic; antickling; antianaemic; haemostatic;
KW antileptic; ss.
XX
OS Homo sapiens.
XX
PN WO200173002-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009761.
XX
PR 27-MAR-2000; 2000US-0192176P.
PR 27-MAR-2000; 2000US-0192179P.
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
XX
PA (UYDE ) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC;
XX
DR WPI; 2001-639230/73.
XX
PT Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.
XX
PS Claim 7; Page 257; 294pp; English.
XX
CC The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,

```

CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCCCT 1680
 |||||
 DB 4 CAGCTGGAGCCT 16

RESULT 538
 AAQ67730/c
 ID AAQ67730 standard; cDNA; 17 BP.

XX
 AC AAQ67730;

XX 25-MAR-2003 (revised)
 DT 22-MAR-1995 (first entry)

XX Primer for human spasmodic polypeptide.

XX Primer; polymerase chain reaction; spasmodic;
 KW gastrointestinal disorder; prophylaxis; therapy; ss.

XX Synthetic.

OS
 XX WO9417102-A1.

XX 04-AUG-1994.

XX 20-JAN-1994; 94WO-DK000037.

XX 21-JAN-1993; 93DK-00000068.

XX (NOVO) NOVO-NORDISK AS.

XX Thim L, Norris K, Norris F, Bjorn SE, Christensen M, Nielsen PF;

XX WPI; 1994-264034/32.

XX Human spasmodic polypeptide in glycosylated form - useful for
 PT prophylaxis or treatment of gastrointestinal disorders.

XX Disclosure; Page 13; 52pp; English.

XX The primer (based on the human spasmodic protein (HSP) sequence) is
 CC used to isolate DNA fragments encoding the trefoil domains of HSP by PCR
 CC from human genomic DNA. The HSP (glycosylated at Asn15) is used in a
 CC pharmaceutical composition for the prophylaxis and treatment of
 CC gastrointestinal disorders. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 17 BP; 6 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 CCCTGGTGTCTCC 1689
 |||||
 DB 14 CCCTGGTGTCTCC 2

RESULT 539
 AAX70103

ID AAX70103 standard; RNA; 17 BP.

XX
 AC AAX70103;

XX 28-JUL-1999 (first entry)

XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1398.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.

OS Homo sapiens.

XX
 PN WO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

XX (CHIR) CHIRON CORP.

XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 89; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention

SQ Sequence 17 BP; 4 A; 1 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 61.5%; Pred. No. 4.7e+02;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1725 ATGGAGTTGGCT 1737
 :|||:|:|:|:
 DB 1 AUGGAUAUUGGCU 13

RESULT 540

AAX70102

ID AAX70102 standard; RNA; 17 BP.

XX
 AC AAX70102;

XX 28-JUL-1999 (first entry)

XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1397.

```

XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WIPI; 1997-259017/23.
XX CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 89; 218pp; English.
XX CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX SQ Sequence 17 BP; 4 A; 2 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 61.5%; Pred. No. 4.7e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1725 ATGGAGTTGGCT 1737
DB 3 AUGGAUAUUGGCU 15

RESULT 541
AAX62178/c
ID AAX62178 standard; RNA; 17 BP.
XX AC AAX62178;
XX 16-JUL-1999 (first entry)
XX DE Granule bound starch synthase hammerhead substrate SEQ ID NO:53.
XX KW Maize; corn; Zea mays; delta-9 desaturase; GBS; target; substrate;
KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KW modulation; gene expression; transgenic plant; cleavage; canola plant;
KW caffeine synthesis; coffee plant; nicotine production; tobacco;
KW fruit ripening; flower pigmentation; lignin production; ss.
XX OS Zea mays.
XX PN WO9710328-A2.

PD 20-MAR-1997.
XX PF 12-JUL-1996; 96WO-US011689.
XX PR 13-JUL-1995; 95US-0001135P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (DOWC ) DOWELANCO.
XX PI Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;
XX Young SA, Folkerts O, Merlo DJ;
XX WIPI; 1997-202224/18.
XX CC Ribozyme which modulates plant gene expression - preferably modulates
PT expression of DELTA-9 desaturase or granule bound starch synthase in
PT maize or canola.
XX PS Claim 41; Page 73; 155pp; English.
XX CC The present invention describes an enzymatic nucleic acid molecule (I)
CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBS)
CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
CC modulate caffeine synthesis in a coffee plant, nicotine production in a
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
XX SQ Sequence 17 BP; 4 A; 7 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1636 GGGCTTGTAGCAG 1648
DB 16 GCGCTTGTAGCAG 4

RESULT 542
AAV97519
ID AAV97519 standard; RNA; 17 BP.
XX AC AAV97519;
XX 17-MAR-1999 (first entry)
XX DE Human EGF-R target sequence nucleotide position 2613.
XX KW Human; epidermal growth factor receptor; EGF-R; target sequence;
KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW cancer; genetic drift; detection; mutation; ss.
XX OS Homo sapiens.
XX PN WO9833893-A2.
XX PD 06-AUG-1998.
XX PF 14-JAN-1998; 98WO-US000730.
XX PR 31-JAN-1997; 97US-0036476P.
XX PR 04-DEC-1997; 97US-00985162.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (UYAS-) UNIV ASTON.
XX PI Akhtar S, Fell P, Mcswiggen JA;
XX

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DR WPI; 1998-437449/37.
 XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and for
 PT treating cancers.
 XX
 PS Claim 5; Page 74; 109pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules (NAMs)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGF-R
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMs can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell
 XX
 SQ Sequence 17 BP; 5 A; 5 C; 3 G; 0 T; 4 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 69.2%; Pred. No. 4.7e+02;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1729 AGATTGGCTCCCA 1741
 ||:|||||
 Db 5 AUAUUGGCCUCCA 17
 RESULT 543
 AAA18625/c
 ID AAA18625 standard; RNA; 17 BP.
 XX
 AC AAA18625;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Human TIE-2 substrate sequence SEQ ID NO:1851.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US006507.
 XX
 PR 27-MAR-1998; 98US-0079678P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 PS Claim 56; Page 107; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with RNA

CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA34422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tubercous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1661 AGGCTCACAGCTG 1673
 |||||
 Db 16 AGGCTCAGAGCTG 4
 RESULT 544
 AAA18519/c
 ID AAA18519 standard; RNA; 17 BP.
 XX
 AC AAA18519;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Human TIE-2 substrate sequence SEQ ID NO:1745.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US006507.
 XX
 PR 27-MAR-1998; 98US-0079678P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or stability

PT of an mRNA encoding an angiogenic factors.
XX Claim 56; Page 100; 305pp; English.
PS The present invention describes enzymatic cleave RNA encoded by an aryl
XX cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARN1) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAAL16775 to
CC AAAL17167 and AAAL17561 to AAAL17622 represent ribozyme sequences for ARN1,
CC and AAAL17168 to AAAL17560 and AAAL17623 to AAAL17684 represent their
CC corresponding target sequences; AAAL17685 to AAAL18385 and AAAL19087 to
CC AAAL19154 represent ribozyme sequences for Tie-2, and AAAL18386 to AAAL19086
CC and AAAL19155 to AAAL19222 represent their corresponding target sequences;
CC AAAL19223 to AAAL20361 and AAAL21501 to AAAL21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAAL20362 to AAAL21500 and
CC AAAL21596 to AAAL21688 represent their corresponding target sequences;
CC AAAL21689 to AAAL22475 and AAAL23263 to AAAL23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAAL22476 to AAAL23262, AAAL23343 to
CC AAAL23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARN1,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (AMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioblastoma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARN1, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;
SQ

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1716 AGTACGAGATGG 1728
Db 17 AGTACAGAGATGG 5
RESULT 545
AAV92465/C
ID AAV92465 standard; RNA; 17 BP.
XX AAV92465;
AC AAV92465;
XX 18-FEB-1999 (first entry)
DT Human A-Raf substrate position 747.
DE Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX Homo sapiens.
OS WO9850530-A2.
XX 12-NOV-1998.
PD 05-MAY-1998; 98WO-US009249.
XX 09-MAY-1997; 97US-0046059P.
XX 09-JUN-1997; 97US-0049002P.
XX 03-JUL-1997; 97US-0051718P.
XX 22-AUG-1997; 97US-0056808P.
XX 02-OCT-1997; 97US-0061321P.
XX 02-OCT-1997; 97US-0061324P.
XX 05-NOV-1997; 97US-0064866P.
XX 19-DEC-1997; 97US-0068212P.

XX (RIBO-) RIBOZYME PHARM INC.
PA Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
XX Parry T, Beigelman L, McSwiggan JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedier D;
XX WPI; 1999-009494/01.
XX Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX Claim 177; Page 158; 259pp; English.
PS A method has been developed for the identification of a nucleic acid
XX capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-raf. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX Sequence 17 BP; 2 A; 10 C; 4 G; 0 T; 1 U; 0 Other;
SQ

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1670 GCTGGAACCTCG 1682
Db 14 GCTGGGACCTCG 2
RESULT 546
AAV92632
ID AAV92632 standard; RNA; 17 BP.
XX AAV92632;
AC AAV92632;
XX 18-FEB-1999 (first entry)
DT Human A-Raf substrate position 2216.
DE Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX Homo sapiens.
OS WO9850530-A2.
XX 12-NOV-1998.
PD 05-MAY-1998; 98WO-US009249.
XX 09-MAY-1997; 97US-0046059P.
XX 09-JUN-1997; 97US-0049002P.
XX

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PR 03-JUL-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX
XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI Parry T, Beigelman L, Mcswigen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
XX WPI; 1999-009494/01.
XX
XX Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
XX Claim 177; Page 161; 259pp; English.
XX
XX A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-rat. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX
XX Sequence 17 BP; 2 A; 9 C; 1 G; 0 T; 5 U; 0 Other;
SQ
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 61.5%; Pred. No. 4.7e-02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1693 TGCTCTCCACG 1695
Db 4 UGUCUCCUCCAU 16
RESULT 547
AAV72307/c
ID AAV72307 standard; DNA; 17 BP.
XX
XX AAV72307;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human blood bacterium intergenic spacer primer 2.
XX
XX 16S rRNA; drug resistant protein; pathophysiology; human blood bacterium;
XX disease; multiple sclerosis; chronic fatigue; treatment; fibromyalgia;
XX lupus erythematosus; rheumatoid arthritis; toxic metabolite; plasma;
XX serum; antibiotic; vaccine; antibiotic; 23S rRNA; primer; ss.
XX
XX Synthetic.
XX Bacteria.
XX
XX W09924613-A1.
XX
PR 20-MAY-1999.
XX
XX 06-NOV-1998; 98WO-US023674.
XX
XX 06-NOV-1997; 97US-0064472P.
XX (PATH-) PATHOBIOOTEK INC.
XX
XX Lindner L, Macphee K;
XX
XX WPI; 1999-327419/27.
XX
XX A human blood bacterium, characterization, culturing and diagnostic
PT methods.
XX
XX Claim 10; Page 92; 95pp; English.
XX
XX This invention describes methods for culturing and detecting a human
CC blood bacterium (HBB), implicated in several disease e.g. multiple
CC sclerosis and chronic fatigue. Quantification of levels of HBB in an
CC individual can be used to determine the efficacy of a treatment for a HBB
CC -related disease. HBB-related diseases include chronic fatigue syndrome,
CC multiple sclerosis, lupus erythematosus, rheumatoid arthritis and
CC fibromyalgia. HBB vaccines can be used to treat diseased individuals.
CC Engineered HBB is administered to individuals where the disease has the
CC condition of a toxic metabolite being accumulated in plasma or serum of
CC the individual. A range of antibiotics can be used to treat
CC pathophysiological states associated with HBB. The invention describes
CC the isolation of HBB 16S rRNA, 23S rRNA and drug resistant protein
CC encoding nucleic acid. The products of the invention have antibiotic
CC activity
XX
XX Sequence 17 BP; 2 A; 11 C; 1 G; 3 T; 0 U; 0 Other;
SQ
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e-02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1698 GGTGGAAGTGGG 1710
Db 16 GGTGGAAGTGGG 4
RESULT 548
AAA60267/c
ID AAA60267 standard; DNA; 17 BP.
XX
XX AAA60267;
XX
XX 07-DEC-2000 (first entry)
XX
XX Mouse HPC2 cDNA expression construct PCR primer SEQ ID NO: 88.
XX
XX Human; mouse; prostate cancer predisposing gene; HPC2;
XX human chromosome 17p; gene therapy; peptide therapy; drug design;
XX PCR primer; sequencing primer; ss.
XX
XX Homo sapiens.
XX
XX W0200027864-A1.
XX
XX 18-MAY-2000.
XX
XX 05-NOV-1999; 99WO-US026055.
XX
XX 06-NOV-1998; 98US-0107468P.
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Tavtigian SV, Teng DHF, Simard J, Rommens JM;
XX
XX WPI; 2000-376481/32.
XX

```


XX Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX Homo sapiens.
 OS
 XX WO200162911-A2.
 PN
 XX 30-AUG-2001.
 PD
 XX 23-FEB-2001; 2001WO-US005957.
 XX
 XX 24-FEB-2000; 2000US-0184594P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 PA
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 PI WPI; 2001-550088/61.
 DR
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX
 XX Claim 4; Page 64; 108pp; English.
 XX
 XX The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 XX Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;
 SQ
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1719 ACGGAGATGGAGA 1731
 Db |||||
 17 ACAGAGATGGAGA 5
 RESULT 552
 ABL46463/C
 ID ABL46463 standard; RNA; 17 BP.
 XX
 XX ABL46463;
 AC
 XX 27-JUN-2003 (first entry)
 DT
 XX Human GRID hammerhead ribozyme substrate oligonucleotide #96.
 DE
 XX Human; Grb2-related with Insert Domain; GRID; T-cell;
 XX co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200162911-A2.
 PN
 XX 30-AUG-2001.
 PD
 XX 23-FEB-2001; 2001WO-US005957.
 XX
 XX 24-FEB-2000; 2000US-0184594P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (RIBO-) RIBOZYME PHARM INC.

PA (GLAX) GLAXO GROUP LTD.
 XX
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 DR
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX
 XX Claim 4; Page 61; 108pp; English.
 XX
 XX The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 XX Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;
 SQ
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 1719 ACGGAGATGGAGA 1731
 Db |||||
 14 ACAGAGATGGAGA 2
 RESULT 553
 ABL46651/C
 ID ABL46651 standard; RNA; 17 BP.
 XX
 XX ABL46651;
 AC
 XX 27-JUN-2003 (first entry)
 DT
 XX Human GRID NCH ribozyme substrate oligonucleotide #105.
 DE
 XX Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200162911-A2.
 PN
 XX 30-AUG-2001.
 PD
 XX 23-FEB-2001; 2001WO-US005957.
 XX
 XX 24-FEB-2000; 2000US-0184594P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 PA
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 PI WPI; 2001-550088/61.
 DR
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX
 XX Claim 4; Page 65; 108pp; English.
 XX
 XX The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as

CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation, chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention

XX
SQ Sequence 17 BP; 2 A; 6 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGAGA 1731
DB 13 ACAGAGATGGAGA 1

RESULT 554
ABL92148/c
ID ABL92148 standard; cDNA; 17 BP.
XX
AC ABL92148;
XX
DT 30-MAY-2002 (first entry)
XX
DE Long human Tumour Endothelial Marker SEQ ID NO 314.
XX
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cystostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; ss.
XX
OS Homo sapiens.
XX
PN WO200210217-A2.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-US024031.
XX
PR 02-AUG-2000; 2000US-0222599P.
PR 11-AUG-2000; 2000US-0224360P.
PR 11-APR-2001; 2001US-0282850P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI St Croix B, Kinzler KW, Vogelstein B;
XX
DR WPI; 2002-291856/33.
XX
PT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
PS Disclosure; Page 19; 331pp; English.
XX
CC The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995. The present sequence is that of an
CC oligonucleotide marker useful to the invention

XX
SQ Sequence 17 BP; 4 A; 8 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1678 CCTGGTGTCCTCT 1690
DB 14 CCTGGGTCTCTCT 2

RESULT 555
ABN07835
ID ABN07835 standard; DNA; 17 BP.
XX
AC ABN07835;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7827.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 7827; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The

CC useful for detecting an alteration in HPC2, where the alteration is
 CC associated with cancer in a human. The method involves analysing an HPC2
 CC gene or an HPC2 gene expression product from a tissue of the human. The
 CC HPC2 gene is useful as a marker for prostate cancer and can be used in
 CC gene therapy techniques to suppress neoplastic growth of recipient cells
 CC which carry the mutant HPC2 allele. The sequences represent primers used
 CC in the methods of the invention, cDNA encoding human and mouse HPC2 and
 CC cDNA encoding HPC2 paralogues and orthologues
 XX
 SQ Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1657 CACAGGCTGACA 1669
 |||||
 Db 17 CACAGGCTGACA 5

RESULT 558

ABV78964
 ID ABV78964 standard; DNA; 17 BP.

XX AC ABV78964;

XX 03-JAN-2003 (first entry)

XX Human HTPPL scanning oligonucleotide SEQ ID 210.

XX Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX Homo sapiens.

XX EP1229046-A2.

XX 07-AUG-2002.

XX 28-JAN-2002; 2002EP-00001167.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 23-MAY-2001; 2001US-00864761.

XX 09-OCT-2001; 2001US-0327898P.

XX (AEOM-) AEOMICA INC.

XX Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.

XX Example 2; Page 91; 718pp; English.

XX The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was

CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX

SQ Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1646 CAGAAGCGCAAGCA 1658
 |||||
 Db 4 CGGAAGCGCAAGCA 16

RESULT 559

ABV79490

ID ABV79490 standard; DNA; 17 BP.

XX AC ABV79490;

XX 03-JAN-2003 (first entry)

XX Human HTPPL scanning oligonucleotide SEQ ID 736.

XX Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;

KW human testis expressed Patched like protein; testis; adrenal; liver;

KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX Homo sapiens.

XX EP1229046-A2.

XX 07-AUG-2002.

XX 28-JAN-2002; 2002EP-00001167.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 23-MAY-2001; 2001US-00864761.

XX 09-OCT-2001; 2001US-0327898P.

XX (AEOM-) AEOMICA INC.

XX Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.

XX Example 2; Page 160; 718pp; English.

XX The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar

CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention

SQ Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696

Db 5 GTCTCTACAGCG 17

RESULT 560

ABV79494
 ID ABV79494 standard; DNA; 17 BP.

XX AC ABV79494;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 740.

XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EP1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX DR WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.

XX PS Example 2; Page 160; 718pp; English.

XX CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL

CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention

SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;

Best Local Similarity 92.3%; Pred. No. 4.7e+02;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696

Db 1 GTCTCTACAGCG 13

RESULT 561

ABV79491

ID ABV79491 standard; DNA; 17 BP.

XX AC ABV79491;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 737.

XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EP1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX DR WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.

XX PS Example 2; Page 160; 718pp; English.

XX CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the

CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with that of Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1684 GTCTCTCCAGCG 1696
Db 4 GTCTCTACAGCG 16
RESULT 562
ABV79492
ID ABV79492 standard; DNA; 17 BP.
AC ABV79492;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 738.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 160; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like

CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with that of Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1684 GTCTCTCCAGCG 1696
Db 3 GTCTCTACAGCG 15
RESULT 563
ABV79493
ID ABV79493 standard; DNA; 17 BP.
AC ABV79493;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 739.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 160; 718pp; English.
XX

XX The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1684 GTCCTCTCAGCG 1696
 Db |||||
 2 GTCCTCTCAGCG 14
 RESULT 564
 ABV78968
 ID ABV78968 standard; DNA; 17 BP.
 XX
 AC ABV78968;
 XX
 DT 03-JAN-2003 (first entry)
 XX
 DE Human HTPL scanning oligonucleotide SEQ ID 214.
 XX
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1229046-A2.
 XX
 PD 07-AUG-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 XX
 PR 30-JAN-2001; 2001WO-US0000663.
 PR 30-JAN-2001; 2001WO-US0000664.
 PR 30-JAN-2001; 2001WO-US0000665.
 PR 30-JAN-2001; 2001WO-US0000667.
 PR 30-JAN-2001; 2001WO-US0000668.
 PR 30-JAN-2001; 2001WO-US0000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhan J;
 XX
 DR WPI; 2002-676582/73.
 XX
 XX Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.

XX Example 2; Page 91; 718pp; English.
 PS
 XX The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1648 GAAGGCAAGCACC 1660
 Db |||||
 2 GAAGGCAAGCAGC 14
 RESULT 565
 ABV78963
 ID ABV78963 standard; DNA; 17 BP.
 XX
 AC ABV78963;
 XX
 DT 03-JAN-2003 (first entry)
 XX
 DE Human HTPL scanning oligonucleotide SEQ ID 209.
 XX
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1229046-A2.
 XX
 PD 07-AUG-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 XX
 PR 30-JAN-2001; 2001WO-US0000663.
 PR 30-JAN-2001; 2001WO-US0000664.
 PR 30-JAN-2001; 2001WO-US0000665.
 PR 30-JAN-2001; 2001WO-US0000667.
 PR 30-JAN-2001; 2001WO-US0000668.
 PR 30-JAN-2001; 2001WO-US0000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhan J;
 XX
 DR WPI; 2002-676582/73.
 XX
 XX Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.

PT	for identifying agonist and antagonist and specific binding partners, and	PT	Novel isolated human testis expressed Patched like protein (HTPL), useful
PT	for treating subjects having defects in HTPL.	PT	for identifying agonist and antagonist and specific binding partners, and
XX		PT	for treating subjects having defects in HTPL.
PS	Example 2; Page 91; 718pp; English.	XX	
XX	The present invention relates to human testis expressed Patched like	PS	Example 2; Page 91; 718pp; English.
CC	protein (HTPL, see ABV78759 to ABV78762 and AB98519 to ABB98520). HTPL	XX	The present invention relates to human testis expressed Patched like
CC	has two isoforms, with a few single base pair differences between the	CC	protein (HTPL, see ABV78759 to ABV78762 and AB98519 to ABB98520). HTPL
CC	two. One of the single base pair changes introduces a premature stop	CC	has two isoforms, with a few single base pair differences between the
CC	codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL	CC	two. One of the single base pair changes introduces a premature stop
CC	shares an overall structure organisation with the Patched protein. The	CC	codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC	shared structural features strongly imply that HTPL plays a role similar	CC	shares an overall structure organisation with the Patched protein. The
CC	to that of Patched, and is a potential tumour suppressor. HTPL is	CC	shared structural features strongly imply that HTPL plays a role similar
CC	important in regulating male germ cell development, and the HTPL gene was	CC	to that of Patched, and is a potential tumour suppressor. HTPL is
CC	mapped to human chromosome 10p12.1. HTPL and its coding sequence are	CC	important in regulating male germ cell development, and the HTPL gene was
CC	useful for diagnosing a disorder caused by mutation in HTPL, and in	CC	mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC	therapy and manufacture of a medicament for treatment or prevention of	CC	useful for diagnosing a disorder caused by mutation in HTPL, and in
CC	such disorder associated with decreased expression or activity of human	CC	therapy and manufacture of a medicament for treatment or prevention of
CC	HTPL. Such disorders include disorders of testis, or adrenal, adult and	CC	such disorder associated with decreased expression or activity of human
CC	foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,	CC	HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC	skeletal muscle or colon function. HTPL proteins and nucleic acids are	CC	foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC	clinically useful diagnostic markers and potential therapeutic agents for	CC	skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC	male infertility and cancer. The present oligonucleotide was used in an	CC	clinically useful diagnostic markers and potential therapeutic agents for
CC	example from the invention	CC	male infertility and cancer. The present oligonucleotide was used in an
XX		CC	example from the invention
SQ	Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;	XX	
		SQ	Sequence 17 BP; 6 A; 6 C; 5 G; 0 T; 0 U; 0 Other;
		Query Match	8.2%; Score 11.4; DB 1; Length 17;
		Best Local Similarity	92.3%; Pred. No. 4.7e+02;
		Matches	12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1646 CAGAGGCAAGCA 1658	QY	1648 GAAGCGAAGCACC 1660
Db	5 CGGAGGCAAGCA 17	Db	1 GAAGCGAAGCAGC 13
RESULT 566		RESULT 567	
ABV78969		ABV91046/C	
ID	ABV78969 standard; DNA; 17 BP.	ID	ABV91046 standard; DNA; 17 BP.
XX		XX	
AC	ABV78969;	AC	ABV91046;
XX		XX	
DT	03-JAN-2003 (first entry)	DT	23-DEC-2002 (first entry)
XX		XX	
DE	Human HTPL scanning oligonucleotide SEQ ID 215.	DE	Human POSHL1 scanning oligonucleotide SEQ ID NO 1759.
XX		XX	
KW	Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;	XX	Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW	human testis expressed Patched like protein; testis; adrenal; liver;	KW	Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW	male germ cell development; bone marrow; brain; kidney; lung; placenta;	KW	gene therapy; transgenic; ss.
KW	prostate; skeletal muscle; colon; male infertility; cancer; ss.	KW	
XX		XX	
OS	Homo sapiens.	OS	Homo sapiens.
XX		XX	
PN	EP1229046-A2.	PN	EP1239051-A2.
XX		XX	
PD	07-AUG-2002.	PD	11-SEP-2002.
XX		XX	
PF	28-JAN-2002; 2002EP-00001167.	PF	28-JAN-2002; 2002EP-00001165.
XX		XX	
PR	30-JAN-2001; 2001WO-US000663.	PR	30-JAN-2001; 2001WO-US000663.
PR	30-JAN-2001; 2001WO-US000664.	PR	30-JAN-2001; 2001WO-US000664.
PR	30-JAN-2001; 2001WO-US000665.	PR	30-JAN-2001; 2001WO-US000665.
PR	30-JAN-2001; 2001WO-US000666.	PR	30-JAN-2001; 2001WO-US000666.
PR	30-JAN-2001; 2001WO-US000667.	PR	30-JAN-2001; 2001WO-US000667.
PR	30-JAN-2001; 2001WO-US000668.	PR	30-JAN-2001; 2001WO-US000668.
PR	30-JAN-2001; 2001WO-US000669.	PR	30-JAN-2001; 2001WO-US000669.
PR	23-MAY-2001; 2001US-00864761.	PR	30-JAN-2001; 2001WO-US000670.
PR	09-OCT-2001; 2001US-0327898P.	PR	23-MAY-2001; 2001US-00864761.
XX		PR	10-OCT-2001; 2001US-0328205P.
PA	(AEOM-) AEOMICA INC.	XX	
XX		XX	(AEOM-) AEOMICA INC.
PI	Zhan J;	XX	
XX		XX	
XX	WPI; 2002-676582/73.	XX	
DR		XX	

PI Shannon M;
 XX WPI; 2002-684061/74.
 DR Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
 XX -1, useful for treating disorders associated with decreased expression or
 PT activity of human POSHL1.
 PT
 XX Example 2; SEQ ID NO 1759; 60pp + Sequence Listing; English.
 PS The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),
 CC (S1) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1/53 TCCTAAGGCCCA 1765
 Db 16 TCCTAAGTCCCA 4
 RESULT 568
 ABV90586/c
 ID ABV90586 standard; DNA; 17 BP.
 AC ABV90586;
 XX
 XX 23-DEC-2002 (first entry)
 DT Human POSHL1 scanning oligonucleotide SEQ ID NO 1299.
 DE
 XX
 XX Human: POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW Gene therapy; transgenic; ss.
 XX Homo sapiens.
 OS
 XX
 XX EPI2339051-A2.
 PN
 XX
 XX 11-SEP-2002.
 FD
 XX
 XX 28-JAN-2002; 2002EP-00001165.
 PF
 XX
 XX 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 23-MAY-2001; 2001US-00864761.
 PR 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.
 PA Shannon M;
 XX WPI; 2002-684061/74.
 DR Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
 XX -1, useful for treating disorders associated with decreased expression or
 PT activity of human POSHL1.
 PT
 XX Example 2; SEQ ID NO 1299; 60pp + Sequence Listing; English.
 PS The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),
 CC (S1) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1664 CTCACAGCTGGAA 1676
 Db 14 CACACAGCTGGAA 2
 RESULT 569
 ABV90585/c
 ID ABV90585 standard; DNA; 17 BP.
 AC ABV90585;
 XX
 XX 23-DEC-2002 (first entry)
 DT Human POSHL1 scanning oligonucleotide SEQ ID NO 1298.
 DE
 XX
 XX Human: POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW Gene therapy; transgenic; ss.
 XX Homo sapiens.
 OS
 XX
 XX EPI2339051-A2.
 PN
 XX
 XX 11-SEP-2002.
 FD
 XX
 XX 28-JAN-2002; 2002EP-00001165.
 PF
 XX
 XX 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 23-MAY-2001; 2001US-00864761.
 PR 10-OCT-2001; 2001US-0328205P.

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PR 30-JAN-2001; 2001WO-US000667.
PR 23-MAY-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 1298; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, AB883999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
SQ Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1664 CTCACAGCTGGAA 1676
DB 15 CACACAGCTGGAA 3
RESULT 570
ABV91045/C
ID ABV91045 standard; DNA; 17 BP.
XX AC ABV91045;
XX 23-DEC-2002 (first entry)
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1758.
XX Human, POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX Homo sapiens.
XX EP1239051-A2.
XX 11-SEP-2002.
XX 28-JAN-2002; 2002EP-00001165.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 1758; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, AB883999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
SQ Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1753 TCCTAAGGCCCA 1765
DB 17 TCCTAAGGCCCA 5
RESULT 571
ABV90583/C
ID ABV90583 standard; DNA; 17 BP.
XX AC ABV90583;
XX 23-DEC-2002 (first entry)
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1296.
XX Human, POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX Homo sapiens.
XX EP1239051-A2.
XX 11-SEP-2002.
XX 28-JAN-2002; 2002EP-00001165.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.

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PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
XX -1, useful for treating disorders associated with decreased expression or
XX activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1296; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX (S1) having 95% deviations, especially conservative substitutions or a
XX fragment of the sequences comprising at least 8 contiguous amino acids.
XX Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX adaptor protein that interacts with Rho family small GTPases as well as
XX downstream components of the signal transduction pathway. (I) is useful
XX for identifying a specific binding partner. (I) and nucleic acids (II)
XX encoding (I) are useful for diagnosing, monitoring disease and treating
XX caused by altered expression of human POSHL1 including diagnosing and
XX treating cancer, they are useful in the development of vaccines and (II) is
XX useful in gene therapy. (II) is useful for constructing microarrays which
XX are useful for measuring and for surveying gene expression and creating
XX transgenic non-human animals capable of producing the proteins. The
XX present sequence is that of a scanning oligonucleotide useful in examples
XX of the invention. Note: The present sequence did not form part of the
XX printed specification, but is based on sequence information supplied to
XX Derwent by the European Patent Office
XX
XX Sequence 17 BP; 1 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 8.2%; Score 11.4; DB 1; Length 17;
XX Best Local Similarity 92.3%; Pred. NO. 4.7e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1664 CTCACAGCTGGAA 1676
Db 17 CACACAGCTGGAA 5
| | | | | | | | | | | | | | | |
RESULT 572
ABV90587/C
ID ABV90587 standard; DNA; 17 BP.
XX
XX ABV90587;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1300.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX
XX EPI239051-A2.
XX
XX 11-SEP-2002.
XX

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PF 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
XX -1, useful for treating disorders associated with decreased expression or
XX activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1300; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX (S1) having 95% deviations, especially conservative substitutions or a
XX fragment of the sequences comprising at least 8 contiguous amino acids.
XX Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX adaptor protein that interacts with Rho family small GTPases as well as
XX downstream components of the signal transduction pathway. (I) is useful
XX for identifying a specific binding partner. (I) and nucleic acids (II)
XX encoding (I) are useful for diagnosing, monitoring disease and treating
XX caused by altered expression of human POSHL1 including diagnosing and
XX treating cancer, they are useful in the development of vaccines and (II) is
XX useful in gene therapy. (II) is useful for constructing microarrays which
XX are useful for measuring and for surveying gene expression and creating
XX transgenic non-human animals capable of producing the proteins. The
XX present sequence is that of a scanning oligonucleotide useful in examples
XX of the invention. Note: The present sequence did not form part of the
XX printed specification, but is based on sequence information supplied to
XX Derwent by the European Patent Office
XX
XX Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 8.2%; Score 11.4; DB 1; Length 17;
XX Best Local Similarity 92.3%; Pred. NO. 4.7e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1664 CTCACAGCTGGAA 1676
Db 13 CACACAGCTGGAA 1
| | | | | | | | | | | | | | | |
RESULT 573
ABV90584/C
ID ABV90584 standard; DNA; 17 BP.
XX
XX ABV90584;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1297.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX
XX EPI239051-A2.
XX

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XX 11-SEP-2002.
PD 28-JAN-2002; 2002EP-00001165.
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
PA Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 1297; 60pp + Sequence Listing; English.
PS
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, AB883999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 1 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1664 CTCACAGCTGGAA 1676
DB 16 CACACAGCTGGAA 4
RESULT 574
ABL31671/C
ID ABL31671 standard; DNA; 17 BP.
XX ABL31671;
DT 21-MAR-2002 (first entry)
XX Human HLA genotyping oligonucleotide SEQ ID NO 1160.
DE Human, human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
XX Homo sapiens.
OS

XX WO200192572-A1.
XX 06-DEC-2001.
XX 01-JUN-2001; 2001WO-JP004662.
XX 01-JUN-2000; 2000JP-00164798.
XX (NISN) NISSHINBO IND INC.
PA (SYST-) SYSTEM RES INC.
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX WPI; 2002-122074/16.
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT individuals e.g. by determining immunogenetic differences when
PT transplanting between them.
XX Claim 10; Page 313; 345pp; Japanese.
XX The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene
CC polymorphisms. The method is useful for judging HLA genotypes of
CC individuals by determining immunogenetic differences before transplanting
CC between them, providing genetic information to decide compatibility of
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
CC diagnosis of genetic diseases and identifying individuals
XX Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1661 AGGCTCAGCTG 1673
DB 17 AGGCTCAGCTG 5
RESULT 575
ABL31564/C
ID ABL31564 standard; DNA; 17 BP.
XX ABL31564;
XX 21-MAR-2002 (first entry)
XX Human HLA genotyping oligonucleotide SEQ ID NO 1053.
DE Human, human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
XX Homo sapiens.
OS WO200192572-A1.
XX 06-DEC-2001.
XX 01-JUN-2001; 2001WO-JP004662.
XX 01-JUN-2000; 2000JP-00164798.
XX (NISN) NISSHINBO IND INC.
PA (SYST-) SYSTEM RES INC.
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
PI

XX WPI; 2002-122074/16.
 XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
 PT individuals e.g. by determining immunogenetic differences when
 PT transplating between them.
 XX
 XX Claim 10; Page 293; 345pp; Japanese.
 XX
 XX The invention relates to a typing kit for judging human leukocyte antigen
 CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
 CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
 CC genes e.g. belonging to HLA class I antigens on human genome and
 CC containing gene polymorphisms as allciantigens have been immobilised as
 CC primers for amplification of cleaved nucleic acids relating to gene
 CC polymorphisms. The method is useful for judging HLA genotypes of
 CC individuals by determining immunogenetic differences before transplanting
 CC between them, providing genetic information to decide compatibility of
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
 CC pancreas, langerhans islet in pancreas and cornea, susceptibility
 CC diagnosis of genetic diseases and identifying individuals
 XX
 XX Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1661 AGGCTCAGCTG 1673
 Db 17 AGGCTCTCAGCTG 5
 ||||| |||||
 RESULT 576
 ABX72073/c
 ID ABX72073 standard; DNA; 17 BP.
 AC ABX72073;
 XX
 XX 12-MAR-2003 (first entry)
 DT
 DE Human tumour endothelial marker TEM 6 DNA long tag.
 DE Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
 KW Tumour endothelial marker; normal endothelial marker; PEM;
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
 KW neovascularization; immune response; cytostatic; antidiabetic;
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO2002083874-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 10-APR-2002; 2002WO-US008253.
 PF
 XX 11-APR-2001; 2001US-0282850P.
 PR
 XX 06-FEB-2002; 2002US-0354262P.
 PR
 XX (UUYO) UNIV JOHNS HOPKINS.
 PA
 XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 PI
 XX WPI; 2003-093016/08.
 DR
 XX New purified human transmembrane protein, designated as tumor endothelial
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
 PT psoriasis.
 XX
 XX Disclosure; Page 359; 374pp; English.
 PS

XX The present invention relates to a novel method for the isolation of
 CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting,
 CC diagnosing or treating tumours as well as polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
 CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for
 CC inducing an immune response to tumour endothelial cells in a patient, or
 CC for identifying candidate drugs for treating tumours. ABX72067-ABX72116
 CC represent human TEM DNA tags
 XX
 XX Sequence 17 BP; 4 A; 8 C; 5 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1678 CCGTGGTCTCTCT 1690
 Db 14 CCGGGGTCTCTCT 2
 ||||| |||||
 RESULT 577
 ABZ69604
 ID ABZ69604 standard; DNA; 17 BP.
 XX
 AC ABZ69604;
 XX
 XX 11-AUG-2003 (first entry)
 DT
 DE Human telomerase coding sequence PCR primer #5.
 DE
 KW Transient immortalisation; immortalisation protein; transplant; PCR;
 KW primer; ss; cardiant; osteopathic; hepatotropic; antiparkinsonian;
 KW organ regeneration; degenerative disease; cardiac infarct;
 KW bone degeneration; osteoporosis; liver regeneration; Parkinson's disease.
 XX
 OS Homo sapiens.
 XX
 XX WO2003035984-A2.
 PN
 XX 01-MAY-2003.
 PD
 XX 07-OCT-2002; 2002WO-EP011200.
 PF
 XX 18-OCT-2001; 2001DE-01052972.
 PR
 XX (HEAR-) HEART BIOSYSTEMS GMBH.
 PA
 XX Kueper J, Meyer R, Meyer-Ficca M, Kuhn A;
 PI
 XX WPI; 2003-430421/40.
 DR
 XX Transient immortalization of cells, useful for preparing transplant
 PT material and for organ regeneration, by supplying immortalizing proteins
 PT externally.
 XX
 XX Example 5; Page 29; 59pp; German.
 PS
 XX The present invention relates to a method for the transient
 CC immortalisation of cells by introducing immortalisation proteins into
 CC them from the outside. The method is used to immortalise cells
 CC transiently to allow their expansion, particularly to produce transplant
 CC material for regenerating organs, for treating chronic (degenerative)
 CC diseases, e.g. in cases of cardiac infarct (with simultaneous reduction
 CC in the risk of congestive heart failure and future infarcts) or chronic
 CC bone degeneration (osteoporosis), for regeneration of the liver, for
 CC treating Parkinson's disease (using dopaminergic cells) and for ex vivo
 CC production of heart and venous valves. The present sequence is a PCR
 CC primer used in the exemplification of the invention
 CC

XX SQ Sequence 17 BP; 0 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. NO. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCCIC 1691
 |||||
 2 CTGGTGTCTGCTC 14

Db

RESULT 578
 ABT35614
 ID ABT35614 standard; DNA; 17 BP.
 XX AC
 XX ABT35614;
 DT 12-JUN-2003 (first entry)
 XX DE Tumour suppression related human fukutin oligo SEQ ID No 1251.
 XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX OS Homo sapiens.
 XX PN WO2003025175-A2.
 XX PD 27-MAR-2003.
 XX PF 17-SEP-2002; 2002WO-IB004208.
 XX PR 17-SEP-2001; 2001FR-00011978.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX DR New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX PS Disclosure; Page 179; 720pp; French.
 XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX given in the specification, a sequence containing at least 15 consecutive
 XX nucleotides from the 17 mer sequence, a sequence with, after optimal
 XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 XX hybridizes to them under highly stringent conditions, or the complement
 XX of any of them, or the corresponding RNA. The novel isolated nucleic
 XX acids of the invention are useful as probes and primers for detecting,
 XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 XX component of a gene chip, in vitro as (anti)sense reagents, and for
 XX production of recombinant polypeptides. Any of the nucleic acids,
 XX polypeptides, vectors containing the nucleic acids, cells containing the
 XX vector or antibodies directed against the polypeptides are useful for
 XX preparation of pharmaceuticals for prevention and/or treatment of viral
 XX diseases that are characterised by development of tumours or cell
 XX degeneration, specifically cancer but also Alzheimer's disease and
 XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX patient samples is useful for diagnosis and/or prognosis of these
 XX diseases. The polypeptides can also be used to generate antibodies, and
 XX both the polypeptide and antibodies are useful as components of protein
 XX chips. The nucleic acid sequences of the invention can be used in gene
 XX therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention

XX SQ Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. NO. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCCIC 1691
 |||||
 2 CTGGTGTCTGCTC 14

Db

RESULT 579
 ABT36109
 ID ABT36109 standard; DNA; 17 BP.
 XX AC
 XX ABT36109;
 DT 12-JUN-2003 (first entry)
 XX DE Tumour suppression related human fukutin oligo SEQ ID No 1746.
 XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX OS Homo sapiens.
 XX PN WO2003025175-A2.
 XX PD 27-MAR-2003.
 XX PF 17-SEP-2002; 2002WO-IB004208.
 XX PR 17-SEP-2001; 2001FR-00011978.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX DR New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX PS Disclosure; Page 237; 720pp; French.
 XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX given in the specification, a sequence containing at least 15 consecutive
 XX nucleotides from the 17 mer sequence, a sequence with, after optimal
 XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 XX hybridizes to them under highly stringent conditions, or the complement
 XX of any of them, or the corresponding RNA. The novel isolated nucleic
 XX acids of the invention are useful as probes and primers for detecting,
 XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 XX component of a gene chip, in vitro as (anti)sense reagents, and for
 XX production of recombinant polypeptides. Any of the nucleic acids,
 XX polypeptides, vectors containing the nucleic acids, cells containing the
 XX vector or antibodies directed against the polypeptides are useful for
 XX preparation of pharmaceuticals for prevention and/or treatment of viral
 XX diseases that are characterised by development of tumours or cell
 XX degeneration, specifically cancer but also Alzheimer's disease and
 XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX patient samples is useful for diagnosis and/or prognosis of these
 XX diseases. The polypeptides can also be used to generate antibodies, and
 XX both the polypeptide and antibodies are useful as components of protein
 XX chips. The nucleic acid sequences of the invention can be used in gene
 XX therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention

XX SQ Sequence 17 BP; 1 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. NO. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1685 TCTCCTCCAGCGT 1697
 |||||
 3 TCTCCTCAAGCGT 15

Db

RESULT 579
 ABT36109
 ID ABT36109 standard; DNA; 17 BP.
 XX AC
 XX ABT36109;
 DT 12-JUN-2003 (first entry)
 XX DE Tumour suppression related human fukutin oligo SEQ ID No 1746.
 XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX OS Homo sapiens.
 XX PN WO2003025175-A2.
 XX PD 27-MAR-2003.
 XX PF 17-SEP-2002; 2002WO-IB004208.
 XX PR 17-SEP-2001; 2001FR-00011978.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX DR New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX PS Disclosure; Page 237; 720pp; French.
 XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX given in the specification, a sequence containing at least 15 consecutive
 XX nucleotides from the 17 mer sequence, a sequence with, after optimal
 XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 XX hybridizes to them under highly stringent conditions, or the complement
 XX of any of them, or the corresponding RNA. The novel isolated nucleic
 XX acids of the invention are useful as probes and primers for detecting,
 XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 XX component of a gene chip, in vitro as (anti)sense reagents, and for
 XX production of recombinant polypeptides. Any of the nucleic acids,
 XX polypeptides, vectors containing the nucleic acids, cells containing the
 XX vector or antibodies directed against the polypeptides are useful for
 XX preparation of pharmaceuticals for prevention and/or treatment of viral
 XX diseases that are characterised by development of tumours or cell
 XX degeneration, specifically cancer but also Alzheimer's disease and
 XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX patient samples is useful for diagnosis and/or prognosis of these
 XX diseases. The polypeptides can also be used to generate antibodies, and
 XX both the polypeptide and antibodies are useful as components of protein
 XX chips. The nucleic acid sequences of the invention can be used in gene
 XX therapy. This polynucleotide sequence represents a tumour suppression
 XX related human fukutin oligonucleotide of the invention

acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule

Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAGAG 1651
Db 17 CTTGTAGCGGAG 5
|||||

RESULT 582
ACA06207/C
ID ACA06207 standard; RNA; 17 BP.
AC ACA06207;
XX
XX 03-JUN-2003 (first entry)
XX
XX NFkB sub-unit modulating inozyme substrate #26.
XX
XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
KW G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
XX Homo sapiens.
OS
XX
XX US2002177568-A1.
XX
XX 28-NOV-2002.
XX
XX 23-MAY-2001; 2001US-00864785.
XX
XX 07-DEC-1992; 92US-00987132.
PR 18-MAY-1994; 94US-00245466.
PR 15-AUG-1994; 94US-00291932.
PR 23-DEC-1996; 96US-0077916.
XX
XX (STIN/) STINCHOMB D T.
PA
PA (MCSW/) MCSWIGGEN J.
PA
XX (DRAP/) DRAPER K G.
XX
XX Stinchcomb DT, Mcswiggen J, Draper KG;
XX
XX WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
XX Claim 3; Page 27; 72pp; English.
PS
XX The invention describes an enzymatic nucleic acid molecule (I) which down
XX regulates expression of a sequence encoding a subunit of nuclear factor
CC

kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberyne configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg²⁺. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule

Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAGAG 1651
Db 14 CTTGTAGCGGAG 2
|||||

RESULT 583
ACA07619/C
ID ACA07619 standard; RNA; 17 BP.
AC ACA07619;
XX
XX 03-JUN-2003 (first entry)
XX
XX NFkB sub-unit modulating zinzyme substrate #18.
XX
XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
KW G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
XX Homo sapiens.
OS
XX
XX US2002177568-A1.
XX
XX 28-NOV-2002.
XX
XX 23-MAY-2001; 2001US-00864785.
XX
XX 07-DEC-1992; 92US-00987132.
PR 18-MAY-1994; 94US-00245466.
PR 15-AUG-1994; 94US-00291932.
PR 23-DEC-1996; 96US-0077916.
XX
XX (STIN/) STINCHOMB D T.
PA
PA (MCSW/) MCSWIGGEN J.
PA

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PA (DRAP/) DRAPER K G.
XX
XX Stinchcomb DT, Mcswiggen J, Draper KG;
XX
XX WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
XX Claim 3; Page 38; 72pp; English.
XX
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg2+. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC gencitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel enzymatic
CC nucleic acid molecule
XX
XX Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
SQ
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1639 CTTGTAGCGAAG 1651
Db 16 CTTGTAGCGAAG 4
RESULT 584
ACA08196/C
XX ACA08196;
XX
XX 03-JUN-2003 (first entry)
DT
XX NFkB sub-unit modulating DNazyme substrate #3.
DE
XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gencitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
XX Homo sapiens.
OS

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XX US2002177568-A1.
PN
XX 28-NOV-2002.
XX
XX 23-MAY-2001; 2001US-00864785.
PF
XX 07-DEC-1992; 92US-00987132.
PR
XX 18-MAY-1994; 94US-00245466.
PR
XX 15-AUG-1994; 94US-00291932.
PR
XX 23-DEC-1996; 96US-00777916.
XX
XX (STIN/) STINCHOMB D T.
PA
XX (MCSW/) MCSWIGGEN J.
PA
XX (DRAP/) DRAPER K G.
XX
XX Stinchcomb DT, Mcswiggen J, Draper KG;
PI
XX WPI; 2003-340953/32.
DR
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
XX Claim 3; Page 42; 72pp; English.
XX
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg2+. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC gencitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel enzymatic
CC nucleic acid molecule
XX
XX Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
SQ
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1639 CTTGTAGCGAAG 1651
Db 13 CTTGTAGCGAAG 1
RESULT 585
ADB03602
XX ADB03602 standard; DNA; 17 BP.
ID
XX ADB03602;
AC
XX 20-NOV-2003 (first entry)
XX
XX Human MDZ7 scanning oligonucleotide SEQ ID 4588.
DE
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW

```

KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 4588; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 7 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 GTAGCAGAGGCA 1654

DB 2 GTAGCAGAGGAA 14

RESULT 586

ADA99413

ID ADA99413 standard; DNA; 17 BP.

AC ADA99413;

XX 20-NOV-2003 (first entry)

XX Human MDZ3 scanning oligonucleotide SEQ ID 402.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

KW developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.

XX

PD 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 402; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 2 A; 8 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1744 TCCTCCTATCCT 1756

DB 2 TCCTCCTATCCT 14

RESULT 587

ADA99414

ID ADA99414 standard; DNA; 17 BP.

AC ADA99414;

XX 20-NOV-2003 (first entry)

XX Human MDZ3 scanning oligonucleotide SEQ ID 403.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX

```
PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 403; 103pp; English.
PS
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
SQ Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1744 TCCTCCCTATCCT 1756
Db 1 TCCTCACTATCCT 13
RESULT 588
ADA99411
ID ADA99411 standard; DNA; 17 BP.
XX
XX ADA99411;
AC
XX 20-NOV-2003 (first entry)
DT
XX Human MDZ3 scanning oligonucleotide SEQ ID 400.
DE
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) ABOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
```

```
XX Example 8; SEQ ID NO 400; 103pp; English.
PS
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
SQ Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1744 TCCTCCCTATCCT 1756
Db 4 TCCTCACTATCCT 16
RESULT 589
ADB03600
ID ADB03600 standard; DNA; 17 BP.
XX
XX ADB03600;
AC
XX 20-NOV-2003 (first entry)
DT
XX Human MDZ7 scanning oligonucleotide SEQ ID 4586.
DE
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) ABOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
```


QY 1642 GTAGCAGAGGCA 1654
 DB 1 GTAGCAGAGGAA 13

RESULT 592
 ADA99412

ID ADA99412 standard; DNA; 17 BP.
 XX
 AC
 XX
 DT
 XX
 DE
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 DR WPI; 2003-423107/40.
 XX
 PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 PS Example 8; SEQ ID NO 401; 103pp; English.
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 2 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1744 TCCTCCCTATCTCT 1756
 DB 3 TCCTCACTATCTCT 15

RESULT 593
 ADB03599

ID ADB03599 standard; DNA; 17 BP.
 XX
 AC ADB03599;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD27 scanning oligonucleotide SEQ ID 4585.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 DR WPI; 2003-423107/40.
 XX
 PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 PS Example 8; SEQ ID NO 4585; 103pp; English.
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 7 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 GTAGCAGAGGCA 1654
 DB 5 GTAGCAGAGGAA 17

RESULT 594
 ABZ65291

ID ABZ65291 standard; RNA; 17 BP.
 XX
 AC ABZ65291;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human HER2 DNazyme substrate #748.
 XX

KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX Homo sapiens.

OS WO200297114-A2.

PN WO200297114-A2.

XX 05-DEC-2002.

PF 29-MAY-2002; 2002WO-US016840.

XX 29-MAY-2001; 2001US-0294140P.

PR 06-JUN-2001; 2001US-0296249P.

PR 10-SEP-2001; 2001US-0318471P.

XX (RIBO-) RIBOZYME PHARM INC.

PA Mcswiggen J;

PI WPI; 2003-140484/13.

DR Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 4; Page 147; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ5531, ABZ6520 - ABZ6524,
 CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
 CC ribozymes of the invention

XX Sequence 17 BP; 3 A; 5 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 76.9%; Pred. No. 4.7e+02;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGGA 1675
 DB 2 GCUCACUGGUGGA 14

RESULT 595
 ABZ65290
 ID ABZ65290 standard; RNA; 17 BP.

AC ABZ65290;

XX 21-MAR-2003 (first entry)

DE Human HER2 DNzyme substrate #747.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.

OS Homo sapiens.

XX WO200297114-A2.

PN 05-DEC-2002.

PD 29-MAY-2002; 2002WO-US016840.

XX 29-MAY-2002; 2002WO-US016840.

XX 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.

XX (RIBO-) RIBOZYME PHARM INC.

PA Mcswiggen J;

PI WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 4; Page 147; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ5531, ABZ6520 - ABZ6524,
 CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
 CC ribozymes of the invention

XX Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 76.9%; Pred. No. 4.7e+02;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGGA 1675
 DB 5 GCUCACUGGUGGA 17

RESULT 596
 ACD63408

ID ACD63408 standard; RNA; 17 BP.

AC ACD63408;

XX 30-SEP-2003 (first entry)

XX HCV minus strand DNzyme substrate sequence #1047.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.

OS WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00677478.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Claim 1; Page 293; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyms, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention
 XX
 SQ Sequence 17 BP; 4 A; 4 C; 3 G; 0 T; 6 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 63.5%; Pred. No. 4.7e+02;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 1675 AACCTGTGTCT 1687
 Db 2 AACCCUGGUGAU 14
 RESULT 597
 ACDS5657/c
 ID ACDS5657 standard; RNA; 17 BP.
 XX
 AC ACDS5657;
 XX
 DT 23-SEP-2003 (first entry)
 XX
 DE HBV amberyms substrate sequence #167.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyms; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX

PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Example 1; Page 206; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyms, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberyms sequences
 CC disclosed in the present invention
 XX
 SQ Sequence 17 BP; 4 A; 0 C; 11 G; 0 T; 2 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1736 CTCGCCAATCCTC 1748
 Db 13 CCCCACTCTCTC 1
 RESULT 598
 ACDS9262/c
 ID ACDS9262 standard; RNA; 17 BP.
 XX
 AC ACDS9262;
 XX
 DT 24-SEP-2003 (first entry)
 XX
 DE HCV DNazyme substrate sequence #1232.
 XX

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
 KW amzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAPV/) PAVCO P.
 PA (LEEF/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 XX Claim 1; Page 256; 387pp; English.
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
 CC inozymes, zinzymes, amberyzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNzyme or minus strand DNzyme sequences disclosed in the present
 CC invention
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
 Query Match 8.2%; Score 11.4; DB 1; Length 17;
 Best Local Similarity 92.3%; Pred. NO. 4.7e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1673 GGAACCTGGTGT 1685
 DB 13 GCAACCTGGTGT 1

RESULT 599
 ACD59261/C
 ID ACD59261 standard; RNA; 17 BP.
 XX
 AC ACD59261;
 XX
 DT 24-SEP-2003 (first entry)
 XX
 DE HCV DNzyme substrate sequence #1231.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
 KW amzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAPV/) PAVCO P.
 PA (LEEF/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 XX Claim 1; Page 256; 387pp; English.
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
 CC inozymes, zinzymes, amberyzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNzyme or minus strand DNzyme sequences disclosed in the present
 CC invention


```

XX 21-NOV-2002.
PD
XX
XX
PF 13-MAY-2002; 2002WO-US014877.
XX
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
XX
XX Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
PI WPI; 2003-129214/12.
XX
XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT diagnosing a HBM-like phenotype in a subject and for preparing a
PT composition for modulating bone mass and/or lipid levels in a subject
PT suffering from e.g. osteoporosis.
XX
XX Disclosure; Page 53; 629pp; English.
XX
XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC level modulation. The invention is useful for diagnosing a HBM-like
CC phenotype in a subject and for preparing a composition for modulating
CC bone mass and/or lipid levels in a subject suffering from e.g.
CC osteoporosis. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
SQ
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1722 GAGATGGAGATTG 1734
DB 14 GAGAGGGAGATTG 2
RESULT 603
ADB42129
ID ADB42129 standard; DNA; 17 BP.
XX
XX ADB42129;
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #2452.
DE
XX cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT

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DR WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX Disclosure; Page 318; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX Sequence 17 BP; 1 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1679 CTGGTGTCCTCC 1691
DB 4 CTGGTGTCCTCC 16
RESULT 604
ADB39940/c
ID ADB39940 standard; DNA; 17 BP.
XX
XX ADB39940;
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #263.
DE
XX
XX cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT

```

PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 62; 77lpp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and anti-sense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 7 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1637 GGCTTGTAGCAGA 1649
Db |||||||||
15 GGTTGTAGCAGA 3
RESULT 605
ADB39941/C
ID ADB39941 standard; DNA; 17 BP.
XX
XX ADB39941;
AC
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #264.
DE
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX WO2003040369-A2.
PN
XX 15-MAY-2003.
PD
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX 17-SEP-2001; 2001FR-00011981.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
FA
XX Tellerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
DR
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX

PS Disclosure; Page 63; 77lpp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and anti-sense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1637 GGCTTGTAGCAGA 1649
Db |||||||||
15 GGTTGTAGCAGA 3
RESULT 606
ADC37717
ID ADC37717 standard; DNA; 17 BP.
XX
XX ADC37717;
AC
XX 18-DEC-2003 (first entry)
DT
XX Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:66.
DE
XX human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
KW
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO2003037931-A2.
PN
XX 08-MAY-2003.
PD
XX 01-NOV-2002; 2002WO-US035129.
PF
XX 01-NOV-2001; 2001US-0334773P.
PR
XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
FA
XX Shannon M, Phan T;
XX
XX WPI; 2003-430501/40.
DR
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
XX Example 2; SEQ ID NO 66; 172pp; English.
PS
XX The present invention describes the human angiominotin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC

CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of NMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 17 BP; 7 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
SQ

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGACA 1731
Db 1 ACGGTGATGGAGA 13

RESULT 607
ADB44320/c
ID ADB44320 standard; DNA; 17 BP.
XX
AC ADB44320;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #4643.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001PR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Teleman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 574; 771pp; French.
XX

CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.
XX Sequence 17 BP; 5 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
SQ

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGAAC 1677
Db 13 TCACAGCTGGATC 1

RESULT 608
AAT66085/c
ID AAT66085 standard; DNA; 20 BP.
XX
AC AAT66085;
XX
DT 25-MAR-2003 (revised)
DT 18-JUN-1997 (first entry)
XX
DE Plasminogen activator/urokinase gene repeat sequence primer #1.
XX
KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW linkage analysis; genetic disease; animal; plant; breeding; locus;
KW hybridisation; chromosome; ds.
XX
OS Synthetic.
XX
PN US5582979-A.
XX
PD 10-DEC-1996.
XX
PF 04-APR-1994; 94US-00222177.
XX
PR 21-APR-1989; 89US-00341562.
PR 05-SEP-1991; 91US-00754351.
XX
PA (MARS-) MARSHFIELD CLINIC.
XX
PI Weber JL;
XX
DR WPI; 1997-042299/04.
XX
PT Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
PT using novel nucleic acid moles. as primers.
XX
PS Example 9; Col 59-60; 186pp; English.
XX

CC The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g paternity or maternity testing, human
CC genetic analysis such as linkage analysis of genetic disease, commercial
CC animal or plant breeding or pedigree analysis. The sequences AAT66084-
CC 166107 represent repeat sequences of low informativeness found in
CC specific human genes. The primers AAT66085-6 were used to amplify a 111
CC bp fragment of the plasminogen activator/urokinase gene which contains
CC the repeat sequence of AAT66084. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 20 BP; 5 A; 1 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 20;
Best Local Similarity 92.3%; Pred. No. 5.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 GCTCCCAACTCCT 1747
Db 13 GCTCCTAACTCCT 1


```

RESULT 609
AAQ29795/c
ID AAQ29795 standard; DNA; 16 BP.
XX AC
XX AAQ29795;
XX DT
XX 25-MAR-2003 (revised)
XX 19-MAR-1993 (first entry)
XX DE
XX A allele probe VP52.
XX KW
XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
XX KW
XX paternity; forensic; ss.
XX OS
XX Synthetic.
XX PN
XX EP512342-A2.
XX PD
XX 11-NOV-1992.
XX PF
XX 25-APR-1992; 92EP-00107084.
XX PR
XX 07-MAY-1991; 91US-00696793.
XX PA
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI
XX Saiki RK, Nasarabadi SL;
XX DR
XX WPI; 1992-374679/46.
XX PT
XX Determn. of an individuals genotype at the gamma-globin locus - using
XX sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
XX PS
XX Disclosure; Page 15; 29pp; English.
XX CC
XX The sequences given in AAQ29787-816 are probes which were used within the
XX method of the invention for detecting the presence of a variant sequence
XX in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
XX distinguished from one another by the polymorphic sequence corresponding
XX to the HindIII site of the A allele. The sequences of the three alleles
XX are given in AAQ29842-44. The methods for determining an individuals
XX genotype at the GGG locus with respect to a set of alleles improves the
XX discriminatory power of GGG typing methodology compared to previous
XX methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ
XX Sequence 16 BP; 4 A; 8 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Determn. of an individuals genotype at the gamma-globin locus - using
XX sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
XX PS
XX Disclosure; Page 15; 29pp; English.
XX CC
XX The sequences given in AAQ29787-816 are probes which were used within the
XX method of the invention for detecting the presence of a variant sequence
XX in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
XX distinguished from one another by the polymorphic sequence corresponding
XX to the HindIII site of the A allele. The sequences of the three alleles
XX are given in AAQ29842-44. The methods for determining an individuals
XX genotype at the GGG locus with respect to a set of alleles improves the
XX discriminatory power of GGG typing methodology compared to previous
XX methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ
XX Sequence 16 BP; 4 A; 8 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 16;
XX Best Local Similarity 81.2%; Pred. No. 4.8e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1669 AGCTGGAACCCCTGGTG 1684
XX || || || || || || || ||
XX 16 AGGTGGAAGCTTGCTG 1
XX
XX Db
XX
XX RESULT 610
AAQ29793/c
ID AAQ29793 standard; DNA; 16 BP.
XX AC
XX AAQ29793;
XX DT
XX 25-MAR-2003 (revised)
XX 19-MAR-1993 (first entry)
XX DE
XX A allele probe VP50.
XX KW
XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
XX KW
XX paternity; forensic; ss.
XX OS
XX Synthetic.
XX PN
XX EP512342-A2.
XX PD
XX 11-NOV-1992.
XX PF
XX 25-APR-1992; 92EP-00107084.
XX PR
XX 07-MAY-1991; 91US-00696793.
XX PA
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI
XX Saiki RK, Nasarabadi SL;
XX DR
XX WPI; 1992-374679/46.
XX PT
XX Determn. of an individuals genotype at the gamma-globin locus - using
XX sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
XX PS
XX Disclosure; Page 15; 29pp; English.
XX CC
XX The sequences given in AAQ29787-816 are probes which were used within the
XX method of the invention for detecting the presence of a variant sequence
XX in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
XX distinguished from one another by the polymorphic sequence corresponding
XX to the HindIII site of the A allele. The sequences of the three alleles
XX are given in AAQ29842-44. The methods for determining an individuals
XX genotype at the GGG locus with respect to a set of alleles improves the
XX discriminatory power of GGG typing methodology compared to previous
XX methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ
XX Sequence 16 BP; 4 A; 8 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 16;
XX Best Local Similarity 81.2%; Pred. No. 4.8e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1669 AGCTGGAACCCCTGGTG 1684
XX || || || || || || || ||
XX 16 AGGTGGAAGCTTGCTG 1
XX
XX Db
XX
XX RESULT 610
AAQ29793/c
ID AAQ29793 standard; DNA; 16 BP.
XX AC
XX AAQ29793;
XX DT
XX 25-MAR-2003 (revised)
XX 19-MAR-1993 (first entry)
XX DE
XX A allele probe VP50.
XX KW
XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
XX KW
XX paternity; forensic; ss.
XX OS
XX Synthetic.
XX PN
XX EP512342-A2.
XX PD
XX 11-NOV-1992.
XX PF
XX 25-APR-1992; 92EP-00107084.
XX PR
XX 07-MAY-1991; 91US-00696793.
XX PA
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI
XX Saiki RK, Nasarabadi SL;
XX DR
XX WPI; 1992-374679/46.
XX PT
XX Determn. of an individuals genotype at the gamma-globin locus - using
XX sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
XX PS
XX Disclosure; Page 14; 29pp; English.
XX CC
XX The sequences given in AAQ29787-816 are probes which were used within the
XX method of the invention for detecting the presence of a variant sequence
XX in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
XX distinguished from one another by the polymorphic sequence corresponding
XX to the HindIII site of the A allele. The sequences of the three alleles
XX are given in AAQ29842-44. The methods for determining an individuals
XX genotype at the GGG locus with respect to a set of alleles improves the
XX discriminatory power of GGG typing methodology compared to previous
XX methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ
XX Sequence 16 BP; 5 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 16;
XX Best Local Similarity 81.2%; Pred. No. 4.8e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1670 GCTGGAAACCCCTGGTGT 1685
XX || || || || || || || ||
XX 16 GGTGGAAGCTTGCTGT 1
XX
XX Db
XX
XX RESULT 611
AAQ52859
ID AAQ52859 standard; RNA; 16 BP.
XX AC
XX AAQ52859;
XX DT
XX 25-MAR-2003 (revised)
XX 26-MAY-1994 (first entry)
XX DE
XX Cytomegalovirus target sequence 36.
XX KW
XX RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HbRNA;
XX picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
XX papilloma virus; HPV; Epstein-Barr virus; EBV; TCV;
XX T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
XX influenza virus; HSV; herpes simplex virus; vector; immune response;
XX antibody; ribozyme; viral RNA; treatment; ss.
XX OS
XX Synthetic.
XX PN
XX WO9323569-A1.
XX PD
XX 25-NOV-1993.
XX PF
XX 29-APR-1993; 93WO-US004020.
XX PR
XX 11-MAY-1992; 92US-00882689.
XX PR
XX 14-MAY-1992; 92US-00882712.
XX PR
XX 14-MAY-1992; 92US-00882713.
XX PR
XX 14-MAY-1992; 92US-00882714.
XX PR
XX 14-MAY-1992; 92US-00882823.
XX PR
XX 14-MAY-1992; 92US-00882824.
XX PR
XX 14-MAY-1992; 92US-00882886.

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XX WPI; 2001-611503/70.
XX
XX Novel polypeptides that are the regulators of BRCA-1, useful for treating
PT cancer and diagnosing the presence of neoplastic cells in biological
PT sample.
XX
XX Disclosure; Fig 8; 97pp; English.
XX
XX Sequences AAS56729-AAS5698 represent DNA encoding BRCA-1 regulators,
CC ribozyme target recognition RNA sequences, DNA fragments encoding the RNA
CC and primers used in the methods of the invention. Hybridisation of
CC ribozymes to their targets results in cleavage of the RNA target. The
CC ribozymes can be used to cleave regulators of the tumour suppressor BRCA-
CC 1, resulting in upregulation or downregulation of BRCA-1 in a cell. The
CC mRNA targets include those encoding the BRCA-1 regulator BR1, inhibitor
CC dominant negative 4 (ID4), breast basic conserved protein 1 (BBC1),
CC CHIR2, AF6, BR2 and BR3. Regulation of BRCA-1 is useful for treating and
CC diagnosing cancer and other proliferative disorders. The severity of an
CC incidence of cancer can be lessened by regulating tumour proliferation
CC through modulation of BRCA-1 expression. The sequences of the invention
CC are useful in the development of anti-cancer drugs
XX
XX Sequence 16 BP; 3 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1679 CTGGTGTCTCCTCCAG 1694
Db 1 CTGCTGTCTACTACAG 16
RESULT 614
AAI68609/c
ID AAI68609 standard; DNA; 16 BP.
XX
XX AC AAI68609;
XX
XX 14-JAN-2002 (first entry)
DE ICAM-1 triple helix associated oligonucleotide SEQ ID 11.
XX
XX ICAM-1; triple helix; transcription inhibition; antipsoriatic;
KW intracellular adhesion molecule; dermatological; antiasthmatic;
KW antiinflammatory; immunosuppressive; gastrointestinal; psoriasis;
KW neurodermatitis; allergic asthma; Crohn's disease; autoimmune disease;
KW transplant rejection; psoralen; photo-ultra-violet therapy; ds.
XX
XX Unidentified.
OS
XX WO200179487-A2.
PN
XX 25-OCT-2001.
XX
XX 18-APR-2001; 2001WO-DE0001509.
PF
XX 18-APR-2000; 2000DE-01019252.
PR
XX (DEGI/) DEGITZ K K.
PA (BESC/) BESCH R.
XX
XX Degitz KK, Besch R;
PI
XX WPI; 2002-017614/02.
XX
XX Triple-helix forming polydeoxyribonucleotides, useful for treating
PT intracellular adhesion molecule-1 related diseases, e.g. psoriasis, are
PT directed against transcribed or promoter regions of the ICAM-1 gene.
XX
XX Claim 5; Page 4; 61pp; German.
PS
XX

CC This invention describes novel polydeoxyribonucleotides (A), for use as
CC triple-helix forming oligonucleotides, having at least 3 sequential
CC purine and/or pyrimidine bases, capable of inhibiting transcription of
CC ICAM-1. (A) has a sequence specific for the transcribed or promoter
CC regions of the ICAM-1 (intracellular adhesion molecule) gene. The
CC products of the invention have antipsoriatic, dermatological,
CC antiasthmatic, antiinflammatory, immunosuppressive and gastrointestinal
CC activity. (A) are used for treatment or prevention of ICAM-1-associated
CC diseases, specifically psoriasis, neurodermatitis, allergic asthma,
CC Crohn's disease, autoimmune diseases and transplant rejection. Compared
CC with antisense oligonucleotides, (A) provide a longer-lasting effect
CC (they bind directly to the gene, so a compensatory increase in
CC transcription is not possible). (A) may be coupled to psoralen to provide
CC light-regulatable, sequence-specific downregulation of genes; this should
CC make photo-ultra-violet therapy more specific, with reduced side effects.
CC AAI68599-AAI68673 represent oligonucleotides used to illustrate the
XX method of the invention
XX
SQ Sequence 16 BP; 4 A; 0 C; 11 G; 1 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1736 CTCCCACTCTCCTCT 1751
Db 16 CCCCCACCTTCTCCT 1
RESULT 615
ABZ34019/c
ID ABZ34019 standard; DNA; 16 BP.
XX
XX AC ABZ34019;
XX
XX 31-JAN-2003 (first entry)
XX
XX HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:261.
DE
XX Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;
KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
KW probe; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX Synthetic.
XX
XX WO200255741-A2.
PN
XX 18-JUN-2002.
PD
XX 09-JAN-2002; 2002WO-EP000153.
PF
XX 11-JAN-2001; 2001EP-00870005.
PR
XX 20-APR-2001; 2001EP-00870085.
PR
XX 24-APR-2001; 2001US-0286102P.
XX
XX (INNO-) INNOGENETICS NV.
PA
XX De Smet K, Stuyver L;
PI
XX WPI; 2002-590680/63.
DR
XX
XX Detecting mutations associated with anti-HIV drug resistance comprises
PT detecting at least one of the mutations in the HIV reverse transcriptase
PT gene by using probes optimized to function together in a reverse-
PT hybridization assay.
XX
XX Claim 2; Page 19; 117pp; English.
PS
XX The present invention describes a method for detecting mutations
CC associated with anti-HIV drug resistance in a patient by detecting at
CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188U,
CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
CC

of HIV strains in a biological sample using a specific set of probes optimised to function together in a reverse-hybridisation assay. The method and the nucleic acid sequences used in the method are useful for determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic detection, preferably in vitro detection of the mutations K103N/R, V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides a rapid, reliable and precise assay or determination and monitoring of antiviral drug resistance or mutations associated with drug resistance of viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT sequences and probes which are used in the exemplification of the present invention

XX Sequence 16 BP; 5 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 16;
 Best Local Similarity 81.2%; Pred. No. 4.8e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1690 TCCAGCGTGTGGAAG 1705
 Db 16 TCCATCCTGTGGAAG 1

RESULT 616
 ADE14208/c
 ID ADE14208 standard; DNA; 16 BP.
 AC ADE14208;
 XX
 DT 29-JAN-2004 (first entry)
 DE Optineurin promoter motif, repeat element or regulatory region #317.
 XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
 KW SNP; glaucoma; progressive ocular hypertensive disorder;
 KW glaucoma related disorder; motif; repeat element; regulatory region.
 XX Homo sapiens.
 OS
 XX US2003190617-A1.
 PN
 XX 09-OCT-2003.
 PD
 XX 06-MAR-2002; 2002US-00091281.
 PF
 XX 06-MAR-2002; 2002US-00091281.
 PR
 XX (SIEB/) SI E.
 PA (RAYM/) RAYMOND V.
 PA (MORI/) MORISSETTE J.
 XX
 XX Raymond V, Morissette J, Si E;
 PI WPI; 2003-864168/80.
 XX
 DR
 XX New nucleic acid sequences of the optineurin gene are useful to detect
 PT polymorphisms particularly single nucleotide polymorphisms in the
 PT optineurin promoter to diagnose, prognose and treat glaucoma and related
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 319; 159pp; English.
 XX
 CC The invention relates to an isolated nucleic acid (N1) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ADE13890. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism

CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient for the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 CC capable of detecting a SNP located within an optineurin promoter, and
 CC detecting the polymorphism). The invention is used to diagnose and
 CC prognose glaucoma and also to treat glaucoma related disorders. The
 CC present sequence is an optineurin promoter motif, repeat element or
 CC putative regulatory region.
 XX
 SQ Sequence 16 BP; 4 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
 XX Query Match 8.1%; Score 11.2; DB 1; Length 16;
 Best Local Similarity 81.2%; Pred. No. 4.8e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCACGCTGGAACC 1678
 Db 16 GCTCACGCTGTAATC 1

RESULT 617
 ADA99593
 ID ADA99593 standard; DNA; 17 BP.
 AC ADA99593;
 XX
 DT 20-NOV-2003 (first entry)
 DE Human MDZ3 scanning oligonucleotide SEQ ID 582.
 XX
 DE Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 XX Homo sapiens.
 OS
 PN EP1281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00C16874.
 XX
 PR 02-AUG-2001; 2001US-00522181.
 XX
 XX (AEOM-) AEOMICA INC.
 PA
 XX Shannon M, Gu Y, Nguyen C;
 PI WPI; 2003-423107/40.
 XX
 DR New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
 XX
 PS Example 8; SEQ ID NO 582; 103pp; English.
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences; MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7 or MDZ12, e.g. cancer.

CC MD24, MD27, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MD24, MD27, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MD24, MD27, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 XX Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1659 CCAGGCTCACAGCTGG 1674
 Db 1 CCAGGCATCCAGCTGG 16

RESULT 618

ABZ65014/C

ID ABZ65014 standard; RNA; 17 BP.

XX AC ABZ65014;

XX AC

XX 21-MAR-2003 (first entry)

XX DE Human HER2 DNzyme substrate #471.

XX DE

KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX

OS Homo sapiens.
 XX

XX WO200297114-A2.
 XX

XX 05-DEC-2002.
 PD

XX 29-MAY-2002; 2002WO-US016840.
 PF

XX 29-MAY-2001; 2001US-0294140P.
 PR

XX 06-JUN-2001; 2001US-0296249P.
 PR

XX 10-SEP-2001; 2001US-0318471P.
 XX

XX (RIBO-) RIBOZYME PHARM INC.
 PA

XX

XX Mcswiggen J;

XX WPI; 2003-140484/13.
 XX

XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX

XX Claim 4; Page 142; 185pp; English.
 PS

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention

XX Sequence 17 BP; 3 A; 9 C; 1 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1636 GGGCTTGATGACAGAG 1651
 Db 16 GGGCATGTAGGAGAGG 1

RESULT 619

ADA99592

ID ADA99592 standard; DNA; 17 BP.

XX AC ADA99592;
 XX

XX 20-NOV-2003 (first entry)
 XX

XX Human MDZ3 scanning oligonucleotide SEQ ID 581.
 XX

KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MD24; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX

OS Homo sapiens.
 XX

XX EP1281758-A2.
 XX

XX 05-FEB-2003.
 XX

XX 30-JUL-2002; 2002EP-00016874.
 PF

XX 02-AUG-2001; 2001US-00922181.
 PR

XX (ABOM-) ABOMICA INC.
 XX

XX Shannon M, Gu Y, Nguyen C;
 XX

XX WPI; 2003-423107/40.
 DR

XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
 XX

XX Example 8; SEQ ID NO 581; 103pp; English.
 PS

XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MD24, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MD24, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MD24, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MD24, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX

XX Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1659 CCAGGCTCACAGCTGG 1674
 Db 2 CCAGGCATCCAGCTGG 17

RESULT 620
 AAQ29810/C
 ID AAQ29810 standard; DNA; 17 BP.
 XX AC AAQ29810;
 XX DT 25-MAR-2003 (revised)
 DT 19-MAR-1993 (first entry)
 XX DE C allele probe VP12.
 XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
 KW paternity; forensic; ss.
 XX Synthetic.
 XX EP512342-A2.
 XX PD 11-NOV-1992.
 XX PF 25-APR-1992; 92EP-00107084.
 PR 07-MAY-1991; 91US-00696793.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Saiki RK, Nasarabadi SL;
 XX WPI; 1992-374679/46.
 XX Determn. of an individuals genotype at the gamma-globin locus - using
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
 XX Disclosure; Page 18; 29pp; English.
 XX The sequences given in AAQ2987-816 are probes which were used within the
 CC method of the invention for detecting the presence of a variant sequence
 CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
 CC distinguished from one another by the polymorphic sequence corresponding
 CC to the HindIII site of the A allele. The sequences of the three alleles
 CC are given in AAQ29842-44. The methods for determining an individuals
 CC genotype at the GGG locus with respect to a set of alleles improves the
 CC discriminatory power of GGG typing methodology compared to previous
 CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 17 BP; 6 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1670 GCTGGAACCTGGTGT 1685
 | | | | | | | | | |
 17 GGTGGAATCTGGTGT 2
 RESULT 621
 AAQ29815
 ID AAQ29815 standard; DNA; 17 BP.
 XX AC AAQ29815;
 XX DT 25-MAR-2003 (revised)
 DT 19-MAR-1993 (first entry)
 XX DE C allele probe VP42.
 XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
 KW paternity; forensic; ss.
 XX Synthetic.
 XX EP512342-A2.
 XX PD 11-NOV-1992.
 XX PF 25-APR-1992; 92EP-00107084.
 PR 07-MAY-1991; 91US-00696793.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Saiki RK, Nasarabadi SL;
 XX WPI; 1992-374679/46.
 XX Determn. of an individuals genotype at the gamma-globin locus - using
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
 XX Disclosure; Page 18; 29pp; English.
 XX The sequences given in AAQ2987-816 are probes which were used within the
 CC method of the invention for detecting the presence of a variant sequence
 CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
 CC distinguished from one another by the polymorphic sequence corresponding
 CC to the HindIII site of the A allele. The sequences of the three alleles
 CC are given in AAQ29842-44. The methods for determining an individuals
 CC genotype at the GGG locus with respect to a set of alleles improves the
 CC discriminatory power of GGG typing methodology compared to previous
 CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 17 BP; 6 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1670 GCTGGAACCTGGTGT 1685
 | | | | | | | | | |
 17 GGTGGAATCTGGTGT 2

PN EP512342-A2.
 XX 11-NOV-1992.
 XX 25-APR-1992; 92EP-00107084.
 XX 07-MAY-1991; 91US-00696793.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Saiki RK, Nasarabadi SL;
 XX WPI; 1992-374679/46.
 XX Determn. of an individuals genotype at the gamma-globin locus - using
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
 XX Disclosure; Page 20; 29pp; English.
 XX The sequences given in AAQ2987-816 are probes which were used within the
 CC method of the invention for detecting the presence of a variant sequence
 CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
 CC distinguished from one another by the polymorphic sequence corresponding
 CC to the HindIII site of the A allele. The sequences of the three alleles
 CC are given in AAQ29842-44. The methods for determining an individuals
 CC genotype at the GGG locus with respect to a set of alleles improves the
 CC discriminatory power of GGG typing methodology compared to previous
 CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 17 BP; 2 A; 1 C; 8 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1670 GCTGGAACCTGGTGT 1685
 | | | | | | | | | |
 1 GGTGGAATCTGGTGT 16
 RESULT 622
 AAQ29814
 ID AAQ29814 standard; DNA; 17 BP.
 XX AC AAQ29814;
 XX DT 25-MAR-2003 (revised)
 DT 19-MAR-1993 (first entry)
 XX DE C allele probe VP41.
 XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
 KW paternity; forensic; ss.
 XX Synthetic.
 XX EP512342-A2.
 XX PD 11-NOV-1992.
 XX PF 25-APR-1992; 92EP-00107084.
 PR 07-MAY-1991; 91US-00696793.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Saiki RK, Nasarabadi SL;
 XX WPI; 1992-374679/46.
 XX Determn. of an individuals genotype at the gamma-globin locus - using
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
 XX

PS Disclosure; Page 19; 29pp; English.

XX The sequences given in AAQ29787-816 are probes which were used within the
CC method of the invention for detecting the presence of a variant sequence
CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
CC distinguished from one another by the polymorphic sequence corresponding
CC to the HindIII site of the A allele. The sequences of the three alleles
CC are given in AAQ29842-44. The methods for determining an individual's
CC genotype at the GGG locus with respect to a set of alleles improves the
CC discriminatory power of GGG typing methodology compared to previous
CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 17 BP; 2 A; 1 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1672 TGGAAACCTGGTGCT 1687

Db 2 TGGAAATCTGGTGCT 17

RESULT 623

AAQ29789/c
ID AAQ29789 standard; DNA; 17 BP.

XX AC AAQ29789;

XX 25-MAR-2003 (revised)

DT 19-MAR-1993 (first entry)

XX A allele probe VP11.

XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
KW paternity; forensic; ss.

XX Synthetic.

XX EP512342-A2.

XX 11-NOV-1992.

XX 25-APR-1992; 92EP-00107084.

XX 07-MAY-1991; 91US-00696793.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Saiki RK, Nasarabadi SL;

XX WPI; 1992-374679/46.

XX Determ. of an individuals genotype at the gamma-globin locus - using
PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
XX Disclosure; Page 13; 29pp; English.

XX The sequences given in AAQ29787-816 are probes which were used within the
CC method of the invention for detecting the presence of a variant sequence
CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
CC distinguished from one another by the polymorphic sequence corresponding
CC to the HindIII site of the A allele. The sequences of the three alleles
CC are given in AAQ29842-44. The methods for determining an individual's
CC genotype at the GGG locus with respect to a set of alleles improves the
CC discriminatory power of GGG typing methodology compared to previous
CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 17 BP; 6 A; 7 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1672 TGGAAACCTGGTGCT 1687

Db 17 TGGAAAGCTGGTGCT 2

RESULT 624

AAQ29812/c
ID AAQ29812 standard; DNA; 17 BP.

XX AC AAQ29812;

XX 25-MAR-2003 (revised)

DT 19-MAR-1993 (first entry)

XX C allele probe VP24.

XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
KW paternity; forensic; ss.

XX Synthetic.

XX EP512342-A2.

XX 11-NOV-1992.

XX 25-APR-1992; 92EP-00107084.

XX 07-MAY-1991; 91US-00696793.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Saiki RK, Nasarabadi SL;

XX WPI; 1992-374679/46.

XX Determ. of an individuals genotype at the gamma-globin locus - using
PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
XX Disclosure; Page 19; 29pp; English.

XX The sequences given in AAQ29787-816 are probes which were used within the
CC method of the invention for detecting the presence of a variant sequence
CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
CC distinguished from one another by the polymorphic sequence corresponding
CC to the HindIII site of the A allele. The sequences of the three alleles
CC are given in AAQ29842-44. The methods for determining an individual's
CC genotype at the GGG locus with respect to a set of alleles improves the
CC discriminatory power of GGG typing methodology compared to previous
CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 17 BP; 8 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1672 TGGAAACCTGGTGCT 1687

Db 17 TGGAAATCTGGTGCT 2

RESULT 625

AAQ29788/c
ID AAQ29788 standard; DNA; 17 BP.

XX AC AAQ29788;

XX 25-MAR-2003 (revised)

DT 19-MAR-1993 (first entry)

XX A allele probe VP10.

XX

KW G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
 XX paternity; forensic; ss.
 OS Synthetic.
 XX
 PN EP512342-A2.
 XX
 PD 11-NOV-1992.
 XX
 XX 25-APR-1992; 92EP-00107084.
 XX
 XX 07-MAY-1991; 91US-00696793.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Saiki RK, Nasarabadi SL;
 XX
 DR WPI; 1992-374679/46.
 XX
 PT Determn. of an individuals genotype at the gamma-globin locus - using
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
 XX
 PS Disclosure; Page 13; 29pp; English.
 XX
 CC The sequences given in AAQ29787-816 are probes which were used within the
 CC method of the invention for detecting the presence of a variant sequence
 CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
 CC distinguished from one another by the polymorphic sequence corresponding
 CC to the HindIII site of the A allele. The sequences of the three alleles
 CC are given in AAQ29842-44. The methods for determining an individuals
 CC genotype at the GGG locus with respect to a set of alleles improves the
 CC discriminatory power of GGG typing methodology compared to previous
 CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 17 BP; 5 A; 9 C; 1 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
 XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1670 GCTGGAACCTGTGTCT 1685
 DB 17 GGTGGAAGCTGTGTCT 2
 XX
 RESULT 626
 AAQ29811/c
 ID AAQ29811 standard; DNA; 17 BP.
 XX
 AC AAQ29811;
 XX
 DT 25-MAR-2003 (revised)
 DT 19-MAR-1993 (first entry)
 XX
 DE C allele probe VP17.
 XX
 XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
 KW paternity; forensic; ss.
 XX
 OS Synthetic.
 XX
 PN EP512342-A2.
 XX
 PD 11-NOV-1992.
 XX
 XX 25-APR-1992; 92EP-00107084.
 XX
 XX 07-MAY-1991; 91US-00696793.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Saiki RK, Nasarabadi SL;
 XX
 DR WPI; 1992-374679/46.
 XX
 PT Determn. of an individuals genotype at the gamma-globin locus - using
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
 XX
 PS Disclosure; Page 13; 29pp; English.
 XX
 CC The sequences given in AAQ29787-816 are probes which were used within the
 CC method of the invention for detecting the presence of a variant sequence
 CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
 CC distinguished from one another by the polymorphic sequence corresponding
 CC to the HindIII site of the A allele. The sequences of the three alleles
 CC are given in AAQ29842-44. The methods for determining an individuals
 CC genotype at the GGG locus with respect to a set of alleles improves the
 CC discriminatory power of GGG typing methodology compared to previous
 CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 17 BP; 5 A; 9 C; 1 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
 XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1670 GCTGGAACCTGTGTCT 1685
 DB 17 GGTGGAAGCTGTGTCT 2
 XX
 RESULT 626
 AAQ29811/c
 ID AAQ29811 standard; DNA; 17 BP.
 XX
 AC AAQ29811;
 XX
 DT 25-MAR-2003 (revised)
 DT 19-MAR-1993 (first entry)
 XX
 DE C allele probe VP17.
 XX
 XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
 KW paternity; forensic; ss.
 XX
 OS Synthetic.
 XX
 PN EP512342-A2.
 XX
 PD 11-NOV-1992.
 XX
 XX 25-APR-1992; 92EP-00107084.
 XX
 XX 07-MAY-1991; 91US-00696793.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Saiki RK, Nasarabadi SL;
 XX
 DR WPI; 1992-374679/46.
 XX
 PT Determn. of an individuals genotype at the gamma-globin locus - using
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
 XX
 PS Disclosure; Page 19; 29pp; English.
 XX
 CC The sequences given in AAQ29787-816 are probes which were used within the
 CC method of the invention for detecting the presence of a variant sequence
 CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
 CC distinguished from one another by the polymorphic sequence corresponding
 CC to the HindIII site of the A allele. The sequences of the three alleles
 CC are given in AAQ29842-44. The methods for determining an individuals
 CC genotype at the GGG locus with respect to a set of alleles improves the
 CC discriminatory power of GGG typing methodology compared to previous
 CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 17 BP; 7 A; 6 C; 1 G; 3 T; 0 U; 0 Other;
 XX
 XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
 XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1672 TCGAACCCTGTGTCT 1687
 DB 17 TGGATCTTGGTGTCT 2
 XX
 RESULT 627
 AAQ66711/c
 ID AAQ66711 standard; DNA; 17 BP.
 XX
 AC AAQ66711;
 XX
 DT 22-DEC-1994 (first entry)
 XX
 DE Primer to amplify HHV6 derived sequences.
 XX
 XX HHV6; Human Herpes Virus 6; Primers; Probes; PCR; amplify;
 KW polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN JP06133799-A.
 XX
 PD 17-MAY-1994.
 XX
 XX 27-OCT-1992; 92JP-00311416.
 PF
 XX 27-OCT-1992; 92JP-00311416.
 PR
 XX (KOKU-) KOKUSAI SHIVAKU KK.
 PA
 XX WPI; 1994-196175/24.
 DR
 XX HHV-6 derived nucleotide(s) - useful for identification of HHV-6 DNA.
 PT
 XX Claim 4; Page 2; 13pp; Japanese.
 PS
 XX The inventors provide human Herpes virus 6 derived nucleotide sequences
 CC useful for identification of HHV-6 DNA. AAQ66705-12 are primer set 1 (I),
 CC are used in the invention
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
 XX
 XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
 XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1665 TCACAGCTGGRACCT 1680
 DB 16 TCACAGATGGAAGACT 1

RESULT 628
 AAT53734/c
 ID AAT53734 standard; RNA; 17 BP.
 XX AC AAT53734;
 XX DT 25-MAR-2003 (revised)
 DT 03-APR-1997 (first entry)
 XX DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2847).
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.
 XX OS Rattus rattus.
 XX PN WO9523225-A2.
 XX PD 31-AUG-1995.
 XX PF 23-FEB-1995; 95WO-IB000156.
 XX PR 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291433.
 PR 16-AUG-1994; 94US-00292620.
 PR 17-AUG-1994; 94US-00291433.
 PR 16-AUG-1994; 94US-00291433.
 PR 19-AUG-1994; 94US-00292620.
 PR 12-SEP-1994; 94US-00300000.
 PR 02-SEP-1994; 94US-00300000.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311486.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowira B, Dizenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kislich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 XX Ribozymes having modified bases and methods for producing them - for use
 PT in inhibiting disease related genes.
 XX Claim 2; Page 204; 407pp; English.

CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
 CC nucleotide base position indicated in the DE line. Regions of the mRNA
 CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 CC inhibit ICAM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX Sequence 17 BP; 3 A; 10 C; 0 G; 0 T; 4 U; 0 Other;
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1704 AGTTGGGTAGGACTA 1719
 DB |||||||
 17 AGGTGGGTAGGGGTA 2
 RESULT 629
 AAT53501/c
 ID AAT53501 standard; RNA; 17 BP.
 XX AC AAT53501;
 XX DT 25-MAR-2003 (revised)
 DT 27-MAR-1997 (first entry)
 XX DE Rat ICAM hammerhead ribozyme target sequence (nt. position 374).
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.
 XX OS Rattus rattus.
 XX PN WO9523225-A2.
 XX PD 31-AUG-1995.
 XX PF 23-FEB-1995; 95WO-IB000156.
 XX PR 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291433.
 PR 16-AUG-1994; 94US-00292620.
 PR 17-AUG-1994; 94US-00291433.
 PR 19-AUG-1994; 94US-00292620.
 PR 12-SEP-1994; 94US-00300000.
 PR 02-SEP-1994; 94US-00300000.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311486.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.


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XX PI Fildes NJ, Reynolds RL;
XX DR WPI; 1997-350231/32.
XX PT Detection of glycoporphin A allele(s) - by hybridisation assay using
XX PT sequence-specific oligo:nucleotide probes.
XX PS Example 3; Col 15-16; 16pp; English.
XX CC Glycophorin A is a major sialoglycoprotein of the human erythrocyte
XX CC membrane. Glycophorin A carries the M or N blood group antigen, which is
XX CC determined by the amino acid at residues 1 and 5. Allele A encodes the
XX CC protein carrying the M blood group antigen and allele B encodes the
XX CC protein carrying the N blood group antigen. Three additional alleles have
XX CC been discovered, designated A', A'', and B'. Detecting an A', A'', or B'
XX CC allele of the Glycophorin A locus in a human nucleic acid sample
XX CC comprises mixing the sample under stringent hybridisation conditions with
XX CC a sequence-specific oligonucleotide probe that distinguishes the A', A'',
XX CC or B' allele from A and B alleles, and detecting any hybridisation. The
XX CC method and probes are used for determining an individual's Glycophorin A
XX CC genotype, especially useful for determining individual identity for
XX CC forensic purposes. AAT70558-67 (and also AAT70582-83) are primers from
XX CC the AmpliType (R) PM kit used in a Glycophorin A typing system developed
XX CC by Hoffmann-La Roche. The primers direct the simultaneous amplification
XX CC of specific regions of the following six genetic loci: Glycophorin A, HLA
XX CC DQA1, low density lipoprotein receptor, Haemoglobin G gamma-globin, D7S8
XX CC and group specific component. Probe strips are also provided in the kit
XX CC (AAT70568-81)
XX SQ Sequence 17 BP; 2 A; 1 C; 8 G; 6 T; 0 U; 0 Other;

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1670 GCTGGAACCCCTGGTGT 1685
Db 1 GGTGGAATCTTGGTGT 16

RESULT 632
AAAX68727/c
ID AAAX68727 standard; RNA; 17 BP.
XX AC AAAX68727;
XX DT 28-JUL-1999 (first entry)
XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #22.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX DR WPI; 1997-259017/23.
XX CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 134; 218pp; English.
XX CC The present invention describes nucleic acid molecules which modulate the
XX CC synthesis, expression and/or stability of a mRNA encoding 1 or more
XX CC receptors of vascular endothelial growth factor (VEGF). A patient
XX CC (preferably human) having a condition associated with the level of the
XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX CC treated by administering the nucleic acid molecule or the expression
XX CC vector to the patient. AAx67275 to AAx75752 represent specific examples
XX CC of nucleic acid molecules from the present invention.
XX SQ Sequence 17 BP; 1 A; 5 C; 7 G; 0 T; 4 U; 0 Other;

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAAACCCCTG 1681
Db 17 CACAGCAGGACCCCGG 2

RESULT 633
AAAX72948/c
ID AAAX72948 standard; RNA; 17 BP.
XX AC AAAX72948;
XX DT 28-JUL-1999 (first entry)
XX DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #381.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX OS Mus sp.
XX PN WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX DR WPI; 1997-259017/23.
XX CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 134; 218pp; English.
XX CC The present invention describes nucleic acid molecules which modulate the
XX CC synthesis, expression and/or stability of a mRNA encoding 1 or more
XX CC receptors of vascular endothelial growth factor (VEGF). A patient

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CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1642 GTAGCAGAGGCAAGC 1657
 Db 16 GCATCATAGGCAAGC 1
 RESULT 634
 AAX73306/C
 ID AAX73306 standard; RNA; 17 BP.
 XX
 AC AAX73306;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #739.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; flt-1; flk-1;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Mus sp.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX
 DR WPI; 1997-259017/23.
 XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 146; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 1 A; 3 C; 7 G; 0 T; 6 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1666 CACAGCTGGAACCCCTG 1681
 Db 16 CCCAGCAGAAACCCCTG 1
 RESULT 635
 AAX73324
 ID AAX73324 standard; RNA; 17 BP.
 XX
 AC AAX73324;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #757.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; flt-1; flk-1;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Mus sp.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX
 DR WPI; 1997-259017/23.
 XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 147; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 4 A; 7 C; 2 G; 0 T; 4 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 56.2%; Pred. No. 5.2e+02;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1738 CCCAACTCCTCCCTAT 1753
 Db 2 CCCAAGUCCUAGUUAU 17
 RESULT 636
 AAX69487/C
 ID AAX69487 standard; RNA; 17 BP.


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XX PI Zupi G;
XX DR WPI; 1997-489662/45.
XX PT Inhibiting proliferation of human melanoma cells with anti-c-myc
XX PT oligo:nucleotide(s) - particularly used together with cis-platin,
XX PT inhibits metastasis, induces regression or prevents further growth.
XX PS Claim 1; Page 22; 68pp; English.
XX CC This c-myc oligonucleotide is complementary to a sequence of human c-myc
XX CC mRNA and is used for inhibiting the proliferation of human melanoma cells
XX CC (HMC). The c-myc oligonucleotide is at least 10 bases long and inhibits
XX CC proliferation of HMC by at least 10 percent at 10 mu M, when the cells
XX CC are cultured at 37 degree. C in presence of serum. The method is
XX CC particularly used to treat human melanoma, and inhibits metastasis,
XX CC promotes regression or prevents any increase in tumour mass. The c-myc
XX CC oligonucleotide can be used together with cis-platin and which then
XX CC reduces resistance of tumour cells to cis-platin. The oncogene c-myc is
XX CC found to be essential for growth and metastasis of melanoma, and the c-
XX CC myc oligonucleotides are designed to target double-stranded DNA or single
XX CC stranded RNA. A combination of c-myc oligonucleotide and cis-platin is
XX CC more effective than either component used alone
XX SQ Sequence 17 BP; 3 A; 6 C; 1 G; 7 T; 0 U; 0 Other;

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATGGCTCCCACTCC 1746
DB 2 ATGTTTTCCACTCC 17

RESULT 639
AAV14126/C
ID AAV14126 standard; DNA; 17 BP.
XX AC AAV14126;
XX DT 27-AUG-2003 (revised)
XX DT 19-MAY-1998 (first entry)
XX DE Probe HBP42 for preCore region of HBV.
XX KW Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;
XX KW preCore region; HBsAg region; genotype specific target;
XX KW mutation detection; ss.
XX OS Synthetic.
XX OS Hepatitis B virus.
XX PN WO9740193-A2.
XX PD 30-OCT-1997.
XX PF 21-APR-1997; 97WO-EP002002.
XX PR 19-APR-1996; 96EP-00870053.
XX PA (INNO-) INNOGENETICS NV.
XX STuyver L, Rossau R, Maertens G;
XX WPI; 1997-535867/49.
XX DR Detection and/or genetic analysis of hepatitis B virus - specifically
XX PT genotype, preCore mutations, vaccine escape mutations and RT gene
XX PT mutations selected by treatment with drugs.
XX PS Claim 5; Page 27; 80pp; English.

XX CC This sequence represents a probe for the preCore region of hepatitis b
XX CC virus (HBV). This sequence can be used in the method of the invention for
XX CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.
XX CC The method comprises: (a) optionally releasing, isolating or
XX CC concentrating polynucleic acids (I) in the sample, and amplifying the
XX CC relevant part of a suitable HBV gene in the sample with at least 1
XX CC suitable primer pair; (b) hybridising (I) with a combination of at least
XX CC 2 nucleotide probes, which are applied to known locations on a solid
XX CC support and hybridise specifically to mutant target sequences chosen from
XX CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV
XX CC genotype specific target sequences, or their complements or U for T
XX CC homologues; (c) detecting the hybrids formed in step (b), and inferring
XX CC the HBV genotype and/or mutants present in the sample from the
XX CC differential hybridisation signal(s). The composition can be used to
XX CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,
XX CC specifically genotype, preCore mutations, vaccine escape mutations and RT
XX CC gene mutations selected by treatment with drugs, e.g. lamivudine and
XX CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 17 BP; 4 A; 2 C; 6 G; 5 T; 0 U; 0 Other;

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1747 TCCCTATCCTAAAGCC 1762
DB 17 TCCATGTCCTAAAGCC 2

RESULT 640
AAV62812/C
ID AAV62812 standard; RNA; 17 BP.
XX AC AAV62812;
XX DT 16-JUL-1999 (first entry)
XX DE Delta-9 desaturase hamerhead ribozyme target SEQ ID NO:687.
XX KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
XX KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
XX KW modulation; gene expression; transgenic plant; cleavage; canola plant;
XX KW caffeine synthesis; coffee plant; nicotine production; tobacco;
XX KW fruit ripening; flower pigmentation; lignin production; ss.
XX OS Zea mays.
XX OS WO9710328-A2.
XX PN 20-MAR-1997.
XX PF 12-JUL-1996; 96WO-US011689.
XX PR 13-JUL-1995; 95US-0001135P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (DOWC) DOWELANCO.
XX PI Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;
XX PI Young SA, Folkerts O, Merlo DJ;
XX DR WPI; 1997-202224/18.
XX CC Ribozyme which modulates plant gene expression - preferably modulates
XX PT expression of DELTA-9 desaturase or granule bound starch synthase in
XX PT maize or canola.
XX PS Claim 38; Page 85; 155pp; English.
XX CC The present invention describes an enzymatic nucleic acid molecule (I)
XX CC with RNA cleaving activity, which modulates the expression of a plant

```

CC gene. Also described is a gene comprising a cDNA sequence encoding maize
 CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
 CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
 CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
 CC modulate caffeine synthesis in a coffee plant, nicotine production in a
 CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
 CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
 CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
 CC plant

XX SQ Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1733 TGGCTCCCAACTCTTC 1748
 Db 17 TGGCTGCCAACACTTC 2

RESULT 641
 AAV44920/c
 ID AAV44920 standard; DNA; 17 BP.

XX AC AAV44920;

XX DT 28-OCT-1998 (first entry)

XX DE Promoter molecule.

XX KW Promoter molecule; activator sequence; E2F protein; CDF-1 protein;
 KW tumour; leukaemia; cardiovascular disease; autoimmune disease; allergy;
 KW arthritis; psoriatic disease; CNS damage; infectious disease;
 KW blood clotting disorder; therapy; ss.

XX OS Synthetic.

XX PN EP860445-A1.

XX PD 26-AUG-1998.

XX PF 18-FEB-1997; 97EP-00102547.

XX PR 18-FEB-1997; 97EP-00102547.

XX PA (FARH) HOECHST AG.

XX PI Mueller R, Liu N, Zwicker J, Sedlacek H;

XX DR WPI; 1998-439301/38.

XX PT DNA construct comprising activator, chimeric promoter and structural gene
 PT - where promoter has E2F and CDF-1 protein binding sequences.

XX PS Disclosure; Page 16; 34pp; English.

XX CC This sequence represents a promoter molecule that can be used in the
 CC nucleic acid construct of the invention. The nucleic acid construct
 CC comprises: (a) at least one activator sequence; (b) at least one promoter
 CC module comprising a nucleotide sequence which binds a protein of the E2F
 CC family and a protein of the CDF-1 family; and (c) at least one structural
 CC gene. The construct, or a vector containing it can be used for local
 CC application or injection for treating or preventing disease, i.e.
 CC tumours, leukaemia, cardiovascular disease, autoimmune disease, allergy,
 CC arthritis, psoriatic disease, impending rejection of a transplanted
 CC organ, CNS damage, infectious disease or a blood clotting disorder

XX SQ Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GGCTCCCAACTCTTCC 1749
 Db 17 GCCTCCCAACACCTGC 2

RESULT 642

AAV97520

ID AAV97520 standard; RNA; 17 BP.

XX AC AAV97520;

XX DT 17-MAR-1999 (first entry)

XX DE Human EGF-R target sequence nucleotide position 2618.

XX KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KW cancer; genetic drift; detection; mutation; ss.

XX OS Homo sapiens.

XX PN WO9833893-A2.

XX PD 06-AUG-1998.

XX PF 14-JAN-1998; 98WO-US000730.

XX PR 31-JAN-1997; 97US-0036476P.

XX PR 04-DEC-1997; 97US-00985162.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI (UYAS-) UNIV ASTON.

XX PI Akhtar S, Fell P, Mcswiggen JA;

XX DR WPI; 1998-437449/37.

XX PT Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and for
 PT treating cancers.

XX PS Claim 5; Page 74; 109pp; English.

XX CC The present invention describes enzymatic nucleic acid molecules (NAMS)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV9721 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to 9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMS can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell

XX SQ Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. No. 5.2e+02;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCAACTCC 1746

Db 2 AATGGCUCCAGUACC 17

RESULT 643

AAV97591/c

ID AAV97591 standard; RNA; 17 BP.

XX AC AAV97591;

DT 17-MAR-1999 (first entry)
 XX Human EGF-R target sequence nucleotide position 3177.
 DE
 XX
 KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KW cancer; genetic drift; detection; mutation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9833893-A2.
 PN
 XX
 PD 06-AUG-1998.
 XX
 XX 14-JAN-1998; 98WO-US000730.
 PF
 XX 31-JAN-1997; 97US-0036476P.
 PR
 PR 04-DEC-1997; 97US-00985162.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (UYAS-) UNIV ASTON.
 PA
 XX Akhtar S, Fell P, Mcswiggen JA;
 PI
 XX WPI; 1998-437449/37.
 DR
 XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and for
 PT treating cancers.
 PT
 XX Claim 5; Page 75; 109pp; English.
 PS
 XX The present invention describes enzymatic nucleic acid molecules (NAMs)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMs can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell
 CC
 XX Sequence 17 BP; 3 A; 7 C; 2 G; 0 T; 5 U; 0 Other;
 SQ

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1694 GCGTGGTGAAGTTGG 1709
 DB || ||| ||||| |||
 17 GCACGGTAGAAGTTGG 2

RESULT 644
 AAV49878/c
 ID AAV49878 standard; DNA; 17 BP.
 XX
 AC AAV49878;
 XX
 DT 17-OCT-2003 (revised)
 DT 02-NOV-1998 (first entry)
 XX
 XX Myo-D E-box muscle-specific helix-loop-helix binding site.
 DE
 XX cdc25B promoter; murine; medicament; treatment; tumour; disease; CNS;
 KW leukaemia; autoimmune disease; allergy; arthritis; inflammation;
 KW organ rejection; graft-versus-host reaction; blood clot; infection;
 KW circulation; anaemia; hormonal disorders; central nervous system; ss.
 XX
 OS unidentified.
 XX

PN EP864651-A2.
 XX
 PD 16-SEP-1998.
 XX
 PF 13-MAR-1998; 98EP-00104597.
 XX
 PR 14-MAR-1997; 97DE-01010643.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Koerner K, Mueller R, Sedlacek H;
 PI
 XX WPI; 1998-469235/41.
 DR
 XX New cdc25B gene promoter used to produce medicaments to treat - e.g.
 PT tumours, leukaemia, autoimmune diseases, allergies, arthritis,
 PT inflammation, organ rejection, blood clotting and circulatory disorders,
 PT anaemia and hormonal disorders.
 XX
 PS Disclosure; Page 9; 30pp; German.
 XX
 CC This sequence is a muscle-specific binding site for the Myo-D E-box helix
 CC -loop-helix protein. This sequence is used to describe a method resulting
 CC in the isolation of a cdc25B gene promoter. Identification of cdc25B
 CC promoters comprising labelling the promoter (preferably radioactively)
 CC and using it to screen genomic DNA libraries (preferably of mammalian
 CC cells) by hybridisation under stringent conditions. Isolation of the
 CC murine cdc25B promoter comprises screening a murine genomic phage library
 CC obtained from mouse strain 129FVJ with a probe comprising part of the
 CC promoter. Constructs containing this promoter can be used to produce a
 CC medicament for treating tumour diseases, leukaemia, autoimmune diseases,
 CC allergies, arthritis, inflammations, organ rejection, graft-versus-host
 CC reactions, blood clotting disorders, circulatory disorders, anaemia,
 CC infections, hormonal disorders and/or CNS damage. (Updated on 17-OCT-2003
 CC to standardise OS field)
 XX
 SQ Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
 XX

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1734 GGCTCCCAACTCTCTCC 1749
 DB ||||| ||||| |||
 17 GCCTCCCAACACTGC 2

RESULT 645
 AAV43831/c
 ID AAV43831 standard; DNA; 17 BP.
 XX
 AC AAV43831;
 XX
 DT 22-OCT-1998 (first entry)
 DT
 XX
 DE Artificial promoter sequence 1 to be used as an activator sequence.
 XX
 XX E2F; CDF-1; chimeric promoter module; B-myb promoter; cdc25C promoter;
 KW tumour; leukaemia; cardiovascular disease; psoriatic disease; allergy;
 KW arthritis; inflammatory reaction; auto-immune disease; CNS damage;
 KW transplanted organ rejection; infectious disease; CDE-CHR motif;
 KW blood clotting disorder; chronic viral infection; ss.
 XX
 OS Synthetic.
 XX
 PN EP859008-A2.
 XX
 PD 19-AUG-1998.
 PD
 XX 18-FEB-1998; 98EP-00102812.
 PF
 XX 18-FEB-1997; 97EP-00102547.
 PR
 XX

PA (FARH) HOECHST AG.
 XX
 PI Mueller R, Liu N, Zwicker J, Sedlacek H;
 XX
 DR WPI; 1998-429649/37.
 XX
 XX New nucleic acid construct comprises activator, chimeric promoter which
 PT binds to E2F and CDF-1 proteins and structural gene - used to treat e.g.
 PT tumours, leukaemia, cardiovascular diseases, inflammatory reactions and
 PT auto-immune disorders.
 XX
 XX Disclosure; Page 11; 21pp; English.
 PS
 XX This represents an artificial promoter sequence that can be used as an
 CC activator sequence in the nucleic acid construct of the invention. The
 CC construct comprises at least one activator sequence, at least one
 CC chimeric promoter module comprising a nucleotide sequence which binds a
 CC protein of the E2F family and a protein of the CDF-1 family and at least
 CC one structural gene, where the chimeric promoter module causes an up-
 CC regulation of gene expression in the cell cycle later than the B-myb
 CC promoter but earlier than the cdc25C promoter. The nucleic acid construct
 CC or a vector comprising such a nucleic acid construct can be used for the
 CC treatment of tumours, leukaemia, cardiovascular diseases, inflammatory
 CC reactions, auto-immune diseases, allergies, arthritis, psoriatic
 CC diseases, impending rejection of a transplanted organ, CNS damage,
 CC infectious disease, blood clotting disorders and chronic viral
 CC infections. A CDF-1 protein obtained by preparing a nuclear extract from
 CC HeLa cells and purifying by affinity chromatography in the presence of an
 CC oligonucleotide containing a CDE-CHR sequence motif can be used to
 CC identify inhibitors or stimulators of CDF-1
 XX
 XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1734 GGCTCCCAACTCTCC 1749
 DB 17 GCCTCCCAACACTGTC 2
 RESULT 646
 AAV44681/C
 ID AAV44681 standard; DNA; 17 BP.
 XX
 AC AAV44681;
 XX
 XX 25-MAR-2003 (revised)
 DT 21-OCT-1998 (first entry)
 XX
 DE Bromocontryphan-specific probe.
 XX
 KW bromo-tryptophan; conopeptide; antihelminthic; hypnotic; anticonvulsant;
 KW neuroprotective; anaesthesia; epilepsy; N-methyl-D-aspartate receptor;
 KW 5HT3 serotonin receptor; bromocontryphan; probe; primer; PCR; ss.
 XX
 OS Synthetic.
 OS Conus radiatus.
 XX
 XX WO9831705-A1.
 FN
 XX 23-JUL-1998.
 PD
 XX 16-JAN-1998; 98WO-US000851.
 PF
 XX 17-JAN-1997; 97US-00785534.
 PR
 XX (UTAH) UNIV UTAH RES FOUND.
 PA (SALK) SALK INST.
 PA (REGC) UNIV CALIFORNIA.
 XX
 XX Cruz LJ, Olivera BM, McIntosh JM, Jimenez E, Craig AG, Rivier JA;

PI Julius D, England L;
 XX
 DR WPI; 1998-414034/35.
 XX
 XX New conopeptide(s) containing bromo-tryptophan residue - useful as
 PT antihelminthic, anti-emetic, hypnotic, anticonvulsant and neuro:protective
 PT agents, and as adjuncts to anaesthesia.
 XX
 PS Example 1; Page 18; 64pp; English.
 XX
 XX The invention relates to bromo-tryptophan conopeptides which are useful
 CC as anti-helminthics, anti-emetics, hypnotics, anticonvulsants, neuro-
 CC protective agents and adjuncts for anaesthesia, especially for treating
 CC epilepsy; for reducing neurotoxic injury caused by hypoxia, anoxia or
 CC ischaemia (of any origin); for treating Alzheimer's, Huntington's or
 CC Parkinson's diseases, Down's syndrome, amyotrophic lateral sclerosis,
 CC AIDS-related dementia, chemical toxicity etc.; also for control of pain
 CC and for treatment or prevention of migraine. Some of these peptides act
 CC by antagonising the N-methyl-D-aspartate receptor, others bind to the
 CC 5HT3 serotonin receptor. The present sequence represents a bromo-
 CC contryphan-specific probe. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 17 BP; 3 A; 8 C; 2 G; 1 T; 0 U; 3 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 76.9%; Pred. No. 5.2e+02;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1673 GGAACTCTGGTGT 1685
 DB 15 GGARCCNTGGTGY 3
 RESULT 647
 AAV42344/C
 ID AAV42344 standard; DNA; 17 BP.
 XX
 AC AAV42344;
 XX
 XX 25-MAR-2003 (revised)
 DT 25-SEP-1998 (first entry)
 XX
 DE E box nucleotide sequence.
 XX
 KW Activation sequence; structural gene; transcription factor protein;
 KW prevention; ameliorate; disease; ss.
 XX
 OS Synthetic.
 XX
 XX EP848061-A2.
 FN
 XX 17-JUN-1998.
 PD
 XX 10-DEC-1997; 97EP-00121752.
 PF
 XX 11-DEC-1996; 96DE-01051443.
 PR
 XX (FARH) HOECHST AG.
 PA
 XX Mueller R, Sedlacek H;
 PI
 XX WPI; 1998-314476/28.
 DR
 XX Self-enhancing nucleic acid construct - containing transcription factor
 PT coding sequence and binding site.
 PT
 XX Disclosure; Page 15; 56pp; English.
 PS
 XX The present sequence represents an E box sequence. The sequence is used
 CC to exemplify the invention. The specification describes a nucleic acid
 CC construct which comprises at least one structural gene that encodes an
 CC active compound, at least one structural gene that encodes a
 CC transcription factor protein and at least one activation sequence that

CC contains a sequence that binds the transcription factor protein and one
 CC promoter sequence. Each activation sequence activates the expression of a
 CC structural gene and the expression of the transcription factor protein.
 CC The construct is used to prevent or ameliorate disease. (Updated on 25-
 CC MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI
 CC field.)

XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1734 GCTCCGCACTCTCTCC 1749
 DB 17 GCTCCCAACACCTGC 2
 |||||

RESULT 648
 AAV80328
 ID AAV80328 standard; DNA; 17 BP.
 XX
 AC AAV80328;
 XX
 DT 29-MAR-1999 (first entry)
 XX
 DE Phage lambda PCR primer OMS178.
 XX
 KW RCE1; hrCE1; hrCE1p; CAAX processing enzyme; human; tumour; cancer;
 KW therapy; diagnosis; Ras protein; endoproteinase; PCR; primer; ss.
 XX
 OS Synthetic.
 OS Bacteriophage lambda.
 XX
 PN WO9854333-A2.
 XX
 PD 03-DEC-1998.
 XX
 PF 02-JUN-1998; 98WO-US011415.
 XX
 PR 02-JUN-1997; 97US-00047369.
 PR 14-JUL-1997; 97US-0052389P.
 XX
 PA (ACAC-) ACACIA BIOSCIENCES INC.

XX Ashby MN, Dimster-Denk DG, Phillips JW;
 XX WPI; 1999-059843/05.
 XX New DNA encoding mammalian CAAX-processing enzymes - used e.g. to treat
 PT CAAX-protein mediated diseases such as cancers and tumours associated
 PT with mutant Ras.
 XX
 PS Example 1; Page 54; 98pp; English.
 XX
 CC This is the nucleotide sequence of lambda phage primer OMS178. It was
 CC used with primers (see AAV80326-28) specific for human hrCE1 cDNA (see
 CC AAV80322) in the PCR amplification of hrCE1 lambda clones. The invention
 CC relates to new mammalian CAAX-processing enzymes, including hrCE1 protein
 CC (see AAV86009), a human functional homologue of yeast Rce1 protein, and
 CC nucleic acids encoding them. The new mammalian DNA and CAAX processing
 CC proteins represent potential targets for blocking the oncogenic action of
 CC mutant Ras protein in tumours or for modulating the activity of
 CC prenylated peripheral membrane proteins

XX Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1634 TGGGGCTTGTAGCAGA 1649
 |||||

Db 1 TGGCGCAGGTAGCAGA 16
 RESULT 649
 AAA20626/c
 ID AAA20626 standard; RNA; 17 BP.
 XX
 AC AAA20626;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:3852.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antiporiatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US006507.
 XX
 PR 27-MAR-1998; 98US-0079678P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Favco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability
 of an mRNA encoding an angiogenic factors.

Claim 55; Page 157; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA24222 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3

SQ Sequence 17 BP; 4 A; 7 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

```
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1704 AGTTGGTTAGGAGTA 1719
DB 17 AGCGGGTTAGCACTA 2

RESULT 650
AA18708
ID AAA18708 standard; RNA; 17 BP.
XX
AC AAA18708;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:1934.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
PS Claim 56; Page 112; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tubercous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC
```

```
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 2 A; 6 C; 3 G; 0 T; 6 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGAACCT 1680
DB 1 UCACUGCUGGACCCU 16

RESULT 651
AA18921/C
ID AAA18921 standard; RNA; 17 BP.
XX
AC AAA18921;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:2147.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
PS Claim 56; Page 125; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
```

CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1685 TCTCTCCAGCGTGGT 1700
 Db 16 TCTCATAAAGCGTGGT 1
 RESULT 652
 AAV91363/c
 ID AAV91363 standard; RNA; 17 BP.
 XX
 AC AAV91363;
 XX
 DT 18-FEB-1999 (first entry)
 DE Human C-raf target site nucleotide position 2735.
 XX
 KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9850530-A2.
 XX
 PD 12-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-US009249.
 XX
 PR 09-MAY-1997; 97US-0046059P.
 PR 09-JUN-1997; 97US-0049002P.
 PR 03-JUL-1997; 97US-0051718P.
 PR 22-AUG-1997; 97US-0056808P.
 PR 02-OCT-1997; 97US-0061321P.
 PR 02-OCT-1997; 97US-0061324P.
 PR 05-NOV-1997; 97US-0064866P.
 PR 19-DEC-1997; 97US-0068212P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX
 DR WPI; 1999-009494/01.
 XX
 XX Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer,
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 PT used as antiviral agents and synthons.
 XX
 PS Claim 177; Page 153; 259pp; English.
 XX
 CC A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with

CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1690 TCCAGCGTGGTGAAG 1705
 Db 17 TTCAGCATGATGAAG 2
 RESULT 653
 AAV92631
 ID AAV92631 standard; RNA; 17 BP.
 XX
 AC AAV92631;
 XX
 DT 18-FEB-1999 (first entry)
 DE Human A-Raf substrate position 2214.
 XX
 KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9850530-A2.
 XX
 PD 12-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-US009249.
 XX
 PR 09-MAY-1997; 97US-0046059P.
 PR 09-JUN-1997; 97US-0049002P.
 PR 03-JUL-1997; 97US-0051718P.
 PR 22-AUG-1997; 97US-0056808P.
 PR 02-OCT-1997; 97US-0061321P.
 PR 02-OCT-1997; 97US-0061324P.
 PR 05-NOV-1997; 97US-0064866P.
 PR 19-DEC-1997; 97US-0068212P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX
 DR WPI; 1999-009494/01.
 XX
 XX Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer,
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 PT used as antiviral agents and synthons.
 XX
 PS Claim 177; Page 161; 259pp; English.
 XX
 CC A method has been developed for the identification of a nucleic acid

capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-rat RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-rat. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene

Sequence 17 BP; 1 A; 10 C; 1 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 5.2e+02;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1678 CCTGGTGTCTCTCCA 1693
|| :||:||||
Db 1 CCCCUGUCUCCUCCA 16

RESULT 654
AAV91075
ID AAV91075 standard; RNA; 17 BP.
XX
AC AAV91075;
DT 18-FEB-1999 (first entry)
XX
DE Human C-rat target site nucleotide position 884.
XX
KW Human; c-rat; A-rat; B-rat; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN W03850530-A2.
XX
PD 12-NOV-1998.
XX
PF 05-MAY-1998; 98WO-US009249.
XX
PR 09-MAY-1997; 97US-0046059P.
PR 09-JUN-1997; 97US-0049002P.
PR 03-JUL-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI Parry T, Beigelman L, Mcswigen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
DR WPI; 1999-009494/01.
XX
PT Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,

restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.

Claim 177; Page 148; 259pp; English.

A method has been developed for the identification of a nucleic acid capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-rat RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-rat. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene

Sequence 17 BP; 2 A; 8 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1747 TCCCTATCCTAAAGGC 1762
:||||:||||
Db 2 UCCCUUCCUCCAGGC 17

RESULT 655
AAV88523/c
ID AAV88523 standard; DNA; 17 BP.
XX
AC AAV88523;
XX
DT 13-SEP-1999 (first entry)
XX
DE Conus radiatus contryphan PCR primer DHOG 550.
XX
KW Contryphan; leu-tryphan; anticonvulsant; neuroprotective; venom;
KW cone snail; neurodegenerative disorder; epilepsy; neurotoxic injury;
KW hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident;
KW brain trauma; spinal cord trauma; myocardial infarct; physical trauma;
KW drowning; suffocation; perinatal asphyxia; hypoglycaemia; migraine;
KW senile dementia; Alzheimer's disease; amyotrophic lateral sclerosis;
KW Parkinson's disease; Huntington's disease; Down's syndrome; PCR primer;
KW Korsakoff's disease; schizophrenia; neuronal damage; seizure; ss.
XX
OS Synthetic.
OS Conus radiatus.
XX
PN W09933865-A1.
XX
PD 08-JUL-1999.
XX
PF 16-DEC-1998; 98WO-US026789.
XX
PR 24-DEC-1997; 97US-0068737P.
PR 16-APR-1998; 98US-00061026.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Jacobsen R, Jimenez E, Cruz LJ, Olivera BM, Gray WR, Grilley M;
PI Watkins M, Hillyard DR;
XX
DR WPI; 1999-419087/35.

XX PT New pure contryphan peptides.
 XX PS Example 4; Page 22; 48pp; English.
 XX CC The present sequence represents a PCR primer for a contryphan
 CC peptide sequence. Contryphan peptides are found in the venom of cone
 CC snails. The contryphan peptides are useful as anticonvulsant agents, as
 CC neuroprotective agents, for managing pain, and for treating
 CC neurodegenerative disorders, especially those resulting from an
 CC overstimulation of excitatory amino acid receptors. The contryphan are
 CC useful for the treatment and alleviation of epilepsy and as a general
 CC anticonvulsant agent. The contryphan are also useful to reduce
 CC neurotoxic injury associated with conditions of hypoxia, anoxia, or
 CC ischaemia which typically follows stroke, cerebrovascular accident, brain
 CC or spinal chord trauma, myocardial infarct, physical trauma, drownings,
 CC suffocation, perinatal asphyxia, or hypoglycaemic events. The contryphan
 CC are further useful for the treatment of Alzheimer's disease, senile
 CC dementia, amyotrophic lateral sclerosis, Parkinson's disease,
 CC Huntington's disease, Down's syndrome, Korsakoff's disease,
 CC schizophrenia, AIDS dementia, multi-infarct dementia, and neuronal damage
 CC associated with uncontrolled seizures. The contryphan are further useful
 CC in controlling pain and are effective in the treatment of migraine. They
 CC can be used prophylactically or to relieve the symptoms associated with a
 CC migraine episode
 XX CC
 SQ Sequence 17 BP; 3 A; 8 C; 2 G; 1 T; 0 U; 3 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 76.9%; Pred. No. 5.2e+02;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1673 GGAACTCGTGT 1685
 DB 15 GGARCCGTGTG 3
 RESULT 656
 AAX32865/C
 ID AAX32865 standard; DNA; 17 BP.
 XX AC AAX32865;
 XX DT 27-AUG-2003 (revised)
 XX DT 20-MAR-2003 (revised)
 XX DT 28-JUN-1999 (first entry)
 XX DE HBV pre-S gene promoter fragment binding TFO B4.
 XX KW Triplex-forming oligonucleotide; TFO; promoter region; pre-S gene;
 XX KW inhibition; hepatitis B virus; HBV adr subtype; DR region; ss.
 XX OS Synthetic.
 XX OS Hepatitis B virus.
 XX FH Key Location/Qualifiers
 XX FT misc_feature 17
 XX FT /tag= a
 XX FT /note= "optional monophosphorylation (claim 2)"
 XX PN W09920641-A1.
 XX PD 29-APR-1999.
 XX PF 19-OCT-1998; 98WO-CN000248.
 XX PR 21-OCT-1997; 97CN-00106667.
 XX PA (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
 XX PI Lu C;
 XX DR WPI; 1999-288270/27.

XX PT Triplex-forming oligonucleotides, useful for, e.g. inhibition of
 XX PT hepatitis B virus (HBV).
 XX PS Claim 1, 2; Page 22; 39pp; Chinese.
 XX CC The invention provides triplex-forming oligonucleotides (TFO) and their
 CC modified derivatives. TFO B1-B5 (AAX32862-866) can bind with the promoter
 CC region of pre-S gene in inhibition of hepatitis B virus (HBV) adr subtype
 CC and TFO B11, B12 and B15 (AAX32868-870) can bind with DR region of HBV.
 CC The oligonucleotides are useful for inhibition of HBV and as drug in
 CC treatment of hepatitis B. Since the length of the oligonucleotides can be
 CC suitably increased, the stability and specificity of the formed triplex
 CC DNA with 2 similar homopoly purine/homopoly pyrimidine fragments are
 CC higher. Triplex formation is specifically targeting on the HBV gene
 CC expression, DNA replication and reproduction, or to produce (DNA)2:RNA
 CC hybrid triplex with target sequence of RNA in stopping RNA reverse
 CC transcription, so there is little effect on the human cells. Such
 CC oligonucleotides are chemically modified by 3'-terminal
 CC monophosphorylation, leading to more significant inhibition due to their
 CC higher stability, and the degradation products of the modified
 CC oligonucleotides are not toxic to the body. (Updated on 20-MAR-2003 to
 CC correct DR field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX CC
 SQ Sequence 17 BP; 6 A; 0 C; 11 G; 0 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1736 CTCCTCCCTCTCTCTCT 1751
 DB 16 CTCCTCTCTCTCTCTCT 1
 RESULT 657
 AAX76849/C
 ID AAX76849 standard; DNA; 17 BP.
 XX AC AAX76849;
 XX DT 05-AUG-1999 (first entry)
 XX DE PCR primer for T66Bk gene.
 XX KW Transcription unit; MARK2 kinase; rsk3 kinase; regulatory region; T66Bk;
 XX KW contraceptive; Responder/Distorter signalling cascade; t-Responder;
 XX KW PCR primer; ss.
 XX OS Synthetic.
 XX OS Mus sp.
 XX PN W09925815-A2.
 XX PD 27-MAY-1999.
 XX PF 18-NOV-1998; 98WO-BPC07395.
 XX PR 18-NOV-1997; 97EP-00120190.
 XX PR 02-MAR-1998; 98EP-00103596.
 XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX PI Herrmann B, Koschorz E, Kispert A;
 XX DR WPI; 1999-347466/29.
 XX PT Nucleic acids involved in the Responder phenotype in mice.
 XX PS Example 7; Page 58; 117pp; English.
 XX CC This sequence is a PCR primer for the T66Bk gene. The invention related
 CC to a nucleic acid molecule (I) comprising a transcription unit encoding

CC in its 5' portion a kinase having a homology to MARK2 kinase and the 3'
 CC portion of the nucleotide sequence has a high homology to RSK3 kinase.
 CC Sperm produced by transgenic creatures containing (I) are useful for
 CC production of offspring. T66BK, its regulatory region, recombinant DNA,
 CC vectors, host cells, antibodies, etc., are useful for the isolation of
 CC receptors on the surface of sperm recognising attractants of the egg cell
 CC for the development and/or production of contraceptives. They can also be
 CC used to identify chemicals or biological compounds able to trigger the
 CC (premature) activation or inhibition of the Responder/Distorter
 CC signalling cascade, or to identify and isolate receptors and other
 CC members of the cascade that bind the expression products. The methods for
 CC detecting the sperm of the transgenic animal, and selecting against (I)
 CC also provide a means for distorting the transmission ratio of genetic
 CC traits by altering genes of the Responder/Distorter signal cascade other
 CC than the t-Responder. They also allow distortion, to a non-Mendelian
 CC ratio, of the transmission of a genetic trait, i.e. determination of sex,
 CC from male mammals to their offspring by expressing during
 CC spermatogenesis/spermiogenesis a gene involved in sperm motility and/or
 CC fertilisation. The genes and proteins involved in the responder phenotype
 CC and Responder/Distorter signalling cascade, as well as the inventive
 CC methods are advantageous in breeding strategies by allowing for specific
 CC selection of genetic traits and in particular, of sex

XX
 SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1690 TCCAGCCTGTGTGAAG 1705
 ||||| |||||
 Db 16 TCCAGCCAGGGGAAG 1

RESULT 658
 AAX77880/c
 ID AAX77880 standard; DNA; 17 BP.
 AC AAX77880;
 XX
 XX 13-AUG-1999 (first entry)
 DE HLH protein DNA binding motif.
 XX
 KW Activation sequence; transcription factor; murine; p163; p27; treatment;
 KW binding protein; DNA binding domain; effector gene; disease; infection;
 KW tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;
 KW transplant rejection; graft-versus-host disease; circulatory disorder;
 KW blood clot; anaemia; hormonal disorder; CNS injury; HLH protein; ss.
 XX
 OS Unidentified.
 XX
 XX EP926237-A2.
 PD 30-JUN-1999.
 XX
 XX 12-DEC-1998; 98EP-00123709.
 XX
 XX 20-DEC-1997; 97DE-01056975.
 XX
 XX (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 PA
 PI Eilers M, Buerger A, Sedlacek H;
 XX
 XX WPI; 1999-349238/30.
 DR
 XX
 XX New nucleic acid construct comprising promoter, transcription factor
 PT gene, activation sequence and effector gene - useful for gene therapy
 PT treatment of allergies, inflammation, transplant disorders and leukaemia..
 PT
 XX
 XX Disclosure; Page 15; 90pp; German.
 PS
 XX
 CC This invention describes a novel nucleic acid construct comprising the

CC following components (a) an activation sequence for the transcription of
 CC component b, (b) component b which is constructed from component b1 (a
 CC transcription factor activating domain), component b2 (murine p163 or p27
 CC binding protein) and component b3 (a transcription factor DNA binding
 CC domain), (c) an activation sequence which is activated by binding of the
 CC expression product of component (b) and which induces transcription of
 CC component (d) and (d) an effector gene. The construct, preferably in a
 CC plasmid or viral vector, or cell can be used to treat a disease selected
 CC from infections, tumours, leukaemia, autoimmune diseases, allergies,
 CC arthritis, inflammations, transplant rejection, graft-versus-host
 CC disease, blood clotting disorders, circulatory disorders, anaemia,
 CC hormonal disorders and CNS injuries. This sequence represents the DNA
 CC binding motif of the HLH protein which is used to describe the method of
 CC the invention

XX
 SQ Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1734 GGCTCCCAACTCCTCC 1749
 ||||| |||||
 Db 17 GCCTCCCAACACTCC 2

RESULT 659
 AAZ23521/c
 ID AAZ23521 standard; DNA; 17 BP.
 AC AAZ23521;
 XX
 XX 20-DEC-1999 (first entry)
 DE MyoD E box DNA motif.
 XX
 KW Antigen binding; single chain; variable domain; VH domain; light chain;
 KW heavy immunoglobulin chain; VL domain; anticancer; antiviral; tumor;
 KW antibacterial; antimalarial; antiinflammatory; treatment; prevention;
 KW diagnosis; vaccine; autoimmune disease; inflammation; blood disorder;
 KW transplant rejection; arthritis; nervous system disorder; infection;
 KW Myo D box; ss.
 XX
 OS Unidentified.
 XX
 XX DE19816141-A1.
 PN
 XX 14-OCT-1999.
 PD
 XX
 XX 09-APR-1998; 98DE-01016141.
 PF
 XX
 XX 09-APR-1998; 98DE-01016141.
 PR
 XX
 XX (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 PA
 PI Kontermann R, Sedlacek H, Mueller R;
 XX
 XX WPI; 1999-581511/50.
 DR
 XX
 XX New polyclonal binding agents containing variable heavy and light
 PT constructs connected via peptide linker, used for treatment, prevention
 PT or diagnosis of e.g. cancer.
 PT
 XX
 XX Disclosure; Page 13; 20pp; German.
 PS
 XX
 XX This sequence represents a novel single-chain molecule (I) that binds
 CC multiple antigens and comprises two variable domains of heavy
 CC immunoglobulin chains (VH), having specificities A and B and two variable
 CC domains of light chains (VL), also with specificities A and B. The
 CC domains are provided as two VH-VL constructs which are attached via a
 CC peptide (P). Any VH and VL may be replaced by their functional fragments.
 CC The products of the invention have anticancer, antiviral, antibacterial,
 CC antimalarial and antiinflammatory activity. (I) are used to treat,

CC prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases
 CC and inflammation (e.g. transplant rejection and arthritis), blood
 CC disorders (e.g. of the coagulation and/or circulatory systems, such as
 CC anemia, leucopenia, thrombocytopenia and hypertension), nervous system
 CC disorders and/or infections (by viruses or bacteria, or malaria),
 CC including, when (I) include a fusogenic peptide, use for gene transfer.
 CC (I) are produced simply and in predominantly homogeneous form, in a wide
 CC variety of hosts, either in secreted or membrane-bound forms. This
 CC sequence represents a MyoD E box DNA motif which is used to illustrate
 CC the method of the invention

XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GGCTCCCACTCTCTC 1749
 DB 17 GGCTCCCACTCTCTC 2

RESULT 660
 AAZ24146/C
 ID AAZ24146 standard; DNA; 17 BP.
 XX AC AAZ24146;
 XX 20-MAR-2003 (revised)
 DT 08-FEB-2000 (first entry)
 XX HLH protein E box (Myo D) DNA motif.
 XX Immunoglobulin; light chain; VL region; heavy chain; VH region;
 KW single-chain; antigen binding; variable domain; anticancer; treatment;
 KW antiviral; antibacterial; antimalarial; antiinflammatory; diagnosis;
 KW tumor vaccine; autoimmune disease; inflammation; blood disorder;
 KW nervous system; infection; HLH protein; Myo D; E box; ss.
 XX Unidentified.
 OS DE19827239-A1.
 PN 23-DEC-1999.
 PD 18-JUN-1998; 98DE-01027239.
 XX 09-APR-1998; 98DE-01016141.
 PR 18-JUN-1998; 98DE-01027239.
 XX (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 PA Kontermann R, Sedlacek H, Mueller R;
 PI WPI; 1999-591691/51.
 DR New polyspecific binding agents useful for treatment, prevention and
 PT diagnosis of cancer and autoimmune diseases comprises variable domains of
 PT heavy and light chains of immunoglobulins bound by a peptide.
 XX Disclosure; Page 15; 26pp; German.
 PS This invention describes a novel single-chain molecule (I) that binds
 CC multiple antigens and comprises two variable domains of heavy
 CC immunoglobulin chains (VH) and two variable domains of light chains (VL).
 CC The domains are provided as two VH-VL constructs which are attached via a
 CC peptide (P). Any VH and VL may be replaced by their functional fragments.
 CC The products of the invention have anticancer, antiviral, antibacterial,
 CC antimalarial, and antiinflammatory activity. (I) are used to treat,
 CC prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases
 CC and inflammation (e.g. transplant rejection and arthritis), blood
 CC disorders (e.g. of the coagulation and/or circulatory systems, such as
 CC anemia, leucopenia, thrombocytopenia and hypertension), nervous system

CC disorders and/or infections (by viruses or bacteria, or malaria),
 CC including, when (I) include a fusogenic peptide, use for gene transfer.
 CC This sequence represents an HLH protein E box (Myo D) DNA motif which is
 CC used to illustrate the method of the invention. NOTE: This specification
 CC is a treat as basic for CZ-9901215 in Derwent week 9951. (Updated on 20-
 CC MAR-2003 to correct DR field.)

XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GGCTCCCACTCTCTC 1749
 DB 17 GGCTCCCACTCTCTC 2

RESULT 661
 AAZ29110
 ID AAZ29110 standard; DNA; 17 BP.
 XX AC AAZ29110;
 XX 07-FEB-2000 (first entry)
 DT Antisense primer sequence, used for localisation of GFR alpha 3.
 DE Human Glial cell line-derived neurotrophic factor receptor; GFR alpha 3;
 KW antisense primer; hybridisation probe; mouse; localisation; product;
 KW adult tissue; foetal tissue; detection; peripheral nervous system;
 KW diagnosis; autonomic nervous system; disease; ss.
 XX Synthetic.
 OS Mus musculus.
 PN WO9949039-A2.
 XX 30-SEP-1999.
 PD 19-MAR-1999; 99WO-US006098.
 XX 23-MAR-1998; 98US-0079124P.
 PR 13-APR-1998; 98US-0081569P.
 XX (GETH) GENENTECH INC.
 PA De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;
 PI WPI; 2000-038358/03.
 DR New isolated GFR-alpha3 nucleic acid, used to develop products for
 PT treating diseases or conditions involving peripheral nervous system or
 PT autonomic nervous system.
 XX Example 5; Page 51; 112pp; English.
 PS The present DNA sequence is an antisense primer, that is used to generate
 CC a 378 bp hybridisation probe, from mouse GFR alpha 3. It is used as a
 CC probe, for the localisation of GFR alpha 3 in various foetal and adult
 CC human tissues. The GFR alpha 3 is used to develop products, that can be
 CC used for detection and diagnosis of diseases, involving peripheral or
 CC autonomic nervous system
 XX Sequence 17 BP; 3 A; 1 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1739 CCACCTCTCTCTCTCTC 1754
 DB 2 CCAGTCTCTCTCTCTC 17


```

RESULT 662
AAZ88531/C
ID AAZ88531 standard; DNA; 17 BP.
XX
XX
AC AAZ88531;
XX
XX
DT 27-APR-2000 (first entry)
XX
DE
DE MyoD E-box muscle-specific HLH protein DNA binding site.
XX
XX Promoter; antiinflammatory; cytostatic; antiarthritic; hormone;
XX antianemic; neuroprotective; antimicrobial; immunosuppressive; tumor;
XX anticoagulant; treatment; infection; leukemia; autoimmune disease;
XX allergy; arthritis; inflammation; organ rejection; transplant; anemia;
XX blood clotting disease; circulatory disease; MyoD E-box; HLH protein; ss.
XX
OS Unidentified.
XX
XX DE19831420-A1.
XX
XX 20-JAN-2000.
XX
XX 14-JUL-1998; 98DE-01031420.
XX
XX 14-JUL-1998; 98DE-01031420.
XX
XX (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
XX
XX Mueller R, Nettelbeck D, Sedlacek H;
XX
XX WPI; 2000-137953/13.
XX
XX Chimeric promoter constructs with binding sites for recombinant
XX transcription factors useful for producing agents to treat cancer,
XX inflammation, allergy and autoimmune diseases.
XX
XX Disclosure; Page 27; 52pp; German.
XX
XX This invention describes a novel nucleic acid construct (I) which
XX comprises: (1) a minimal promoter (II); (2) a DNA (III) encoding for a
XX minimal recombinant transactivator, comprising DNA coding for a DNA
XX binding domain and a transactivation domain; (3) a minimal DNA sequence
XX (IV) to bind the expression product of (III); (4) a minimal promoter (V)
XX which contains a CDE-CHR element or an E2F-BS-CHR element; and (5) a
XX minimal effector gene (VI). The products of the invention have
XX antimicrobial; immunosuppressive and anticoagulant activity. (I) and
XX (VII) are useful for the production of remedies for the prevention or
XX treatment of infections, tumors, leukemia, autoimmune disease, allergy,
XX arthritis, inflammation, organ rejection, transplants against host
XX reaction, blood clotting diseases, circulatory diseases, anemia, hormone
XX disease and central nervous system injury. This sequence represents the
XX MyoD E-box/muscle-specific HLH protein DNA binding site which is used in
XX the method of the invention
XX
XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1734 GGCTCCCAACTCTCC 1749
XX | ||||| |||
XX Db 17 GCCTCCCAACACTCTG 2
XX
XX RESULT 663
AAZ47108
ID AAZ47108 standard; DNA; 17 BP.
XX
XX
AC AAZ47108;
XX

```

```

PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX
DR WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX
PS Claim 77; Page 64; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 2 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCTCTCCCTAT 1753
DB ||||| ||||| ||
2 CCCAGCTCTCTCTCAT 17

RESULT 665
AAF02991/C
ID AAF02991 standard; DNA; 17 BP.
XX
XX AAF02991;
AC
XX
XX 16-FEB-2001 (first entry)
DT
XX
DE Hammerhead ribozyme substrate #1286.
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
OS
XX WO200061729-A2.
PN
XX 19-OCT-2000.
PD
XX
XX 11-APR-2000; 2000WO-US009721.
PF
XX
XX 12-APR-1999; 99US-0129390P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
PI
XX WPI; 2000-647423/62.
DR
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
PT
XX
XX Claim 37; Page 85; 164pp; English.
PS
XX
XX The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
XX Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1647 AGAGGCAAGCACCAG 1662
DB ||||| ||||| ||
16 AGCAGGCAAGGCCAG 1

RESULT 666
AAF01814/C
ID AAF01814 standard; DNA; 17 BP.
XX
XX AAF01814;
AC
XX
XX 16-FEB-2001 (first entry)
DT
XX
XX Hammerhead ribozyme substrate #109.
DE
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
OS
XX WO200061729-A2.
PN
XX 19-OCT-2000.
PD
XX
XX 11-APR-2000; 2000WO-US009721.
PF
XX
XX 12-APR-1999; 99US-0129390P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
PI
XX WPI; 2000-647423/62.
DR
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
PT
XX
XX Claim 37; Page 58; 164pp; English.
PS
XX
XX The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
XX Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
SQ

```

CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 QQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1638 GCTGTAGCAGAGGC 1653
 Db 17 GCTGTAGTAGAGGCC 2
 RESULT 667
 ABK00575
 ID ABK00575 standard; RNA; 17 BP.
 XX
 AC ABK00575;
 XX
 DT 12-MAR-2002 (first entry)
 DE Human NOGO Hammerhead Ribozyme #575.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200159103-A2.
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWTIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 DR
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 75; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targetting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a hammerhead ribozyme of the invention
 XX
 SQ Sequence 17 BP; 5 A; 1 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 56.2%; Pred. No. 5.2e+02;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1704 AGTTGGGTTAGGAGTA 1719
 Db 2 AGUUGGUUCAGAGUA 17

RESULT 668
 ABK03212/C
 ID ABK03212 standard; RNA; 17 BP.
 XX
 AC ABK03212;
 XX
 DT 12-MAR-2002 (first entry)
 DE Human CD20 Inozyme #163.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 DR
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX Claim 30; Page 148; 200pp; English.
 PS
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberyzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention
 XX
 SQ Sequence 17 BP; 5 A; 7 C; 3 G; 0 T; 2 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1706 TTGGGTTAGGATACG 1721
 Db ||||| ||||| |||||
 17 TTGGGTTGGACGACG 2
 RESULT 669
 ABK03213/C
 ID ABK03213 standard; RNA; 17 BP.
 XX
 AC ABK03213;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human CD20 Inozyme #164.
 XX
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyzyme; zynzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200159103-A2.
 PN
 XX 16-AUG-2001.
 PD
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 PF
 XX 11-FEB-2000; 2000US-0181797P.
 PR
 PR 28-FEB-2000; 2000US-0185516P.
 PR
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 XX
 DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 XX constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 PT
 XX
 PS Claim 30; Page 148; 200pp; English.
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberyzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention
 XX
 SQ Sequence 17 BP; 5 A; 7 C; 3 G; 0 T; 2 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1706 TTGGGTTAGGATACG 1721
 Db ||||| ||||| |||||
 17 TTGGGTTGGACGACG 2
 RESULT 669
 ABK03213/C
 ID ABK03213 standard; RNA; 17 BP.
 XX
 AC ABK03213;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human CD20 Inozyme #164.
 XX
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyzyme; zynzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

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Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1706 TTGGTTAGGATAGC 1721
DB 16 TTGGGCTCGGAGCAG 1
RESULT 670
ABK02836/c
ID ABK02836 standard; RNA; 17 BP.
XX
AC ABK02836;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human CD20 Hammerhead ribozyme #135.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX
DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 30; Page 142; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg2+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
```

```
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg2+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a hammerhead ribozyme of the invention
SQ Sequence 17 BP; 1 A; 5 C; 3 G; 0 T; 8 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1647 AGAAGGCAAGCACCAG 1662
DB 17 AGAAGGCAAGATCAG 2
RESULT 671
ABK01446
ID ABK01446 standard; RNA; 17 BP.
XX
AC ABK01446;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human NOGO Inozyme #716.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX
DR
```


RESULT 673
 ABA78857/C
 ID ABA78857 standard; DNA; 17 BP.
 XX
 AC ABA78857;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE APC mutation correcting oligonucleotide SEQ ID NO: 1703.
 XX
 DE Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytosolic; antitickling; antianaemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US009761.
 XX
 PF 27-MAR-2000; 2000US-0192176P.
 PR 27-MAR-2000; 2000US-0192179P.
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 PI Kmiec EB, Gamper HB, Rice MC;
 XX
 PI WPI; 2001-639230/73.
 XX
 DR Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification.
 XX
 PS Claim 7; Page 145; 294pp; English.
 XX
 CC The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1674 GAACCCCTGGTCTCC 1689
 Db 16 GAACCCCTGGTCTGC 1

RESULT 674
 ABA78858
 ID ABA78858 standard; DNA; 17 BP.
 XX
 AC ABA78858;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE APC mutation correcting oligonucleotide SEQ ID NO: 1704.
 XX
 DE Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytosolic; antitickling; antianaemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US009761.
 XX
 PF 27-MAR-2000; 2000US-0192176P.
 PR 27-MAR-2000; 2000US-0192179P.
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 PI Kmiec EB, Gamper HB, Rice MC;
 XX
 PI WPI; 2001-639230/73.
 XX
 DR Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification.
 XX
 PS Claim 7; Page 145; 294pp; English.
 XX
 CC The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1674 GAACCCCTGGTCTCC 1689
 Db 2 GAACCCCTGGTCTGC 17

AAFI6612/c
ID AAFI6612 standard; DNA; 17 BP.
XX
AC AAFI6612;
XX
DT 13-MAR-2001 (first entry)
XX
DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 99.
XX
KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
XX
PN WO200071164-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-AU000498.
XX
PR 24-MAY-1999; 99AU-00000510.
XX
PA (TACH/) TACHAS G.
XX
PI Tachas G;
XX
XX WPI; 2001-025093/03.
XX
PT Treating gastric acid disturbance by administering an oligonucleotide
PT which modulates the activity of a polypeptide involved in gastric acid
PT production or secretion.
XX
PS Example 3; Page 149; 164pp; English.
XX
CC The present invention provides oligonucleotides, and methods for their
CC use, which are useful in modulating the action of proteins involved in
CC gastric acid production. The target protein is preferably the histamine
CC H2 receptor or one of the proteins which form part of the gastric proton
CC pump. The sequences and methods of the invention are useful in the
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC duodenal ulcers and other gastric acid disturbances, most of which are
CC caused by Helicobacter pylori
XX
SQ Sequence 17 BP; 5 A; 0 C; 11 G; 1 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1736 CTCCCAACTCTCCTCCT 1751
Db 17 CTCCCTCTCACTCCT 2
RESULT 677
ABL46487/c
ID ABL46487 standard; RNA; 17 BP.
XX
AC ABL46487;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human GRID hammerhead ribozyme substrate oligonucleotide #120.
XX
KW Human; Grb2-related with Insert Domain; GRID; T-cell;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200162911-A2.
XX

RESULT 675
AAH24608
ID AAH24608 standard; DNA; 17 BP.
XX
AC AAH24608;
XX
DT 07-AUG-2001 (first entry)
XX
DE Human endometrium cDNA clone 18-4-SP6 PCR primer #2.
XX
KW Human; endometrium; gynaecological; cytostatic; gene therapy;
KW peptide therapy; endometriosis; gene expression; drug screening;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200132920-A2.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-GB004228.
XX
PR 03-NOV-1999; 99GB-00026074.
PR 03-NOV-1999; 99GB-00026076.
PR 03-NOV-1999; 99GB-00026079.
PR 03-NOV-1999; 99GB-00026081.
XX
PA (MEIR-) METRIS THERAPEUTICS LTD.
XX
PI Pappa H, Lnenicek M;
XX
DR WPI; 2001-328804/34.
XX
XX Screening for a gene or gene product associated with endometriosis, for
XX diagnosing or treating endometriosis, comprises selecting a gene whose
XX level of expression differs between healthy and diseased endometrium
XX tissues.
XX
XX Example; Fig 3; 106pp; English.
XX
CC The invention relates to a method for screening for a gene or gene
CC product associated with endometriosis. The method comprises comparing the
CC pattern of gene expression in a diseased endometrium tissue from a
CC patient suffering from endometriosis to the pattern of gene expression in
CC healthy endometrium tissue from the same patient, and selecting a gene
CC whose level of expression differs between healthy and diseased tissues.
CC The gene, gene product and their antagonists and agonists are useful in
CC the manufacture of a medicament for diagnosing or treating endometriosis.
CC The method is useful for screening genes or gene products that are
CC implicated in endometriosis. It is particularly useful in diagnosing
CC endometriosis, as well as for screening for agents for treating
CC endometriosis. Prior methods of diagnosing endometriosis are more
CC difficult to perform and are more expensive, normally involving surgery.
CC The present method allows the disease to be diagnosed and treated at
CC earlier stage. The present sequence is a primer used in a reverse
CC transcription polymerase chain reaction (RT-PCR) procedure to validate
CC the results of differential gene expression studies. It was used to
CC amplify human endometrium cDNA encoding stromelysin
XX
SQ Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1647 AGAAGGCAAGCAGCAG 1662
Db 2 AGAAGGCATGGCCAG 17
RESULT 676

30-AUG-2001.

23-FEB-2001; 2001WO-US005957.

24-FEB-2000; 2000US-0184594P.

(RIBO-) RIBOZYME PHARM INC.

(GLAX) GLAXO GROUP LTD.

Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;

WPI; 2001-550088/61.

New nucleic acid(s) for regulating the Grb2-related with Insert Domain (GRID) gene comprises using antisense and enzymatic nucleic acid molecules such as hammerhead ribozymes.

Claim 4; Page 61; 108pp; English.

The present invention relates to oligonucleotides that downregulate the expression of human Grb2-related with Insert Domain (GRID) gene. GRID is a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful for modulating the expression of GRID, to treat conditions such as tissue/graft rejection and leukaemia. The oligonucleotides can also be administered in conjunction with other therapies such as radiation, chemotherapy and cyclosporin treatment. The present oligonucleotide was used to illustrate the invention

Sequence 17 BP; 6 A; 6 C; 1 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1721 GGAGATGGAGATTGTC 1736

16 GGAGATGGAGATTGTC 1

RESULT 678

ABL46970/C

ID ABL46970 standard; RNA; 17 BP.

AC ABL46970;

27-JUN-2003 (first entry)

Human GRID zinzyme substrate oligonucleotide #54.

Human; Grb2-related with Insert Domain; GRID; T-cell;

co-stimulatory adaptor protein; tissue rejection; graft rejection;

leukaemia; cytostatic; ss.

Homo sapiens.

WO200162911-A2.

30-AUG-2001.

23-FEB-2001; 2001WO-US005957.

24-FEB-2000; 2000US-0184594P.

(RIBO-) RIBOZYME PHARM INC.

(GLAX) GLAXO GROUP LTD.

Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;

WPI; 2001-550088/61.

New nucleic acid(s) for regulating the Grb2-related with Insert Domain (GRID) gene comprises using antisense and enzymatic nucleic acid molecules such as hammerhead ribozymes.

Claim 4; Page 72; 108pp; English.

The present invention relates to oligonucleotides that downregulate the expression of human Grb2-related with Insert Domain (GRID) gene. GRID is a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful for modulating the expression of GRID, to treat conditions such as tissue/graft rejection and leukaemia. The oligonucleotides can also be administered in conjunction with other therapies such as radiation, chemotherapy and cyclosporin treatment. The present oligonucleotide was used to illustrate the invention

Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1753 TCCTAAGGCCCACTG 1768

17 TCCTAAGGCCCACTG 2

RESULT 679

ABL46776

ID ABL46776 standard; RNA; 17 BP.

AC ABL46776;

27-JUN-2003 (first entry)

Human GRID NCH ribozyme substrate oligonucleotide #230.

Human; Grb2-related with Insert Domain; GRID; T-cell;

co-stimulatory adaptor protein; tissue rejection; graft rejection;

leukaemia; cytostatic; ss.

Homo sapiens.

WO200162911-A2.

30-AUG-2001.

23-FEB-2001; 2001WO-US005957.

24-FEB-2000; 2000US-0184594P.

(RIBO-) RIBOZYME PHARM INC.

(GLAX) GLAXO GROUP LTD.

Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;

WPI; 2001-550088/61.

New nucleic acid(s) for regulating the Grb2-related with Insert Domain (GRID) gene comprises using antisense and enzymatic nucleic acid molecules such as hammerhead ribozymes.

Claim 4; Page 67; 108pp; English.

The present invention relates to oligonucleotides that downregulate the expression of human Grb2-related with Insert Domain (GRID) gene. GRID is a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful for modulating the expression of GRID, to treat conditions such as tissue/graft rejection and leukaemia. The oligonucleotides can also be administered in conjunction with other therapies such as radiation, chemotherapy and cyclosporin treatment. The present oligonucleotide was used to illustrate the invention

Sequence 17 BP; 3 A; 2 C; 7 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 56.2%; Pred. No. 5.2e+02;

Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1632 GATGGGCTGTAGCA 1647
 ||:|||| :||
 Db 2 GAUGGCAUGUGGCA 17

RESULT 680
 ABL46486/c
 ID ABL46486 standard; RNA; 17 BP.
 XX
 AC ABL46486;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID hammerhead ribozyme substrate oligonucleotide #119.
 XX
 DE Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Meswigen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 DR
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX
 PS Claim 4; Page 61; 108pp; English.
 XX
 CC The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 SQ Sequence 17 BP; 5 A; 6 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGGC 1736
 ||:||||| :||
 Db 17 GGAGATGGAAATTGTC 2

RESULT 681
 ABL92165
 ID ABL92165 standard; cDNA; 17 BP.
 XX
 AC ABL92165;
 XX
 DT 30-MAY-2002 (first entry)
 XX
 DE Long human Tumour Endothelial Marker SEQ ID NO 331.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210217-A2.
 XX
 PD 07-FEB-2002.
 XX
 DT 01-AUG-2001; 2001WO-US024031.
 PF
 XX
 PR 02-AUG-2000; 2000US-0222599P.
 PR 11-AUG-2000; 2000US-0224360P.
 PR 11-APR-2001; 2001US-0282850P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI St Croix B, Kinzler KW, Vogelstein B;
 XX WPI; 2002-291856/33.
 DR
 XX
 PT An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth.
 XX
 PS Disclosure; Page 22; 331pp; English.
 XX
 CC The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
 CC bearing a vascularised tumour, polycystic kidney disease, diabetic
 CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
 CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
 CC are disclosed, as are marker oligonucleotide sequences: tumour
 CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
 CC (PEM) ABL91903-ABL91995. The present sequence is that of an
 CC oligonucleotide marker useful to the invention
 XX
 SQ Sequence 17 BP; 2 A; 9 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1741 AACTCTCCCTATCCT 1756
 ||:||||| :||
 Db 2 ACCACTCCCTTCT 17

RESULT 682
 ABL10216
 ID ABL10216 standard; DNA; 17 BP.
 XX
 AC ABL10216;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10208.
 XX
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 OS
 XX

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PN WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US016981.
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 05-FEB-2001; 2001US-026860P.
XX (AEOM-) ABOmica INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 10208; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterize and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1750 CTATCCTAAAGGCCCA 1765
Db ||||| |||||
2 CTATCGGAGGCCCA 17
RESULT 683
ABN00537
ID ABN00537 standard; DNA; 17 BP.
XX
AC ABN00537;
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QY 1646 CAGAAGCAAGCACCA 1661
 DB 1 CAGATGACAGCATCA 16
 RESULT 684
 ABN01271/c
 ID ABN01271 standard; DNA; 17 BP.
 AC ABN01271;
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 XX 29-MAY-2002 (first entry)
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1263.
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 XX WO200192524-A2.
 XX 06-DEC-2001.
 XX 25-MAY-2001; 2001WO-US016981.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX (AEOM-) AEOMICA INC.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX Disclosure; SEQ ID NO 1263; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 3 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1730 GATTGGCTCCCACTC 1745
 DB 17 GATCGTCCCCCACTC 2
 RESULT 685
 ABN01293/c
 ID ABN01293 standard; DNA; 17 BP.
 XX
 AC ABN01293;
 XX
 XX 29-MAY-2002 (first entry)
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1285.
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 XX WO200192524-A2.
 XX 06-DEC-2001.
 XX 25-MAY-2001; 2001WO-US016981.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX (AEOM-) AEOMICA INC.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX Disclosure; SEQ ID NO 1285; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 CC
 CC Sequence 17 BP; 6 A; 1 C; 9 G; 1 T; 0 U; 0 Other;
 CC
 CC Query Match 8.1%; Score 11.2; DB 1; Length 17;
 CC Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 CC Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC QY 1678 CCTGCTGCTCTCTCCA 1693
 CC ||||| ||||| |||||
 CC 17 CCTGCTTCTCCCA 2
 CC
 CC RESULT 686
 CC ABN09665/c
 CC ID ABN09665 standard; DNA; 17 BP.
 CC AC ABN09665;
 CC
 CC DT 29-MAY-2002 (first entry)
 CC
 CC DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9657.
 CC
 CC KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 CC muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 CC skeletal muscle disorder; amplicon; screening; ss.
 CC
 CC OS Homo sapiens.
 CC
 CC PN WO200192524-A2.
 CC
 CC PD 06-DEC-2001.
 CC
 CC PF 25-MAY-2001; 2001WO-US016981.
 CC
 CC PR 26-MAY-2000; 2000US-0207456P.
 CC PR 21-SEP-2000; 2000US-0234687P.
 CC PR 27-SEP-2000; 2000US-0236359P.
 CC PR 04-OCT-2000; 2000GB-00024263.
 CC PR 30-JAN-2001; 2001WO-US000661.
 CC PR 30-JAN-2001; 2001WO-US000662.
 CC PR 30-JAN-2001; 2001WO-US000663.
 CC PR 30-JAN-2001; 2001WO-US000664.
 CC PR 30-JAN-2001; 2001WO-US000665.
 CC PR 30-JAN-2001; 2001WO-US000666.
 CC PR 30-JAN-2001; 2001WO-US000667.
 CC PR 30-JAN-2001; 2001WO-US000668.
 CC PR 05-FEB-2001; 2001US-0266860P.
 CC
 CC FA (AEOM-) ABOMICA INC.
 CC
 CC PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 CC
 CC XX WPI; 2002-179446/23.
 CC
 CC XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 CC

PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
 XX Disclosure; SEQ ID NO 9657; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 CC
 CC SQ Sequence 17 BP; 4 A; 4 C; 8 G; 1 T; 0 U; 0 Other;
 CC
 CC Query Match 8.1%; Score 11.2; DB 1; Length 17;
 CC Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 CC Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC QY 1673 GGACCCCTGGTCTCTC 1688
 CC ||||| ||||| |||||
 CC 17 GGACCCCTGGCTCTC 2
 CC
 CC RESULT 687
 CC ABN01294/c
 CC ID ABN01294 standard; DNA; 17 BP.
 CC AC ABN01294;
 CC
 CC DT 29-MAY-2002 (first entry)
 CC
 CC DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1286.
 CC
 CC KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 CC muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 CC skeletal muscle disorder; amplicon; screening; ss.
 CC
 CC OS Homo sapiens.
 CC
 CC PN WO200192524-A2.
 CC
 CC PD 06-DEC-2001.
 CC
 CC PF 25-MAY-2001; 2001WO-US016981.
 CC
 CC PR 26-MAY-2000; 2000US-0207456P.
 CC PR 21-SEP-2000; 2000US-0234687P.
 CC PR 27-SEP-2000; 2000US-0236359P.
 CC PR 04-OCT-2000; 2000GB-00024263.
 CC PR 30-JAN-2001; 2001WO-US000661.
 CC PR 30-JAN-2001; 2001WO-US000662.
 CC PR 30-JAN-2001; 2001WO-US000663.
 CC PR 30-JAN-2001; 2001WO-US000664.
 CC PR 30-JAN-2001; 2001WO-US000665.
 CC PR 30-JAN-2001; 2001WO-US000666.
 CC PR 30-JAN-2001; 2001WO-US000667.
 CC PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 XX WPI; 2002-179446/23.
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 XX Disclosure; SEQ ID NO 1286; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 XX Sequence 17 BP; 5 A; 1 C; 9 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1678 CCGGTGTCCTCCCA 1693
 DB ||||| ||||| |||||
 16 CCGCTTCTCCCA 1
 RESULT 688
 ABN10217
 ID ABN10217 standard; DNA; 17 BP.
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 AC ABN10217;
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 DT 29-MAY-2002 (first entry)
 XX
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10209.
 DE
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200192524-A2.
 PN
 XX 06-DEC-2001.
 PD
 XX 25-MAY-2001; 2001WO-US016981.
 XX
 XX 26-MAY-2000; 2000US-0207456P.
 PR

21-SEP-2000; 2000US-0234687P.
 27-SEP-2000; 2000US-0236359P.
 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
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 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI
 XX WPI; 2002-179446/23.
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 XX Disclosure; SEQ ID NO 10209; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1750 CTATCTCTAAGGCCCA 1765
 DB ||||| ||||| |||||
 1 CTATCCGGAAGCCCA 16
 RESULT 689
 ABN01273/c
 ID ABN01273 standard; DNA; 17 BP.
 XX
 AC ABN01273;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1265.
 DE
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW

KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024283.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 05-FEB-2001; 2001US-0266860P.

XX (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 1265; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

XX Sequence 17 BP; 3 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

XX Query Match 8.1%; Score 11.2; DB 1; Length 17;

XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;

XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1729 AGATTGGTCCCAACT 1744

Db 16 AGATCGTCCCAACT 1

RESULT 690

ABN07992

ID ABN07992 standard; DNA; 17 BP.

XX

AC ABN07992;

XX

XX 29-MAY-2002 (first entry)

XX

XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7984.

XX

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

XX

XX Homo sapiens.

XX

XX WO200192524-A2.

XX

XX 06-DEC-2001.

XX

XX 25-MAY-2001; 2001WO-US016981.

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XX 26-MAY-2000; 2000US-0207456P.

XX

XX 21-SEP-2000; 2000US-0234687P.

XX

XX 27-SEP-2000; 2000US-0236359P.

XX

XX 04-OCT-2000; 2000GB-00024283.

XX

XX 30-JAN-2001; 2001WO-US000661.

XX

XX 30-JAN-2001; 2001WO-US000662.

XX

XX 30-JAN-2001; 2001WO-US000663.

XX

XX 30-JAN-2001; 2001WO-US000664.

XX

XX 30-JAN-2001; 2001WO-US000665.

XX

XX 30-JAN-2001; 2001WO-US000666.

XX

XX 30-JAN-2001; 2001WO-US000667.

XX

XX 30-JAN-2001; 2001WO-US000668.

XX

XX 30-JAN-2001; 2001WO-US000669.

XX

XX 05-FEB-2001; 2001US-0266860P.

XX

XX (AEOM-) AEOMICA INC.

XX

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX

XX WPI; 2002-179446/23.

XX

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 7984; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

XX The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

XX Sequence 17 BP; 8 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1646 CAGAAGGCAAGCACCA 1661
 |||||
 Db 2 CAGCAGGAAACACCA 17

RESULT 691
 ABN07993
 ID ABN07993 standard; DNA; 17 BP.
 XX
 AC ABN07993;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7985.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 XX
 PR 21-SEP-2000; 2000US-0234687P.
 XX
 PR 27-SEP-2000; 2000US-0236359P.
 XX
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PR 30-JAN-2001; 2001WO-US000661.
 XX
 PR 30-JAN-2001; 2001WO-US000662.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 XX
 PR 30-JAN-2001; 2001WO-US000664.
 XX
 PR 30-JAN-2001; 2001WO-US000665.
 XX
 PR 30-JAN-2001; 2001WO-US000666.
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 PR 30-JAN-2001; 2001WO-US000667.
 XX
 PR 30-JAN-2001; 2001WO-US000668.
 XX
 PR 30-JAN-2001; 2001WO-US000669.
 XX
 PR 05-FEB-2001; 2001WO-US000670.
 XX
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 XX or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 PT
 XX Disclosure; SEQ ID NO 7985; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

CC production, and in vaccines or for replacement therapy. The
 CC Polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX
 SQ Sequence 17 BP; 8 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1646 CAGAAGGCAAGCACCA 1661
 |||||
 Db 1 CAGCAGGAAACACCA 16

RESULT 692
 ABN09667/C
 ID ABN09667 standard; DNA; 17 BP.
 XX
 AC ABN09667;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9659.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 XX
 PR 21-SEP-2000; 2000US-0234687P.
 XX
 PR 27-SEP-2000; 2000US-0236359P.
 XX
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PR 30-JAN-2001; 2001WO-US000661.
 XX
 PR 30-JAN-2001; 2001WO-US000662.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 XX
 PR 30-JAN-2001; 2001WO-US000664.
 XX
 PR 30-JAN-2001; 2001WO-US000665.
 XX
 PR 30-JAN-2001; 2001WO-US000666.
 XX
 PR 30-JAN-2001; 2001WO-US000667.
 XX
 PR 30-JAN-2001; 2001WO-US000668.
 XX
 PR 30-JAN-2001; 2001WO-US000669.
 XX
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 XX or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 PT
 XX Disclosure; SEQ ID NO 9659; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1672 TGGAACCCCTGGTGCT 1687
Db ||||| ||||| |||||
16 TGGAACCCCTGGCCTCT 1
RESULT 693
ABN07840
ID ABN07840 standard; DNA; 17 BP.
AC AEN07840;
XX
XX 29-MAY-2002 (first entry)
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7832.
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
OS Homo sapiens.
XX
XX WO200192524-A2.
PN
XX 06-DEC-2001.
PD
XX 25-MAY-2001; 2001WO-US016981.
PF
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001WO-US026860P.
XX
XX (ABCOM-) ABOMICA INC.
PA
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI

XX WPI; 2002-179446/23.
DR
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
PT
XX Disclosure; SEQ ID NO 7832; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1662 GGCTCACAGCTGGAAC 1677
Db ||||| ||||| |||||
1 GCCTCACAGCTGAAGC 16
RESULT 694
ABQ63738
ID ABQ63738 standard; DNA; 17 BP.
XX
XX ABQ63738;
AC
XX 20-AUG-2002 (first entry)
XX
XX Human KTOM1a portion (ABQ63232) probe # 451.
DE
XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
XX gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
XX kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
OS Homo sapiens.
XX
XX WO200224750-A2.
PN
XX 28-MAR-2002.
PD
XX 21-SEP-2001; 2001WO-US029656.
PF
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001WO-US026860P.
XX
XX (ABCOM-) ABOMICA INC.
PA
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI

XX WPI; 2002-147801/19.

XX Novel retroviral display library, useful for isolating a virus that can

PT transfer its nucleic acid to a host cell, i.e. for gene therapy.

PT comprises retroviruses which differ from each other in the Env protein

PT amino acid sequence.

XX Example 1; Fig 8; 59pp; English.

PS This invention relates to a method for creating a retroviral display

XX library, comprising several retroviruses, where each retrovirus in the

CC library differs in relation to other retroviruses in the amino acid

CC sequence of an Env protein and comprises a nucleic acid coding for both

CC the Env protein and a cell-selection marker. The method of the invention

CC is useful for isolating a virus that can transfer its nucleic acid to a

CC host cell. The libraries are useful as pools of viral vehicles from which

CC an appropriate vehicle can be selected to transfer a gene to a host cell.

CC The virus vectors created using the above mentioned methods are useful

CC for gene therapy applications, and can be used to target specific cell

CC types for gene therapy applications and for delivery of toxic genes to

CC tumours or virus infected cells for therapeutic applications. Selected

CC Env variants can also be used to target genes to heart cells to deliver

CC factors which promote tissue regeneration in diseased states. The library

CC allows direct selection of fully functional novel Env proteins. The

CC advantage of this approach over using prescreened ligands with known cell

CC -binding is that it does not require a predetermined conformationally

CC active orientation to fit onto the Env protein and does not necessarily

CC entail foreknowledge of a cell-type specific receptor. The random library

CC method entails minimal disruption of the Env structure due to the precise

CC substitution of the receptor binding domain by random amino acids. Using

CC this technique, more than one million different variant constructs can be

CC screened at a time for gene transfer function. The present sequence

CC represents a synthetic oligonucleotide used to create a randomised amino

CC acid sequence in the Env protein to create the retroviral display library

XX of the invention

XX Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1673 GGACCTCGGTGCTC 1688

DB 2 GGTCCCGAGGTGCTC 17

RESULT 697

AAD42386

XX AAD42386 standard; DNA; 17 BP.

XX AAD42386;

XX 04-NOV-2002 (first entry)

DT A. ochraceus 11 alpha hydroxylase DNA specific primer, 45624-for1.

DE 11 alpha hydroxylase; enzyme; sitosterol; eplerenone; cell therapy;

XX steroid bioconversion; antiinflammatory; antiarthritic; cytostatic;

KW cardiant; cytochrome P450; oxidoreductase; primer; ss.

KW Aspergillus ochraceus.

OS WO200246386-A2.

XX 13-JUN-2002.

XX 26-OCT-2001; 2001WO-US051070.

XX 30-OCT-2000; 2000US-0244300P.

XX (PHAA) PHARMACIA CORP.

PA (BOLT/) BOLTON S.

PA (CLAY/) CLAYTON R.

PA (EAST/) EASTON A.

PA (ENGE/) ENGEL L.

PA (MESS/) MESSING D.

XX Bolton S, Clayton R, Easton A, Engel L, Messing D;

PI WPI; 2002-547772/58.

XX New isolated Aspergillus ochraceus 11 alpha-hydroxylase or

PT oxidoreductase, for bioconversion of steroid substances to their 11 alpha

PT hydroxy counterparts in heterologous cells.

XX Example 11; Page 164; 181pp; English.

XX The present invention relates to novel cytochrome P450-like enzyme

CC (Aspergillus ochraceus 11 alpha hydroxylase protein), oxidoreductases and

CC polynucleotides encoding such proteins. Host cells comprising the

CC sequences of the invention are useful for making one or more enzymes from

CC the metabolic pathway for the synthesis of sitosterol to eplerenone. They

CC are useful for selective oxidation of a compound to an hydroxylated

CC product. Compositions of the invention are useful for producing spores

CC from A. ochraceus, A. niger, A. nidulans, Rhizopus oryzae, R. stolonifer,

CC R. arrhizus Trichothecium roseum, Fusarium oxysporum and M. olivaceum

CC etc, preferably to produce spores from A. ochraceus. Sequences of the

CC invention are useful in bioconversion of steroid substances to their 11

CC alpha-hydroxy counterparts. They are also used in cell therapy. The

CC present sequence is A. ochraceus 11 alpha hydroxylase DNA specific

CC primer. This sequence is used in the exemplification of the invention

XX Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 U; 0 Other;

SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1722 GAGATGGAGATTGGCT 1737

DB 1 GAGATCAAGATTGGCT 16

RESULT 698

ABK27291

ID ABK27291 standard; DNA; 17 BP.

XX ABK27291;

XX 09-APR-2002 (first entry)

DT Reduced linolenic acid production genome altering oligonucleotide #187.

DE Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;

XX o-methyl modification; DNA modification; phosphorothioate linkage;

KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;

KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;

KW amino acid over production; herbicide resistance; glyphosate resistance;

KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;

KW porphyric herbicide resistance; triazine resistance; disease resistance;

KW modified oil production; modified starch production; waxy starch;

KW altered floral morphology; male-sterile plant; albino mutant;

KW modified fatty acid content; reduced palmitate production; albino plant;

KW increased stearate production; reduced linolenic acid production;

KW photosynthetic process.

OS Triticum aestivum.

XX Synthetic.

XX WO200192512-A2.

XX 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 PR 27-MAR-2001; 2001US-00818875.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 XX Kmiec BB, Gamper HB, Rice MC, Kim J;
 PI WPI; 2002-106307/14.
 XX
 DR New oligonucleotides with modified nuclease-resistant termini, useful for
 XX creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.
 PT
 XX Claim 7; Page 201; 220pp; English.
 PS
 XX The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention
 XX
 XX Sequence 17 BP; 4 A; 4 C; 8 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1642 GTAGCAGAGGCAAGC 1657
 Db 2 GGAGCAGTAGGCGAGC 17
 RESULT 699
 ABK27292/c
 ID ABK27292 standard; DNA; 17 BP.
 XX
 AC ABK27292;
 XX
 DT 09-APR-2002 (first entry)
 XX
 XX Reduced linolenic acid production genome altering oligonucleotide #188.
 DE
 XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; LNA modification; phosphorothioate linkage;
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW modified fatty acid content; reduced palmitate production; albino plant;
 KW increased stearate production; reduced linolenic acid production;
 KW

KW photosynthetic process.
 XX
 OS Triticum aestivum.
 OS Synthetic.
 XX
 PN WO200192512-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 01-JUN-2001; 2001WO-US017672.
 XX
 XX 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 PR 27-MAR-2001; 2001US-00818875.
 XX
 XX (UYDE) UNIV DELAWARE.
 PA
 XX Kmiec BB, Gamper HB, Rice MC, Kim J;
 PI WPI; 2002-106307/14.
 XX
 DR New oligonucleotides with modified nuclease-resistant termini, useful for
 XX creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.
 PT
 XX Claim 7; Page 201; 220pp; English.
 PS
 XX The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention
 XX
 XX Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1642 GTAGCAGAGGCAAGC 1657
 Db 16 GGAGCAGTAGGCGAGC 1
 RESULT 700
 ABV79505
 ID ABV79505 standard; DNA; 17 BP.
 XX
 AC ABV79505;
 XX
 DT 03-JAN-2003 (first entry)
 XX
 XX Human HPL scanning oligonucleotide SEQ ID 751.
 DE Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW

KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 OS Homo sapiens.
 EN EPI229046-A2.
 XX 07-AUG-2002.
 XX 28-JAN-2002; 2002EP-000011167.
 XX 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX (ABOM-) ABOMICA INC.
 PA Zhan J;
 XX WPI; 2002-676582/73.
 DR Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.
 XX Example 2; Page 162; 718pp; English.
 XX The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1662 GGCTCACAGCTGGAC 1677
 DB 2 GACTCACTGCTGGACC 17
 RESULT 701
 ABV79023
 ID ABV79023 standard; DNA; 17 BP.
 XX AC ABV79023;
 XX 03-JAN-2003 (first entry)
 XX Human HTPL scanning oligonucleotide SEQ ID 269.

XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX Homo sapiens.
 OS EPI229046-A2.
 XX 07-AUG-2002.
 XX 28-JAN-2002; 2002EP-000011167.
 XX 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX (ABOM-) ABOMICA INC.
 PA Zhan J;
 XX WPI; 2002-676582/73.
 DR Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.
 XX Example 2; Page 99; 718pp; English.
 XX The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX Sequence 17 BP; 2 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1671 CTGAACCCCTGCTC 1686
 DB 2 CAGGACCCCTGCGTC 17
 RESULT 702
 ABV79024
 ID ABV79024 standard; DNA; 17 BP.
 XX AC ABV79024;
 XX 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 270.

XX DE Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

KW human testis expressed Patched like protein; testis; adrenal; liver;

KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

OS Homo sapiens.

XX EP1229046-A2.

XX 07-AUG-2002.

XX 28-JAN-2002; 2002EP-00001167.

XX 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 23-MAY-2001; 2001US-00864761.

PR 09-OCT-2001; 2001US-0327898P.

XX (AEOM-) AEOMICA INC.

XX Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.

XX Example 2; Page 99; 718pp; English.

XX The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB38519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potential therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention

XX Sequence 17 BP; 2 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 CTGGACCCCTGGTGC 1686

DB 1 CAGGACCCCTGGTGC 16

RESULT 703

ABK19420

ID ABK19420 standard; RNA; 17 BP.

XX

AC ABK19420;

XX DT 09-APR-2002 (first entry)

XX DE Human ERG Amberzyme target sequence Seq ID No 2067.

XX DE Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;

KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;

KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;

KW tumour angiogenesis; diabetic retinopathy; macular degeneration;

KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;

KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;

KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;

KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;

XX amberzyme.

XX Homo sapiens.

XX WO2001188124-A2.

XX 22-NOV-2001.

XX 16-MAY-2001; 2001WO-US015866.

XX 16-MAY-2000; 2000US-00572021.

XX (RIBO-) RIBOZYME PHARM INC.

XX (GLAXO) GLAXO GROUP LTD.

XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;

XX WPI; 2002-082995/11.

XX Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

XX Claim 4; Page 128; 149pp; English.

XX The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, Sturge vascular angiofibroma of tuberosus sclerosis, port-wine stains, verruca Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg²⁺. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention

XX Sequence 17 BP; 7 A; 1 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 5.2e+02;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1710 GTTAGAGTACGAGA 1725

DB 2 GUTAGGAGAAAGGACA 17

Sequence 17 BP; 7 A; 0 C; 7 G; 0 T; 3 U; 0 Other;

XX SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1691 CCAGCGTGGTGAAGT 1706
||||| |||||
Db 2 CCAGCTCCGTGAAGT 17
RESULT 706
ABV91247
ID ABV91247 standard; DNA; 17 BP.
XX AC ABV91247;
XX DT 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1960.
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX OS Homo sapiens.
XX FN EP1239051-A2.
XX PD 11-SEP-2002.
XX PF 28-JAN-2002; 2002EP-00001165.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 10-OCT-2001; 2001US-0328205P.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M;
XX WPI; 2002-684061/74.
XX DR Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 1960; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, AB883999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples

CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX SQ Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1724 GATGGAGATTGGCTCC 1739
||||| |||||
Db 1 GGTGGAGATGGGTCC 16
RESULT 707
ABV90073
ID ABV90073 standard; DNA; 17 BP.
XX AC ABV90073;
XX DT 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 786.
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX OS Homo sapiens.
XX FN EP1239051-A2.
XX PD 11-SEP-2002.
XX PF 28-JAN-2002; 2002EP-00001165.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 10-OCT-2001; 2001US-0328205P.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M;
XX WPI; 2002-684061/74.
XX DR Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 786; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, AB883999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples

CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office

XX SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CAGCGTGGTGGAGT 1706
Db 1 CCGAGCTCCGTGGAGT 16

RESULT 708
ABV90892
ID ABV90892 standard; DNA; 17 BP.
AC ABV90892;
DT 23-DEC-2002 (first entry)
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1605.
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX Homo sapiens.
OS EP1239051-A2.
PN 11-SEP-2002.
PD 28-JAN-2001; 2002EP-00001165.
PF 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
XX -1, useful for treating disorders associated with decreased expression or
XX activity of human POSHL1.
XX Example 2; SEQ ID NO 1605; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX (S1) having 95% deviations, especially conservative substitutions or a
XX fragment of the sequences comprising at least 8 contiguous amino acids.
XX Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX adaptor protein that interacts with Rho family small GTPases as well as
XX downstream components of the signal transduction pathway. (I) is useful
XX for identifying a specific binding partner. (II) and nucleic acids (II)
XX encoding (I) are useful for diagnosing, monitoring disease and treating

CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office

XX SQ Sequence 17 BP; 1 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 CTGGACCCCTGGTGTCTC 1686
Db 2 CCGGAGCCCTGGTGTCTC 17

RESULT 709
ABV91245
ID ABV91245 standard; DNA; 17 BP.
AC ABV91245;
DT 23-DEC-2002 (first entry)
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1958.
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX Homo sapiens.
OS EP1239051-A2.
PN 11-SEP-2002.
PD 28-JAN-2001; 2002EP-00001165.
PF 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
XX -1, useful for treating disorders associated with decreased expression or
XX activity of human POSHL1.
XX Example 2; SEQ ID NO 1958; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX (S1) having 95% deviations, especially conservative substitutions or a
XX fragment of the sequences comprising at least 8 contiguous amino acids.
XX Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX adaptor protein that interacts with Rho family small GTPases as well as
XX downstream components of the signal transduction pathway. (I) is useful
XX for identifying a specific binding partner. (II) and nucleic acids (II)
XX encoding (I) are useful for diagnosing, monitoring disease and treating

CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (II) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office

XX SQ Sequence 17 BP; 2 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1696 GTGGTGGAGTGGGT 1711
 Db 1 GTGGTGGAGTGGGT 16

RESULT 710
 ABV91051/c
 ID ABV91051 standard; DNA; 17 BP.

AC ABV91051;

XX 23-DEC-2002 (first entry)

DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1764.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EP1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 23-MAY-2001; 2001WO-US000670.

XX 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
 PT -1, useful for treating disorders associated with decreased expression or
 PT activity of human POSHL1.

XX Example 2; SEQ ID NO 1764; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (SI, ABB8999), a sequence having 65% sequence identity to (SI),
 CC (SI) having 95% deviations, especially conservative substitutions or a

CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (II) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office

XX SQ Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1748 CCTATCTCTAAAG3CC 1763

Db 16 CCTTGTCTTAAAGTCC 1

RESULT 711

ABV91071/c

ID ABV91071 standard; DNA; 17 BP.

AC ABV91071;

XX 23-DEC-2002 (first entry)

DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1784.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EP1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 23-MAY-2001; 2001WO-US000670.

XX 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
 PT -1, useful for treating disorders associated with decreased expression or
 PT activity of human POSHL1.

XX Example 2; SEQ ID NO 1784; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling

CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
 CC (SI) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX
 SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCTCTAA 1758

Db 17 CTCGGCCCTTCCGAA 2

RESULT 712

ABV91248

ID ABV91248 standard; DNA; 17 BP.

AC ABV91248;

DT 23-DEC-2002 (first entry)

DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1961.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.

OS Homo sapiens.

XX EP1239051-A2.

PN 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

PF 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 23-MAY-2001; 2001US-00864761.

PR 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

PA Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL

PT -1, useful for treating disorders associated with decreased expression or

PT activity of human POSHL1.

PS Example 2; SEQ ID NO 1961; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
 CC (SI) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX

SQ Sequence 17 BP; 4 A; 2 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1726 TGGAGATTGCTCCCA 1741

Db 2 TGGAGATGGGTCCTCA 17

RESULT 713

ABV90896

ID ABV90896 standard; DNA; 17 BP.

AC ABV90896;

DT 23-DEC-2002 (first entry)

DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1609.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.

OS Homo sapiens.

XX EP1239051-A2.

PN 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

PF 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 23-MAY-2001; 2001US-00864761.

PR 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

PA Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL

PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1609; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1674 GAACCTGGTCTCTCC 1699
Db 1 GAGCCCTGCTCTAC 16
RESULT 714
ABV90900
ID ABV90900 standard; DNA; 17 BP.
AC ABV90900;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1613.
XX
XX Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX Homo sapiens.
XX EP1239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
XX 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
XX Shannon M;
PI

DR WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1613; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1678 CCTGGTCTCTCTCA 1693
Db 1 CCTGGTCTCTACCA 16
RESULT 715
ABV91072/c
ID ABV91072 standard; DNA; 17 BP.
XX
XX AC ABV91072;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1785.
XX
XX Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX Homo sapiens.
XX EP1239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
XX 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
PA

XX Shannon M;
 PI WPI; 2002-684061/74.
 XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
 PT -1, useful for treating disorders associated with decreased expression or
 PT activity of human POSHL1.
 XX Example 2; SEQ ID NO 1785; 60pp + Sequence Listing; English.
 XX The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
 CC (S1) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1743 CTCCTCCCTATCTCTAA 1758
 Db |||||
 16 CTCGCCCTTCGGAA 1
 RESULT 716
 ABV91244
 ID ABV91244 standard; DNA; 17 BP.
 AC ABV91244;
 DT 23-DEC-2002 (first entry)
 XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1957.
 DE Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.
 XX Homo sapiens.
 OS EP1239051-A2.
 PN 11-SEP-2002.
 PD 28-JAN-2002; 2002EP-00001165.
 XX 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 23-MAY-2001; 2001US-00864761.

PR 10-OCT-2001; 2001US-0328205P.
 XX (AEOM-) AEOMICA INC.
 PA Shannon M;
 XX WPI; 2002-684061/74.
 PI Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
 DR -1, useful for treating disorders associated with decreased expression or
 DR activity of human POSHL1.
 XX Example 2; SEQ ID NO 1957; 60pp + Sequence Listing; English.
 XX The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
 CC (S1) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX SQ Sequence 17 BP; 2 A; 0 C; 11 G; 4 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1696 GTGGTGGAGTGGGT 1711
 Db |||||
 2 GTGGTGGAGTGGGT 17
 RESULT 717
 ABV91246
 ID ABV91246 standard; DNA; 17 BP.
 AC ABV91246;
 DT 23-DEC-2002 (first entry)
 XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1959.
 DE Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.
 XX Homo sapiens.
 OS EP1239051-A2.
 PN 11-SEP-2002.
 PD 28-JAN-2002; 2002EP-00001165.
 XX 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.

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PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
PA (AEOM-) ABOMICA INC.
PI Shannon M;
PI WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1959; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 2 A; 2 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1724 GATGGAGATTGGCTCC 1739
Db 2 GCTGGAGATGGGGTCC 17
RESULT 718
ABV91249
AC ABV91249 standard; DNA; 17 BP.
XX
XX ABV91249;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1962.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX
XX EP1239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.

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PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
PA (AEOM-) ABOMICA INC.
PI Shannon M;
PI WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1952; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 4 A; 2 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1726 TGGAGATTGGCTCCCA 1741
Db 1 TGGAGATGGGGTCCCA 16
RESULT 719
ABV90898
ID ABV90898 standard; DNA; 17 BP.
XX
XX ABV90898;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1611.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX
XX EP1239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX

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PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 23-MAY-2001; 2001US-00864761.
 PR 10-OCT-2001; 2001US-0328205P.
 XX (AEOM-) AEOMICA INC.
 XX Shannon M;
 XX WPI; 2002-684061/74.
 XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
 PT -1, useful for treating disorders associated with decreased expression or
 PT activity of human POSHL.
 XX Example 2; SEQ ID NO 1611; 60pp + Sequence Listing; English.
 PS The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),
 CC (S1) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present invention is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1677 CCTGGTGCTCTCTCC 1692
 Db | | | | | | | | | |
 2 CCTGGTGCTCTACAC 17
 RESULT 720
 ABL30789
 ID ABL30789 standard; DNA; 17 BP.
 XX ABL30789;
 XX 21-MAR-2002 (first entry)
 XX Human HLA genotyping oligonucleotide SEQ ID NO 278.
 DE Human; human leukocyte antigen; HLA; genotype; polymorphism;
 KW immunogenetic; transplantation; genetic disease; ss.
 XX Homo sapiens.
 XX WO200192572-A1.
 PN 06-DEC-2001.
 XX 06-DEC-2001.

PF 01-JUN-2001; 2001WO-JP004662.
 XX 01-JUN-2000; 2000JP-00164798.
 PR (NISHN) NISSHINBO IND INC.
 PA (SYST-) SYSTEM RES INC.
 XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
 PI WPI; 2002-122074/16.
 DR Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
 PT individuals e.g. by determining immunogenetic differences when
 PT transplanting them.
 XX Claim 10; Page 146; 345pp; Japanese.
 XX The invention relates to a typing kit for judging human leukocyte antigen
 CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
 CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
 CC genes e.g. belonging to HLA class I antigens on human genome and
 CC containing gene polymorphisms as alloantigens have been immobilised as
 CC primers for amplification of cleaved nucleic acids relating to gene
 CC polymorphisms. The method is useful for judging HLA genotypes of
 CC individuals by determining immunogenetic differences before transplanting
 CC between them, providing genetic information to decide compatibility of
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
 CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
 CC diagnosis of genetic diseases and identifying individuals
 XX Sequence 17 BP; 5 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1716 ACTACGGAGTGTGAGA 1731
 Db | | | | | | | | | |
 2 ACTACGGAGTGTGTGA 17
 RESULT 721
 ABL31672/C
 ID ABL31672 standard; DNA; 17 BP.
 XX ABL31672;
 XX 21-MAR-2002 (first entry)
 XX Human HLA genotyping oligonucleotide SEQ ID NO 1161.
 DE Human; human leukocyte antigen; HLA; genotype; polymorphism;
 KW immunogenetic; transplantation; genetic disease; ss.
 XX Homo sapiens.
 XX WO200192572-A1.
 PN 06-DEC-2001.
 XX 01-JUN-2001; 2001WO-JP004662.
 XX 01-JUN-2000; 2000JP-00164798.
 XX (NISHN) NISSHINBO IND INC.
 PA (SYST-) SYSTEM RES INC.
 XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
 PI WPI; 2002-122074/16.
 DR Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
 PT individuals e.g. by determining immunogenetic differences when

transplanting between them.

Claim 10; Page 313; 345pp; Japanese.

The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucleotides (ABL30512-ABL31809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them, providing genetic information to decide compatibility of organ and tissue for transplantation e.g. of bone marrow, kidney, liver, pancreas, Langerhans islet in pancreas and cornea, susceptibility diagnosis of genetic diseases and identifying individuals

Sequence 17 BP; 4 A; 4 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1734 GGCTCCCACTCTCC 1749

Db 17 GGCTCTCCACTGTCC 2

RESULT 722

ABK56128
ID ABK56128 standard; RNA; 17 BP.

AC ABK56128;

DT 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #499.

Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.

Homo sapiens.

WO200211674-A2.

14-FEB-2002.

09-AUG-2001; 2001WO-US024970.

09-AUG-2000; 2000US-0224383P.

(RIBO-) RIBOZYME PHARM INC.

(SYNT) SYNTEX USA LLC.

(THOM/) THOMPSON J.

Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

Grupe A;

WPI; 2002-217145/27.

Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.

Claim 4; Page 61; 152pp; English.

The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic

obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention

Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 50.0%; Pred. No. 5.2e+02;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1743 CTCCTCCTATCCATA 1758

Db 1 CUGCUCUUGUCUUA 16

RESULT 723

ABK56803
ID ABK56803 standard; RNA; 17 BP.

AC ABK56803;

DT 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #1174.

Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.

Homo sapiens.

WO200211674-A2.

14-FEB-2002.

09-AUG-2001; 2001WO-US024970.

09-AUG-2000; 2000US-0224383P.

(RIBO-) RIBOZYME PHARM INC.

(SYNT) SYNTEX USA LLC.

(THOM/) THOMPSON J.

Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

Grupe A;

WPI; 2002-217145/27.

Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.

Claim 4; Page 81; 152pp; English.

The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or

tissue. The sequences are useful for reducing CLCAL activity in a cell, hence, are useful for treatment of a patient having a condition comprising associated with the level of CLCAL, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCAL RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention

Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. NO. 5.2e+02;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

1743 CTCCTCCCTATCTTAA 1758
}:|:|:|:|:|:|
2 CUGCCUUGUCCUAA 17

RESULT 724
ACA61316/c
IIID ACA61316 standard; DNA; 17 BP.
ACA61316;
16-JUL-2003 (first entry)
Human cytochrome p450 gene CYP2D6, ASO probe WT C5816-5'.
Human; ss; cytochrome P450; CYP2D6; chromosome 22; probe; ASO;
drug metabolism; cardiovascular disorder; psychiatric disorder;
drug sensitivity; allele specific oligonucleotide.
XX XX
OS Homo sapiens.
PN EP1281755-A2.
XX XX
PD 05-FEB-2003.
XX XX
PF 16-JUL-2002; 2002EP-00254972.
XX XX
PR 31-JUL-2001; 2001US-0309111P.
XX XX
PA (PFIZ) PFIZER PROD INC.
XX XX
PI Milos PM, Webb SM;
XX XX
WPI; 2003-373769/36.
XX XX
New cytochrome P450 2D6 gene variants and polypeptides, useful for
PT determining if a subject has or is at risk of developing a drug
PT sensitivity condition or disorder that is associated with an aberrant
PT CYP2D6 activity.
XX XX
XX XX
PS Disclosure; Page 13; 88pp; English.
XX XX
The invention relates to an isolated nucleic acid comprising a cytochrome
CC P450 2D6 gene variant, e.g. G5799C or C5816AT (referring to the genomic
CC sequence or the same variant nucleotide in the corresponding cDNA
CC sequences). Also included are probes, primers (allele specific
CC oligonucleotides) and arrays used to detect and or amplify the CYP2D6
CC gene polymorphic regions, the variant polypeptides, antibodies which are
CC capable of distinguishing between the variant and wild-type polypeptides,
CC determining whether a subject has a genetic deficiency for metabolising a
CC drug, evaluating therapy with a drug metabolised by P450 CYP2D6 and
CC determining whether an individual is susceptible to being a poor
CC metaboliser of drugs. The DNA probe is useful for hybridising to a
CC variant form of the CYP2D6 gene. The primer is useful for amplifying the
CC C5816TA allelic variant. The allele specific nucleotide is useful for the

CC oligonucleotides) and arrays used to detect and or amplify the CYP2D6
 CC gene polymorphic regions, the variant polypeptides, antibodies which are
 CC capable of distinguishing between the variant and wild-type polypeptides,
 CC determining whether a subject has a genetic deficiency for metabolising a
 CC drug, evaluating therapy with a drug metabolised by p450 CYP2D6 and
 CC determining whether an individual is susceptible to being a poor
 CC metaboliser of drugs. The DNA probe is useful for hybridising to a
 CC variant form of the CYP2D6 gene. The primer is useful for amplifying the
 CC C58167A allelic variant. The allele specific nucleotide is useful for the
 CC detection of the C58167A allelic variant. The methods are useful for
 CC determining whether a subject has a genetic deficiency for metabolising a
 CC drug, evaluating therapy with a drug metabolised by p450 CYP2D6, and
 CC determining if an individual is susceptible to being a poor metaboliser
 CC of drugs. The nucleic acids are useful as probes or primers for
 CC determining whether a subject has a genetic deficiency for metabolising
 CC drugs that are substrates of p450 CYP2D6. The methods are useful for
 CC determining if a subject has or is at risk of developing a drug
 CC sensitivity condition or disorder that is associated with an aberrant
 CC CYP2D6 activity, e.g. an aberrant level of a CYP2D6 protein or an
 CC aberrant CYP2D6 bioactivity. The methods are also useful in selecting the
 CC appropriate drugs or determining the course of treatment to administer to
 CC a subject to treat cardiovascular or psychiatric disorders, or for
 CC treating a subject with a drug sensitivity or disorder associated with a
 CC specific allelic variant of a polymorphic region of the CYP2D6 gene. The
 CC antibodies are useful for monitoring CYP2D6 protein levels in an
 CC individual for determining whether a subject has a disease or conditions
 CC associated with an aberrant CYP2D6 protein level. The gene is located on
 CC human chromosome 22. The present sequence is an allele specific
 CC oligonucleotide (ASO) probe used to detect the wild-type CYP2D6 gene at
 CC polymorphic site 5916
 XX
 SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1655 AGCACCAGGCTCAG 1670
 Db | | | | | | | | | |
 1 AGCACAAAGCTCATAG 16

RESULT 726
 ACC52643
 ID ACC52643 standard; DNA; 17 BP.
 AC ACC52643;
 DT 27-JUN-2003 (first entry)
 XX Human tumour suppressor sequence #1410.
 DE ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 KW tumour regression; apoptosis; virus resistance; diagnosis;
 KW cellular degeneration.
 XX Homo sapiens.
 XX FR2826373-A1.
 PN 27-DEC-2002.
 XX 20-JUN-2001; 2001PR-00008139.
 XX 20-JUN-2001; 2001PR-00008139.
 XX (MOLE-) MOLECULAR ENGINES LAB SA.
 PA Tuijnder M, Telerman A, Amson R;
 PI WPI; 2003-250498/25.
 DR New nucleic acid sequences associated with tumor suppression, regression,
 XX apoptosis or virus resistance are useful to diagnose and treat viral
 XX disease, development of tumor cells and cell degeneration.
 XX Claim 1; Page 366; 798pp; French.

PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.
 XX Claim 1; Page 366; 798pp; French.
 CC This sequence represents an isolated nucleic acid sequence associated
 CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 XX
 SQ Sequence 17 BP; 4 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1735 GCTCCCAACTCTCTCC 1750
 Db | | | | | | | | | |
 1 GATCCCAAGCTACTCTCC 16

RESULT 727
 ACC52645
 ID ACC52645 standard; DNA; 17 BP.
 AC ACC52645;
 DT 27-JUN-2003 (first entry)
 XX Human tumour suppressor sequence #1412.
 DE ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 KW tumour regression; apoptosis; virus resistance; diagnosis;
 KW cellular degeneration.
 XX Homo sapiens.
 XX FR2826373-A1.
 PN 27-DEC-2002.
 XX 20-JUN-2001; 2001PR-00008139.
 XX 20-JUN-2001; 2001PR-00008139.
 XX (MOLE-) MOLECULAR ENGINES LAB SA.
 PA Tuijnder M, Telerman A, Amson R;
 PI WPI; 2003-250498/25.
 DR New nucleic acid sequences associated with tumor suppression, regression,
 XX apoptosis or virus resistance are useful to diagnose and treat viral
 XX disease, development of tumor cells and cell degeneration.
 XX Claim 1; Page 366; 798pp; French.

This sequence represents an isolated nucleic acid sequence associated
 CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGGACC 1678
 Db 1 GATCCCGAGCTGGACC 16
 RESULT 728
 ACC51350
 ID ACC51350 standard; DNA; 17 BP.
 XX AC ACC51350;
 XX DT 27-JUN-2003 (first entry)
 XX DE Human tumour suppressor sequence #117.
 XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 KW tumour regression; apoptosis; virus resistance; diagnosis;
 KW cellular degeneration.
 OS Homo sapiens.
 XX FR2826373-A1.
 XX PD 27-DEC-2002.
 XX PF 20-JUN-2001; 2001FR-00008139.
 XX PR 20-JUN-2001; 2001FR-00008139.
 XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
 XX PI Tuijnder M, Telerman A, Amson R;
 XX WPI; 2003-250498/25.
 XX New nucleic acid sequences associated with tumor suppression, regression,
 PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.
 XX Claim 1; Page 67; 798pp; French.
 XX This sequence represents an isolated nucleic acid sequence associated
 CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 XX Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1655 AGCACAGGCTCAG 1670
 Db 2 ATCACAGGCTTACAG 17
 RESULT 729
 ACC52642
 ID ACC52642 standard; DNA; 17 BP.
 XX AC ACC52642;
 XX DT 27-JUN-2003 (first entry)
 XX DE Human tumour suppressor sequence #1409.
 XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 KW tumour regression; apoptosis; virus resistance; diagnosis;

KW cellular degeneration.
 XX Homo sapiens.
 XX FR2826373-A1.
 XX PD 27-DEC-2002.
 XX PF 20-JUN-2001; 2001FR-00008139.
 XX PR 20-JUN-2001; 2001FR-00008139.
 XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
 XX PI Tuijnder M, Telerman A, Amson R;
 XX WPI; 2003-250498/25.
 XX New nucleic acid sequences associated with tumor suppression, regression,
 PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.
 XX Claim 1; Page 365; 798pp; French.
 XX This sequence represents an isolated nucleic acid sequence associated
 CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 XX Sequence 17 BP; 2 A; 11 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1735 GCTCCCAACTCTCTCCC 1750
 Db 1 GATCCCGAGCTCTCCC 16
 RESULT 730
 ACC51413/c
 ID ACC51413 standard; DNA; 17 BP.
 XX AC ACC51413;
 XX DT 27-JUN-2003 (first entry)
 XX DE Human tumour suppressor sequence #180.
 XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 KW tumour regression; apoptosis; virus resistance; diagnosis;
 KW cellular degeneration.
 XX Homo sapiens.
 XX FR2826373-A1.
 XX PD 27-DEC-2002.
 XX PF 20-JUN-2001; 2001FR-00008139.
 XX PR 20-JUN-2001; 2001FR-00008139.
 XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
 XX PI Tuijnder M, Telerman A, Amson R;
 XX WPI; 2003-250498/25.

PT New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 81; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated with tumor suppression or regression, apoptosis or virus resistance. The invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumor cells or cellular degeneration.

XX Sequence 17 BP; 6 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGGGAC 1677
Db 16 GTCTCAGCTTGATC 1

RESULT 731

ABX72090
ID ABX72090 standard; DNA; 17 BP.

AC ABX72090;

XX 12-MAR-2003 (first entry)

DE Human tumour endothelial marker TEM 21 DNA long tag #1.

XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW Tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neovascularization; immune response; cytostatic; antidiabetic;
KW ophthalmological; anti-rheumatic; antiarthritic; antipsoriatic; ds.

XX Homo sapiens.

XX WO200283874-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US008253.

XX 11-APR-2001; 2001US-0282850P.

XX 06-FEB-2002; 2002US-0354262P.

XX (UWJO) UNIV JOHNS HOPKINS.

XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2003-093016/08.

XX New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.

XX Disclosure; Page 361; 374pp; English.

XX The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease,

CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neovascularization or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. ABX72067-ABX72116 represent human TEM DNA tags

XX Sequence 17 BP; 2 A; 9 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1741 AACTCCTCCCTATCT 1756

Db 2 ACCACCTCCCTTCT 17

RESULT 732

ABT40040

ID ABT40040 standard; DNA; 17 BP.

XX ABT40040;

XX 13-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 5677.

XX Cytostatic; virucide; neuroprotective; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB034208.

XX 17-SEP-2001; 2001FR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

XX Disclosure; Page 697; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein

CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1655 AGCACCAGGCTCACAG 1670
| | | | | | | | | |
Db 2 ATCAACAGGCTTACAG 17
RESULT 733
ABT34526/c
ID ABT34526 standard; DNA; 17 BP.
XX
XX AC ABT34526;
XX
XX DT 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 163.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO2003025175-A2.
XX
XX PD 27-MAR-2003.
XX
XX PF 17-SEP-2002; 2002WO-IB004208.
XX
XX PR 17-SEP-2001; 2001FR-00011978.
XX
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX PI Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 53; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression

CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 3 A; 9 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1717 GTACGGAGATGGAGAT 1732
| | | | | | | | | |
Db 17 GGATGGGATGGAGAT 2
RESULT 734
ABT37658/c
ID ABT37658 standard; DNA; 17 BP.
XX
XX AC ABT37658;
XX
XX DT 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 3295.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO2003025175-A2.
XX
XX PD 27-MAR-2003.
XX
XX PF 17-SEP-2002; 2002WO-IB004208.
XX
XX PR 17-SEP-2001; 2001FR-00011978.
XX
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX PI Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 419; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression

SQ Sequence 17 BP; 2 A; 8 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1717 GTACGGAGTGGAGAT 1732
DB 17 GGAAGAGCTGGAGAT 2

RESULT 735
ABT38730/c
ID ABT38730 standard; DNA; 17 BP.
XX
AC ABT38730;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4367.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 544; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1651 GGCAAGCACCAGGCTC 1666
DB 16 GTCCAGACCAGGATC 1

RESULT 736
ABT37668/c
ID ABT37668 standard; DNA; 17 BP.
XX
AC ABT37668;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 3305.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 420; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1711 TTAGGAGTACGAGAT 1726
| | | | | | | | | |
Db 17 TCAGGAGCGCGAGAT 2

RESULT 737
ABT37550
ID ABT37550 standard; DNA; 17 BP.
XX AC ABT37550;
XX DT 12-JUN-2003 (first entry)
XX DE Tumour suppression related human fukutin oligo SEQ ID No 3187.
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
XX KW human fukutin; ds.
XX OS Homo sapiens.
XX PN WO2003025175-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004208.
XX PR 17-SEP-2001; 2001FR-00011978.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX PI WPI; 2003-313353/30.
XX PT New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; Page 406; 720pp; French.
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15 consecutive
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX CC hybridizes to them under highly stringent conditions, or the complement
XX CC of any of them, or the corresponding RNA. The novel isolated nucleic
XX CC acids of the invention are useful as probes and primers for detecting,
XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX CC component of a gene chip, in vitro as (anti)sense reagents, and for
XX CC production of recombinant polypeptides. Any of the nucleic acids,
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention
XX SQ Sequence 17 BP; 8 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1752 ATCTAAAGGCCCACT 1767
| | | | | | | | | |
Db 2 ATCATAAAGACCCT 17

RESULT 738
ABT40013/C
ID ABT40013 standard; DNA; 17 BP.
XX AC ABT40013;
XX DT 13-JUN-2003 (first entry)
XX DE Tumour suppression related human fukutin oligo SEQ ID No 5650.
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
XX KW human fukutin; ds.
XX OS Homo sapiens.
XX PN WO2003025175-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004208.
XX PR 17-SEP-2001; 2001FR-00011978.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX PI WPI; 2003-313353/30.
XX PT New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; Page 694; 720pp; French.
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15 consecutive
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX CC hybridizes to them under highly stringent conditions, or the complement
XX CC of any of them, or the corresponding RNA. The novel isolated nucleic
XX CC acids of the invention are useful as probes and primers for detecting,
XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX CC component of a gene chip, in vitro as (anti)sense reagents, and for
XX CC production of recombinant polypeptides. Any of the nucleic acids,
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention
XX SQ Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 16 GCTCACTGCTGGATC 1

RESULT 739
ACA09101/c

ID ACA09101 standard, RNA; 17 BP.

XX ACA09101;

XX 03-JUN-2003 (first entry)

XX NFKB sub-unit modulating amberzyme substrate #264.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.

XX US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

XX 18-MAY-1994; 94US-00245466.

XX 15-AUG-1994; 94US-00291932.

XX 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHOMB D T.

XX (MCSW/) MCSWIGGEN J.

XX (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

XX Claim 3; Page 56; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg²⁺. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft

CC rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule

XX Sequence 17 BP; 4 A; 1 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1740 CAACCTCCTCCCTATCC 1755
Db 17 CAGCTCCCTCCCTTTC 2

RESULT 740
ACA06383

ID ACA06383 standard, RNA; 17 BP.

XX ACA06383;

XX 03-JUN-2003 (first entry)

XX NFKB sub-unit modulating inozyme substrate #202.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.

XX US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

XX 18-MAY-1994; 94US-00245466.

XX 15-AUG-1994; 94US-00291932.

XX 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHOMB D T.

XX (MCSW/) MCSWIGGEN J.

XX (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

XX Claim 3; Page 30; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for

XX	OS	Homo sapiens.
XX	PN	US2002177568-A1.
XX	XX	28-NOV-2002.
XX	PD	
XX	XX	23-MAY-2001; 2001US-00864785.
XX	PF	
XX	XX	07-DEC-1992; 92US-00987132.
PR	PR	18-MAY-1994; 94US-00245466.
PR	PR	15-AUG-1994; 94US-00291932.
PR	PR	23-DEC-1996; 96US-00777916.
XX	XX	(STIN/) STINCHCOMB D T.
PA	PA	(MCSW/) MCSWIGGEN J.
PA	PA	(DRAP/) DRAPER K G.
XX	XX	Stinchcomb DT, Mcswiggen J, Draper KG;
PI		

US2002177568-A1.


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XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX DR WPI; 2003-423107/40.
XX
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MDZ3,
XX PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX PS Example 8; SEQ ID NO 545; 103pp; English.
XX
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MDZ3,
XX CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX
XX SQ Sequence 17 BP; 7 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1680 TGGTGTCTCTCTCCAGC 1695
DB 16 TGGTGTCTCTCTCTCTGC 1
XX
RESULT 745
ADB04488/c
ID ADB04488 standard; DNA; 17 BP.
XX
XX AC ADB04488;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Human MDZ7 scanning oligonucleotide SEQ ID 5474.
XX
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX
XX OS Homo sapiens.
XX
XX FN EP1281758-A2.
XX
XX PD 05-FEB-2003.
XX
XX PF 30-JUL-2002; 2002EP-00016874.
XX
XX PR 02-AUG-2001; 2001US-00922181.
XX
XX PA (AEOM-) AEOMICA INC.
XX
XX PI Shannon M, Gu Y, Nguyen C;
XX PI WPI; 2003-423107/40.
XX
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MDZ3,
XX PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX PS Example 8; SEQ ID NO 474; 103pp; English.
XX
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MDZ3,
XX CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX
XX SQ Sequence 17 BP; 2 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1716 AGTACGAGATCGAGA 1731
DB 16 AGTACGAGATCGAGA 1
XX
RESULT 746
ADA99485/c
ID ADA99485 standard; DNA; 17 BP.
XX
XX AC ADA99485;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Human MDZ3 scanning oligonucleotide SEQ ID 474.
XX
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX
XX OS Homo sapiens.
XX
XX FN EP1281758-A2.
XX
XX PD 05-FEB-2003.
XX
XX PF 30-JUL-2002; 2002EP-00016874.
XX
XX PR 02-AUG-2001; 2001US-00922181.
XX
XX PA (AEOM-) AEOMICA INC.
XX
XX PI Shannon M, Gu Y, Nguyen C;
XX PI WPI; 2003-423107/40.
XX
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MDZ3,
XX PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX PS Example 8; SEQ ID NO 474; 103pp; English.
XX
```

CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 3 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1687 TCCTCAGCTGGTGG 1702
 |||||
 Db 17 TCCTCCACCATGGCGG 2

RESULT 747

ADB03481
 ID ADB03481 standard; DNA; 17 BP.

AC ADB03481;
 XX

DT 20-NOV-2003 (first entry)
 XX

DE Human MDZ7 scanning oligonucleotide SEQ ID 4467.
 XX

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.

XX Homo sapiens.
 OS

PN EP1281758-A2.
 XX

PD 05-FEB-2003.
 XX

PF 30-JUL-2002; 2002EP-00016874.
 XX

PR 02-AUG-2001; 2001US-00922181.
 XX

XX (AEOM-) AEOMICA INC.
 PA

PI Shannon M, Gu Y, Nguyen C;
 XX

DR WPI; 2003-423107/40.
 XX

XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

PS Example 8; SEQ ID NO 4467; 103pp; English.

CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic

CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 4 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCAGCTGGAAC 1678
 |||||
 Db 1 GCTCAAGCTGGGATC 16

RESULT 748

ADA99486/C
 ID ADA99486 standard; DNA; 17 BP.

XX ADA99486;
 AC

XX 20-NOV-2003 (first entry)
 DT

XX Human MDZ3 scanning oligonucleotide SEQ ID 475.
 DE

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.

XX Homo sapiens.
 OS

PN EP1281758-A2.
 XX

XX 05-FEB-2003.
 PD

PF 30-JUL-2002; 2002EP-00016874.
 XX

PR 02-AUG-2001; 2001US-00922181.
 XX

XX (AEOM-) AEOMICA INC.
 PA

PI Shannon M, Gu Y, Nguyen C;
 XX

DR WPI; 2003-423107/40.
 XX

XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

PS Example 8; SEQ ID NO 475; 103pp; English.

CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

```
SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1687 TCCTCAGCGTGGTG 1702
DB 16 TCCTCACCATGGCG 1

RESULT 749
ADB03480
ID ADB03480 standard; DNA; 17 BP.
XX
AC ADB03480;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 4466.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 4466; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, or MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1663 GCTCAGCTGGAACC 1678
DB 16 TCCTCACCATGGCG 1

RESULT 750
ADA99594/c
ID ADA99594 standard; DNA; 17 BP.
XX
AC ADA99594;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 583.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 583; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1666 CACAGCTGGAACCTG 1681
DB 16 CCCAGCTGGATGCTG 1

RESULT 751
ADA99555/c
ID ADA99555 standard; DNA; 17 BP.
XX
AC ADA99555;
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XX 20-NOV-2003 (first entry)
XX Human MD23 scanning oligonucleotide SEQ ID 544.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX Homo sapiens.
XX EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX Example 8; SEQ ID NO 544; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX Sequence 17 BP; 8 A; 3 C; 6 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1680 TGCTGTCTCTCTCCAGC 1695
XX |||||
XX Db 17 TGCTGTCTCTCTCTGC 2
XX
XX RESULT 752
XX ADA99409
XX ID ADA99409 standard; DNA; 17 BP.
XX AC ADA99409;
XX
XX 20-NOV-2003 (first entry)
XX Human MD23 scanning oligonucleotide SEQ ID 398.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX
XX Homo sapiens.
XX EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX Example 8; SEQ ID NO 544; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX Sequence 17 BP; 8 A; 3 C; 6 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1680 TGCTGTCTCTCTCCAGC 1695
XX |||||
XX Db 17 TGCTGTCTCTCTGC 2
XX
XX RESULT 752
XX ADA99409
XX ID ADA99409 standard; DNA; 17 BP.
XX AC ADA99409;
XX
XX 20-NOV-2003 (first entry)
XX Human MD23 scanning oligonucleotide SEQ ID 398.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX
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XX developmental disorder; ss.
XX Homo sapiens.
XX EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX Example 8; SEQ ID NO 398; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1740 CAACTCTCTCTCTATCC 1755
XX |||||
XX Db 2 CAGTTCCTCACTATCC 17
XX
XX RESULT 753
XX ABZ61824/c
XX ID ABZ61824 standard; RNA; 17 BP.
XX AC ABZ61824;
XX 21-MAR-2003 (first entry)
XX Human H-Ras DNazyme target #615.
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX Homo sapiens.
XX WO200297114-A2.
XX 05-DEC-2002.
XX 29-MAY-2002; 2002WO-US016840.
XX
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XX 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Mcswiggen J;
 XX WPI; 2003-140484/13.
 DR Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX Claim 58; Page 122; 185pp; English.
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX SQ Sequence 17 BP; 4 A; 0 C; 11 G; 0 T; 2 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1736 CTCCTCAACTCTCCCT 1751
 |||||
 Db 16 CTCCTCAACTCTCCCT 1
 RESULT 754
 ABZ64589
 ID ABZ64589 standard; RNA; 17 BP.
 AC ABZ64589;
 XX 21-MAR-2003 (first entry)
 XX Human HER2 DNzyme substrate #46.
 DE Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX Homo sapiens.
 OS WO200297114-A2.
 EN 05-DEC-2002.
 XX 29-MAY-2002; 2002WO-US016840.
 XX 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Mcswiggen J;
 XX WPI; 2003-140484/13.
 DR Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX Claim 58; Page 122; 185pp; English.
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX SQ Sequence 17 BP; 4 A; 0 C; 11 G; 0 T; 2 U; 0 Other;

PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX Claim 4; Page 133; 185pp; English.
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX SQ Sequence 17 BP; 0 A; 7 C; 6 G; 0 T; 4 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. No. 5.2e+02;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1677 CCTGTGTCTCTCCCTCC 1692
 |||||
 Db 1 CGCUGGGGGGCCUCC 16
 RESULT 755
 ABZ60463/c
 ID ABZ60463 standard; RNA; 17 BP.
 AC ABZ60463;
 XX 21-MAR-2003 (first entry)
 XX Human K-Ras DNzyme substrate #575.
 DE Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX Homo sapiens.
 OS WO200297114-A2.
 EN 05-DEC-2002.
 XX 29-MAY-2002; 2002WO-US016840.
 XX 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Mcswiggen J;
 XX WPI; 2003-140484/13.
 DR Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX Claim 58; Page 96; 185pp; English.
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-

CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention

XX SQ Sequence 17 BP; 3 A; 9 C; 1 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1633 ATGGGGCTGTGTAGCAG 1648
|||||
Db 17 ATGGGGCATGTGGAAG 2

RESULT 756

ABZ65103

ID ABZ65103 standard; RNA; 17 BP.

XX AC ABZ65103;

XX DT 21-MAR-2003 (first entry)

XX DE Human HER2 DNzyme substrate #560.

XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;

XX KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US016840.

XX PR 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX DR WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX PS Claim 4; Page 143; 185pp; English.
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention

XX SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCTGGT 1683

|||||

Db 2 CAUCUGGAUCCCGAU 17

RESULT 757

ABZ65446

ID ABZ65446 standard; RNA; 17 BP.

XX AC ABZ65446;

XX DT 21-MAR-2003 (first entry)

XX DE Human HER2 DNzyme substrate #903.

XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US016840.

XX PR 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX DR WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX PS Claim 4; Page 150; 185pp; English.
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention

XX SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 50.0%; Pred. No. 5.2e+02;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1675 AACCTGGTGTCTCCT 1690

|||||

Db 2 AGCCUGAUGUGUCCU 17

RESULT 758

ABZ60377/c

ID ABZ60977 standard; RNA; 17 BP.

KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX Hepatitis C virus.
 OS
 XX WO200281494-A1.
 PN
 XX 17-OCT-2002.
 PD
 XX
 XX 26-MAR-2002; 2002WO-US009187.
 PF
 XX
 XX 26-MAR-2001; 2001US-00817879.
 PR
 XX 08-JUN-2001; 2001US-00877478.
 PR
 XX 08-JUN-2001; 2001US-0296876P.
 PR
 XX 24-OCT-2001; 2001US-0335059P.
 PR
 XX 05-DEC-2001; 2001US-0337055P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 PI
 XX WPI; 2003-229207/22.
 DR
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Claim 1; Page 300; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyms, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 7 G; 0 T; 4 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1655 AGCACCAGGCTCACAG 1670
 DB 17 ATCACCAGCTCAGG 2
 RESULT 760
 ACDS5658
 ID ACDS5658 standard; RNA; 17 BP.

XX
 AC ABZ60977;
 XX
 DT 21-MAR-2003 (first entry)
 DE
 XX Human K-Ras DNazyme substrate #1089.
 XX
 XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200297114-A2.
 PN
 XX 05-DEC-2002.
 PD
 XX
 XX 29-MAY-2002; 2002WO-US016840.
 PF
 XX
 XX 29-MAY-2001; 2001US-0294140P.
 PR
 XX 06-JUN-2001; 2001US-0296249P.
 PR
 XX 10-SEP-2001; 2001US-0318471P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Mcswiggen J;
 PI
 XX WPI; 2003-140484/13.
 DR
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX
 PS Claim 58; Page 106; 185pp; English.
 XX
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 5 G; 0 T; 5 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1728 GAGATGGCTCCCAAC 1743
 DB 17 GAGATGGCTCCCAAC 2
 RESULT 759
 ACDS4172/c
 ID ACDS4172 standard; RNA; 17 BP.
 XX
 AC ACDS4172;
 XX
 DT 30-SEP-2003 (first entry)
 DE
 XX HCV minus strand DNazyme substrate sequence #1419.
 XX
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyms; G-cleaver ribozyme; decoy molecule; aptamer;

XX ACDS5658;
 XX
 XX
 XX 23-SEP-2003 (first entry)
 XX
 XX
 XX HBV amberzyme substrate sequence #168.
 XX
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 XX RNA stability; RNA expression; RNA synthesis; antisense;
 XX enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
 XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 XX HBV reverse transcriptase; Enhancer I region; viral replication;
 XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 XX virucide; antiinflammatory; substrate; ss.
 XX
 XX Hepatitis B virus.
 XX
 XX WO200281494-A1.
 XX
 XX 17-OCT-2002.
 XX
 XX 26-MAR-2002; 2002WO-US009187.
 XX
 XX 26-MAR-2001; 2001US-00817879.
 XX 08-JUN-2001; 2001US-00877478.
 XX 08-JUN-2001; 2001US-0296876P.
 XX 24-OCT-2001; 2001US-0335059P.
 XX 05-DEC-2001; 2001US-0337055P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MACE/) MACEJAK D.
 XX (MCSW/) MCSWIGGEN J.
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 XX (PAVC/) PAVCO P.
 XX (LEEP/) LEE P.
 XX (DRAP/) DRAPER K.
 XX (ROBE/) ROBERTS E.
 XX
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
 XX Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 XX
 XX Novel compound useful for treating cirrhosis, liver failure,
 XX hepatocellular carcinoma, or condition associated with hepatitis C virus
 XX infection.
 XX
 XX Example 1; Page 206; 387pp; English.
 XX
 XX The present invention relates to nucleic acid molecules which modulate
 XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 XX and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
 XX inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
 XX as oligonucleotides that specifically bind the Enhancer I region of HBV
 XX DNA. The nucleic acids may be used to modulate the expression of HBV
 XX genes and HBV viral replication. Also disclosed is a method for screening
 XX compounds and/or potential therapies directed against HBV, and compounds
 XX that modulate the expression and/or replication of HCV. The compounds
 XX methods of the invention are useful for the treatment of degenerative and
 XX disease states related to HBV and HCV infection, replication and gene
 XX expression such as cirrhosis, liver failure, and hepatocellular
 XX carcinoma. The present sequence represents a substrate for one of the HBV
 XX ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberzyme sequences
 XX disclosed in the present invention

SQ Sequence 17 BP; 4 A; 0 C; 11 G; 0 T; 2 U; 0 Other;

Query Match

8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 5.2e+02;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1702 GAA GTTGGT TAGGAG 1717
 |||:|||||
 Db 2 GGAGUUGGGGAGGAG 17

RESULT 761

ACDS8401/C

ID ACDS8401 standard; RNA; 17 BP.

XX AC ACDS8401;

XX DT 24-SEP-2003 (first entry)

XX DE HCV DNzyme substrate sequence #819.

XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;

XX KW RNA stability; RNA expression; RNA synthesis; antisense;

XX KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;

XX KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;

XX KW HBV reverse transcriptase; Enhancer I region; viral replication;

XX KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;

XX KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;

XX KW virucide; antiinflammatory; substrate; ss.

XX OS Hepatitis C virus.

XX PN WO200281494-A1.

XX PD 17-OCT-2002.

XX PF 26-MAR-2002; 2002WO-US009187.

XX PR 26-MAR-2001; 2001US-00877879.

XX PR 08-JUN-2001; 2001US-00877478.

XX PR 08-JUN-2001; 2001US-0296876P.

XX PR 24-OCT-2001; 2001US-0335059P.

XX PR 05-DEC-2001; 2001US-0337055P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (BLAT/) BLATT L.

XX PA (MACE/) MACEJAK D.

XX PA (MCSW/) MCSWIGGEN J.

XX PA (MORR/) MORRISSEY D.

XX PA (PAVC/) PAVCO P.

XX PA (LEEP/) LEE P.

XX PA (DRAP/) DRAPER K.

XX PA (ROBE/) ROBERTS E.

XX PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;

XX PI Draper K, Roberts E;

XX PI WPI; 2003-229207/22.

XX PT Novel compound useful for treating cirrhosis, liver failure,

XX PT hepatocellular carcinoma, or condition associated with hepatitis C virus

XX PT infection.

XX PS Claim 1; Page 248; 387pp; English.

XX CC The present invention relates to nucleic acid molecules which modulate

XX CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

XX CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

XX CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,

XX CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

XX CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

XX CC transcriptase and/or HBV reverse transcriptase primer sequences, as well

XX CC as oligonucleotides that specifically bind the Enhancer I region of HBV

XX CC DNA. The nucleic acids may be used to modulate the expression of HBV

XX CC genes and HBV viral replication. Also disclosed is a method for screening

XX CC compounds and/or potential therapies directed against HBV, and compounds

CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNzyme or minus strand DNzyme sequences disclosed in the present
 CC invention
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1677 CCCTGGTGTCTCTCC 1692
 Db 17 CCGCGGTGTCTCCCC 2
 RESULT 762
 ACDS1379
 ID ACDS1379 standard; RNA; 17 BP.
 XX
 AC ACDS1379;
 XX
 DT 23-SEP-2003 (first entry)
 XX
 DE HBV hammerhead ribozyme substrate sequence #539.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 DR Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 PT
 XX Example 1; Page 146; 387pp; English.
 FS
 XX

CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberyne sequences
 CC disclosed in the present invention
 XX
 SQ Sequence 17 BP; 2 A; 6 C; 1 G; 0 T; 8 U; 0 Other;
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 50.0%; Pred. No. 5.2e+02;
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1741 AACTCCTCCTATCCT 1756
 Db 1 AACUCCUUCUUUCCU 16
 RESULT 763
 ACDS5659
 ID ACDS5659 standard; RNA; 17 BP.
 XX
 AC ACDS5659;
 XX
 DT 23-SEP-2003 (first entry)
 XX
 DE HBV amberyne substrate sequence #169.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
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 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX

PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX Example 1; Page 206; 387pp; English.
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
 CC disclosed in the present invention
 XX Sequence 17 BP; 3 A; 0 C; 12 G; 0 T; 2 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 68.8%; Pred. No. 5.2e+02;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1702 GAAGTGGGTAGGAG 1717
 |||||
 Db 1 GGAGUGGGGGAGGAG 16
 |||||
 RESULT 764
 ACDS8497
 ID ACD58497 standard; RNA; 17 BP.
 AC ACD58497;
 XX
 DT 24-SEP-2003 (first entry)
 DE HCV DNazyme substrate sequence #859.
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX Hepatitis C virus.
 OS WO200281494-A1.
 XX 17-OCT-2002.
 XX 26-MAR-2002; 2002WO-US009187.
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
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 PA (PAVC/) PAVCO P.
 PA (LEEF/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX Claim 1; Page 249; 387pp; English.
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention
 XX Sequence 17 BP; 4 A; 7 C; 3 G; 0 T; 3 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 75.0%; Pred. No. 5.2e+02;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1655 AGCACCAGGTCACAG 1670
 |||||
 Db 2 AUCACCAGCCUACCG 17
 |||||
 RESULT 765
 ACDS3921
 ID ACD53921 standard; RNA; 17 BP.
 XX ACD53921;
 AC ACD53921;
 XX
 DT 24-SEP-2003 (first entry)
 DE HBV zinzyme substrate sequence #91.
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX Hepatitis B virus.
 OS

PN WO200281494-A1.
 XX 17-OCT-2002.
 XX 26-MAR-2002; 2002WO-US009187.
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORE/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 DR Novel compound useful for treating cirrhosis, liver failure,
 XX hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX Example 1; Page 175; 387pp; English.
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
 CC disclosed in the present invention
 XX Sequence 17 BP; 4 A; 0 C; 9 G; 0 T; 4 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 56.2%; Pred. No. 5.2e+02;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1698 GGTCGAGCTGGGTTA 1713
 Db 2 GGAGGAGGUAGGUUA 17
 RESULT 766
 ACD55653/C
 ID ACD55653 standard; RNA; 17 BP.
 XX AC
 XX ACD55653;
 XX 23-SEP-2003 (first entry)
 XX HBV amberzyme substrate sequence #163.
 DE
 XX

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX Hepatitis B virus.
 OS WO200281494-A1.
 PN 17-OCT-2002.
 XX 26-MAR-2002; 2002WO-US009187.
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORE/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 DR Novel compound useful for treating cirrhosis, liver failure,
 XX hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX Example 1; Page 206; 387pp; English.
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
 CC disclosed in the present invention
 XX Sequence 17 BP; 5 A; 0 C; 8 G; 0 T; 4 U; 0 Other;
 SQ
 Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1741 AACTCTCTCCCTATCCT 1756
 Db 17 AACTCTCTCCCTATCAT 2

as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HCV DNzyme or minus strand DNzyme sequences disclosed in the present invention

Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1660 CAGGCTCACAGCTGGA 1675
|||||:|||||
Db 2 CAGGCUACCGCGCA 17

RESULT 769
ACD51053
ID ACD51053 standard; RNA; 17 BP.
XX AC ACD51053;
XX
XX
XX 23-SEP-2003 (first entry)
DT
DE HBV hammerhead ribozyme substrate sequence #366.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
XX Hepatitis B virus.
OS
XX
XX WO200281494-A1.
PN
XX 17-OCT-2002.
PD
XX 26-MAR-2002; 2002WO-US009187.
PF
XX 26-MAR-2001; 2001US-00817879.
PR
XX 08-JUN-2001; 2001US-00877478.
PR
XX 08-JUN-2001; 2001US-0296876P.
PR
XX 24-OCT-2001; 2001US-0335059P.
PR
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (NACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
PI
XX WPI; 2003-229207/22.
DR
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus

infection.

XX
XX Example 1; Page 143; 387pp; English.
PS
XX The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberzyme sequences disclosed in the present invention

Sequence 17 BP; 3 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 5.2e+02;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1680 TGGTGTCCTCCAGC 1695
:||||:|||||
Db 1 UGGUGUGUACACCAGC 16

RESULT 770
ACD64268
ID ACD64268 standard; RNA; 17 BP.
XX
XX ACD64268;
AC
XX 30-SEP-2003 (first entry)
DT
XX
XX HCV minus strand DNzyme substrate sequence #1459.
DE
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
XX Hepatitis C virus.
OS
XX
XX WO200281494-A1.
PN
XX 17-OCT-2002.
PD
XX 26-MAR-2002; 2002WO-US009187.
PF
XX 26-MAR-2001; 2001US-00817879.
PR
XX 08-JUN-2001; 2001US-00877478.
PR
XX 08-JUN-2001; 2001US-0296876P.
PR
XX 24-OCT-2001; 2001US-0335059P.
PR
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (NACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
XX

```

PA (LEBP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 301; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, ambezymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNazyme or minus strand DNazyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 0 A; 9 C; 5 G; 0 T; 3 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1677 CCTGGTGTCCTCC 1692
DB 2 CCGCGGUGUCUCCCC 17
RESULT 771
ACD64752/c
ID ACD64752 standard; RNA; 17 BP.
AC ACD64752;
XX
DT 30-SEP-2003 (first entry)
XX
DE HCV minus strand DNazyme substrate sequence #1719.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW ambezyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis C virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US0009187.
XX
PR 26-MAR-2001; 2001US-00817879.

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PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEBP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 305; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, ambezymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNazyme or minus strand DNazyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 2 A; 4 C; 8 G; 0 T; 3 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1660 CAGGCTCACAGCTGCA 1675
DB 17 CAGGCTCACCGCGCA 2
RESULT 772
ACCG67762/c
ID ACCG67762 standard; DNA; 17 BP.
XX
AC ACCG67762;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5009.
XX
KW Cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX

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Mon Aug 30 09:26:45 2004

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PN WO2003025176-A2.
XX
PD
XX
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 616; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCAGCTGGGAAAC 1677
Db 16 GCCTTACAGTGGATC 1
RESULT 773
ACC64522
ID ACC64522 standard; DNA; 17 BP.
XX
XX ACC64522;
XX
XX 01-JUL-2003 (first entry)
DT
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 1769.
DE
XX Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; murine;
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
XX
XX 27-MAR-2003.
PD
XX 17-SEP-2002; 2002WO-IB004210.
PF
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 616; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCAGCTGGGAAAC 1677
Db 16 GCCTTACAGTGGATC 1
RESULT 774
ACC66061/c
ID ACC66061 standard; DNA; 17 BP.
XX
XX ACC66061;
XX
XX 01-JUL-2003 (first entry)
DT
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 3308.
DE
XX Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; murine;
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
XX
XX 27-MAR-2003.
PD
XX 17-SEP-2002; 2002WO-IB004210.
PF
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 417; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 6 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1752 ATCCTAAAGGCCCACT 1767
Db 2 ATCCCAACACCACT 17
RESULT 774
ACC66061/c
ID ACC66061 standard; DNA; 17 BP.
XX
XX ACC66061;
XX
XX 01-JUL-2003 (first entry)
DT
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 3308.
DE
XX Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; murine;
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
XX
XX 27-MAR-2003.
PD
XX 17-SEP-2002; 2002WO-IB004210.
PF
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 417; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 6 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
SQ
```

CC are characterised by development of tumours or cell degeneration,
 XX specifically cancer but also Alzheimer's disease and schizophrenia
 SQ Sequence 17 BP; 1 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1651 GGCAAGCACCAGGCTC 1666
 |||||
 Db 16 GGGAGACACGAGATC 1

RESULT 775
 ACC67106
 ID ACC67106 standard; DNA; 17 BP.
 XX
 AC ACC67106;
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4353.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 539; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX

Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCAGAGCTGGAAAC 1678
 |||||
 Db 1 GATCAGAGCTGAAC 16

RESULT 777
 ACC65714
 ID ACC65714 standard; DNA; 17 BP.
 XX
 AC ACC65714;
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2961.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX

Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGAGCTGGAAAC 1677
 |||||
 Db 16 GGGTACAGCTGGATC 1

RESULT 777
 ACC65714
 ID ACC65714 standard; DNA; 17 BP.
 XX
 AC ACC65714;
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2961.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX

XX OS Mus musculus.
XX PN WO2003025176-A2.
XX XX 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004210.
XX PR 17-SEP-2001; 2001FR-00011979.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX XX WPI; 2003-333167/31.
XX DR New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; Page 377; 738pp; French.
XX CC The present invention relates to murine oligonucleotides (ACC62754-
XX CC ACC6806), which are associated with tumour suppression, tumour
XX CC reversion, apoptosis and virus resistance. The oligonucleotides are
XX CC useful as (1) as probes and primers for detecting, identifying,
XX CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
XX CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
XX CC recombinant polypeptides. The oligonucleotides are useful for preparation
XX CC of pharmaceuticals for prevention and/or treatment of viral diseases that
XX CC are characterised by development of tumours or cell degeneration,
XX CC specifically cancer but also Alzheimer's disease and schizophrenia
XX XX Sequence 17 BP; 4 A; 7 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1658 ACCAGGCTCACAGCTG 1673
XX Db | | | | | | | | | |
XX 2 ATCAGGCCACAGCG 17
XX
XX RESULT 778
XX ACC64616/c
XX ID ACC64616 standard; DNA; 17 BP.
XX AC ACC64616;
XX XX 01-JUL-2003 (first entry)
XX DT Murine oligonucleotide associated with tumour suppression, SEQ ID 1863.
XX DE
XX XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; ss.
XX OS Mus musculus.
XX OS WO2003025176-A2.
XX PN 27-MAR-2003.
XX PD
XX DT 01-JUL-2003 (first entry)
XX XX Murine oligonucleotide associated with tumour suppression, SEQ ID 1863.
XX DE
XX XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; ss.
XX OS Mus musculus.
XX OS WO2003025176-A2.
XX PN 27-MAR-2003.
XX PD
XX PF 17-SEP-2002; 2002WO-IB004210.
XX XX 17-SEP-2001; 2001FR-00011979.
XX PR (MOLE-) MOLECULAR ENGINES LAB.
XX PA Telerman A, Amson R, Tuijnder M;
XX PI

XX WPI; 2003-333167/31.
XX New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; Page 248; 738pp; French.
XX XX The present invention relates to murine oligonucleotides (ACC62754-
XX CC ACC6806), which are associated with tumour suppression, tumour
XX CC reversion, apoptosis and virus resistance. The oligonucleotides are
XX CC useful as (1) as probes and primers for detecting, identifying,
XX CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
XX CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
XX CC recombinant polypeptides. The oligonucleotides are useful for preparation
XX CC of pharmaceuticals for prevention and/or treatment of viral diseases that
XX CC are characterised by development of tumours or cell degeneration,
XX CC specifically cancer but also Alzheimer's disease and schizophrenia
XX XX Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1717 GTACGGAGATGGAGAT 1732
XX Db | | | | | | | | | |
XX 17 GTCCGAATATGGAGAT 2
XX
XX RESULT 779
XX ACC64238/c
XX ID ACC64238 standard; DNA; 17 BP.
XX AC ACC64238;
XX XX 01-JUL-2003 (first entry)
XX DT Murine oligonucleotide associated with tumour suppression, SEQ ID 1485.
XX DE
XX XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; ss.
XX OS Mus musculus.
XX OS WO2003025176-A2.
XX PN 27-MAR-2003.
XX PD
XX PF 17-SEP-2002; 2002WO-IB004210.
XX XX 17-SEP-2001; 2001FR-00011979.
XX PR (MOLE-) MOLECULAR ENGINES LAB.
XX PA Telerman A, Amson R, Tuijnder M;
XX PI WPI; 2003-333167/31.
XX DR New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; Page 204; 738pp; French.
XX XX The present invention relates to murine oligonucleotides (ACC62754-
XX CC ACC6806), which are associated with tumour suppression, tumour
XX CC reversion, apoptosis and virus resistance. The oligonucleotides are
XX CC useful as (1) as probes and primers for detecting, identifying,
XX CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
XX CC

CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterized by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1697 TGGTGAAGTGGGT 1712
Db 17 TGCTAGAGTTGGGAT 2

RESULT 780
ACC83620
ID ACC83620 standard; DNA; 17 BP.
XX
AC ACC83620;
XX
DT 08-SEP-2003 (first entry)
XX
DE Escherichia coli dGTPase dgt gene PCR primer or probe.
XX
KW Deoxyguanosine triphosphate triphosphohydrolase; dGTPase; enzyme;
KW EC-3.1.5.1; enteric bacteria; biosensor; biochip; PCR; primer; probe; ss.
XX
OS Escherichia coli.
XX
PN WO2003046201-A2.
XX
PD 05-JUN-2003.
XX
PF 01-OCT-2002; 2002WO-US031323.
XX
PR 21-NOV-2001; 2001US-00991552.
XX
PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
XX
PI Quirk S;
XX
DR WPI; 2003-482523/45.
XX

PT Detecting enteric bacteria of the family Enterobacteriaceae such as
PT Escherichia in food or water sample, by hybridizing test sample with a
PT probe, and detecting hybridization between probe and a nucleic acid in
PT sample.
XX
PS Claim 3; Page 63; 90pp; English.

XX
CC The present sequence is that of an oligonucleotide that can be used as a
CC hybridisation probe for detecting or identifying Escherichia coli
CC quanosine triphosphate triphosphohydrolase (dGTPase) dgt gene sequences,
CC or as a primer for DNA synthesis, DNA sequencing or DNA amplification of
CC dGTPase nucleic acids. dGTPase is found only in Enterobacteriaceae, such
CC as Escherichia coli, Salmonella and Klebsiella species. Detection of the
CC enzyme is therefore a specific indicator that Enterobacteriaceae
CC pathogens are present in a test sample. The invention relates to the
CC detection of Enterobacteriaceae and to the identification of the genus or
CC genera of Enterobacteriaceae present in a test sample. It is based on the
CC detection of dGTPase nucleic acids or dGTPase enzyme using e.g.
CC hybridisation probes comprising the present nucleic acid, DNA
CC amplification primers, or biosensor chips comprising the present nucleic
CC acid. The methods are useful for determining whether food, water or other
CC samples are contaminated with enteric bacteria

SQ Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1689 CTCGACGCTGGTGGAA 1704
Db 2 CTGCACGCTGGCGGCA 17

RESULT 781
ADB40118/C
ID ADB40118 standard; DNA; 17 BP.
XX
AC ADB40118;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #441.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.

XX Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-000:1981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.

PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 83; 771pp; French.

XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and/or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC cells containing the vectors). The nucleotides (also vectors containing them and
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.

SQ Sequence 17 BP; 6 A; 6 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1711 TTAGGAGTACGGAGAT 1726

```
Db 17 TTAGGAGTATGCGAT 2
|||||
RESULT 782
ADB40655
ID ADB40655 standard; DNA; 17 BP.
XX AC
XX ADB40655;
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
DE
DE Tumour suppression/reversion associated nucleotide #978.
XX
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
XX
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX
XX Disclosure; Page 146; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
XX
XX Sequence 17 BP; 3 A; 10 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1735 GCTCCCAACTCCTCCC 1750
XX | | | | | | | | | |
XX Db 1 GATCCCAACTGCCCC 16
```

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RESULT 783
ADB40250
ID ADB40250 standard; DNA; 17 BP.
XX AC
XX ADB40250;
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
DE
DE Tumour suppression/reversion associated nucleotide #573.
XX
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
XX
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX
XX Disclosure; Page 99; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
XX
XX Sequence 17 BP; 6 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1735 GCTCCCAACTCCTCCC 1750
XX | | | | | | | | | |
XX Db 1 GATCCCAACTCCTCCC 16
```

RESULT 784
ADB39772

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ID ADB39772 standard; DNA; 17 BP.
XX AC
XX ADB39772;
XX DT
XX DE
XX DT 18-DEC-2003 (revised)
XX DT 04-DEC-2003 (first entry)
XX DT
XX DE Tumour suppression/reversion associated nucleotide #95.
XX KW
XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
XX KW primer; probe; tumour suppression; tumour reversion; apoptosis;
XX KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX KW diagnosis.
XX OS
XX OS Homo sapiens.
XX PN WO2003040369-A2.
XX PD
XX PD 15-MAY-2003.
XX PF
XX PF 17-SEP-2002; 2002WO-IB004219.
XX PR
XX PR 17-SEP-2001; 2001PR-00011981.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-441574/41.
XX PT
XX PT New nucleic acid encoding human prostate membrane-specific antigen,
XX PT useful e.g. for treatment of tumors and viral infection, also related
XX PT polypeptide and antibodies.
XX PS
XX PS Disclosure; Page 43; 71pp; French.
XX CC
XX CC The invention relates to the isolation of 6327 nucleotide sequences,
XX CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX CC sequence having at least 80% identity, after optimal alignment, with the
XX CC nucleotides, a sequence that hybridizes under stringent conditions with
XX CC the nucleotides, or the complement, or corresponding RNA, of the
XX CC nucleotides. The nucleotides are used as probes or primers for detecting,
XX CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX CC sense and antisense sequences, of nucleotides involved in tumour
XX CC suppression or reversion, apoptosis and or viral resistance, to produce
XX CC recombinant polypeptides, and to prepare transgenic animals, as
XX CC experimental models. The nucleotides (also vectors containing them and
XX CC cells containing the vectors), the encoded polypeptides and antibodies
XX CC (Ab) against the polypeptide are useful for prevention and/or treatment
XX CC of viral infections or diseases characterized by development of tumours
XX CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX CC Analysis of the expression of the nucleotides can be used for diagnosis
XX CC and/or prognosis of these diseases. The nucleotides and polypeptides can
XX CC also be used to screen for their specific interactive molecules,
XX CC potentially useful for treating diseases associated with abnormal
XX CC expression of the nucleotides.
XX SQ
XX SQ Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Fred. NO. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1663 GCTCACAGCTGGACC 1678
Db 1 GATCACACCGGAAC 16

RESULT 785
ADC04842/c
ID ADC04842 standard; DNA; 17 BP.
XX AC
XX AC ADC04842;

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XX
XX DT
XX XX 18-DEC-2003 (first entry)
XX XX Human Na/H exchanger-like protein 1 gene oligonucleotide #1289.
XX XX ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX KW NHEP1; passive replacement therapy; vaccine; diagnosis.
XX XX
XX OS
XX OS Homo sapiens.
XX PN EP1273660-A2.
XX PD
XX PD 08-JAN-2003.
XX PF
XX PF 25-JAN-2002; 2002EP-00001160.
XX PR
XX PR 30-JAN-2001; 2001WO-US0000666.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 21-DEC-2001; 2001US-0343331P.
XX PA (AEOM-) AEOMICA INC.
XX PI
XX PI Gu Y;
XX DR WPI; 2003-302724/30.
XX XX
XX XX New human sodium-hydrogen exchanger like protein 1 (NHEP1), useful as a
XX PT passive replacement therapy or as a vaccine for treating or preventing
XX PT disorders associated with aberrant expression or activity of human
XX PT NHEP1.
XX PS
XX PS Example 2; SEQ ID NO 1329; 468pp; English.
XX CC
XX CC The invention relates to a nucleic acid molecule which encodes a Na+/H+
XX CC exchanger like protein (NHEP1). The NHEP1 nucleic acid molecule, NHEP1
XX CC polypeptide, an antibody against the protein or its antigen-binding
XX CC fragment is useful in therapy. The NHEP1 nucleic acid molecule, NHEP1
XX CC polypeptide and an agonist are particularly useful for manufacturing a
XX CC medicament for treating or preventing a disorder associated with
XX CC decreased expression or activity of human NHEP1. The antibody or its
XX CC antigen-binding fragment, and an antagonist, are useful for manufacturing
XX CC a medicament for treating or preventing a disorder associated with
XX CC increased expression or activity of human NHEP1. The NHEP1 nucleic acid
XX CC or protein is useful as passive replacement therapy, as a vaccine, or in
XX CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
XX CC spanning the sequence of the human NHEP1 gene (ADC03514).
XX SQ
XX SQ Sequence 17 BP; 0 A; 11 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Fred. NO. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1713 AGGAGTACGGAGATGG 1728
Db 17 AGGAGGAGGAGAGGG 2

RESULT 786
ADC04230
ID ADC04230 standard; DNA; 17 BP.
XX AC
XX AC ADC04230;
XX XX
XX XX 18-DEC-2003 (first entry)
XX XX Human Na/H exchanger-like protein 1 gene oligonucleotide #677.
XX XX ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX KW NHEP1; passive replacement therapy; vaccine; diagnosis.
XX OS
XX OS Homo sapiens.
XX AC

```

```

PN EP1273660-A2.
XX
XX PD
XX
XX PF
XX 25-JAN-2002; 2002EP-00001160.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX PR
XX 23-MAY-2001; 2001US-00864761.
XX PR
XX 21-DEC-2001; 2001US-0343331P.
XX
XX PA
XX (AEOM-) AEOMICA INC.
XX
XX PI
XX Gu Y;
XX
XX DR
XX WPI; 2003-302724/30.
XX
XX PT
XX New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
XX passive replacement therapy or as a vaccine for treating or preventing
XX disorders associated with aberrant expression or activity of human
XX NHEPL1.
XX
XX PS
XX Example 2; SEQ ID NO 717; 468pp; English.
XX
XX CC
XX The invention relates to a nucleic acid molecule which encodes a Na+/H+
XX exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1
XX polypeptide, an antibody against the protein or its antigen-binding
XX fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1
XX polypeptide and an agonist are particularly useful for manufacturing a
XX medicament for treating or preventing a disorder associated with
XX decreased expression or activity of human NHEPL1. The antibody or its
XX antigen-binding fragment, and an antagonist, are useful for manufacturing
XX a medicament for treating or preventing a disorder associated with
XX increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid
XX or protein is useful as passive replacement therapy, as a vaccine, or in
XX diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
XX spanning the sequence of the human NHEPL1 gene (ADC03514).
XX
XX SQ
XX Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 1679 CTGGTGTCTCTCCAG 1694
Db 1 CTGATGTCGTCTACAG 16
XX
XX RESULT 787
XX ADC04229
XX ID ADC04229 standard; DNA; 17 BP.
XX
XX AC
XX ADC04229;
XX
XX DT
XX 18-DEC-2003 (first entry)
XX
XX DE
XX Human Na/H exchanger-like protein 1 gene oligonucleotide #676.
XX
XX KW
XX ss: gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX NHEPL1; passive replacement therapy; vaccine; diagnosis.
XX
XX OS
XX Homo sapiens.
XX
XX PN
XX EP1273660-A2.
XX
XX PD
XX 08-JAN-2003.
XX
XX PF
XX 25-JAN-2002; 2002EP-00001160.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX PR
XX 23-MAY-2001; 2001US-00864761.
XX PR
XX 21-DEC-2001; 2001US-0343331P.
XX
XX PA
XX (AEOM-) AEOMICA INC.
XX
XX PI
XX Gu Y;
XX
XX DR
XX WPI; 2003-302724/30.
XX
XX PT
XX New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
XX passive replacement therapy or as a vaccine for treating or preventing
XX disorders associated with aberrant expression or activity of human
XX NHEPL1.
XX
XX PS
XX Example 2; SEQ ID NO 717; 468pp; English.
XX
XX CC
XX The invention relates to a nucleic acid molecule which encodes a Na+/H+
XX exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1
XX polypeptide, an antibody against the protein or its antigen-binding
XX fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1
XX polypeptide and an agonist are particularly useful for manufacturing a
XX medicament for treating or preventing a disorder associated with
XX decreased expression or activity of human NHEPL1. The antibody or its
XX antigen-binding fragment, and an antagonist, are useful for manufacturing
XX a medicament for treating or preventing a disorder associated with
XX increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid
XX or protein is useful as passive replacement therapy, as a vaccine, or in
XX diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
XX spanning the sequence of the human NHEPL1 gene (ADC03514).
XX
XX SQ
XX Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 1679 CTGGTGTCTCTCCAG 1694
Db 1 CTGATGTCGTCTACAG 16
XX
XX RESULT 788
XX ADC04843/C
XX ID ADC04843 standard; DNA; 17 BP.
XX
XX AC
XX ADC04843;
XX
XX DT
XX 18-DEC-2003 (first entry)
XX
XX DE
XX Human Na/H exchanger-like protein 1 gene oligonucleotide #1290.
XX
XX KW
XX ss: gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX NHEPL1; passive replacement therapy; vaccine; diagnosis.
XX
XX OS
XX Homo sapiens.
XX
XX PN
XX EP1273660-A2.
XX
XX PD
XX 08-JAN-2003.
XX
XX PF
XX 25-JAN-2002; 2002EP-00001160.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX PR
XX 23-MAY-2001; 2001US-00864761.
XX PR
XX 21-DEC-2001; 2001US-0343331P.
XX
XX PA
XX (AEOM-) AEOMICA INC.
XX
XX PI
XX Gu Y;
XX
XX DR
XX WPI; 2003-302724/30.
XX
XX PT
XX New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
XX passive replacement therapy or as a vaccine for treating or preventing
XX disorders associated with aberrant expression or activity of human
XX NHEPL1.

```

XX PS Example 2; SEQ ID NO 1330; 468bp; English.

XX CC The invention relates to a nucleic acid molecule which encodes a Na+/H+ exchanger-like protein (NHEP1). The NHEP1 nucleic acid molecule, NHEP1 polypeptide, an antibody against the protein or its antigen-binding fragment is useful in therapy. The NHEP1 nucleic acid molecule, NHEP1 polypeptide and an agonist are particularly useful for manufacturing a medicament for treating or preventing a disorder associated with decreased expression or activity of human NHEP1. The antibody or its antigen-binding fragment, and an antagonist, are useful for manufacturing a medicament for treating or preventing a disorder associated with increased expression or activity of human NHEP1. The NHEP1 nucleic acid or protein is useful as passive replacement therapy, as a vaccine, or in diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide spanning the sequence of the human NHEP1 gene (ADC03514).

XX SQ Sequence 17 BP; 0 A; 10 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1713 AGGAGTACGGAGATGG 1728
16 AGGAGGAGGAGAGGG 1

Db 1713 AGGAGTACGGAGATGG 1728
16 AGGAGGAGGAGAGGG 1

RESULT 789
ADB45742/c

ID ADB45742 standard; DNA; 17 BP.

AC ADB45742;

DT 18-DEC-2003 (first entry)

DE Tumour suppression/reversion associated nucleotide #6065.

KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.

OS Homo sapiens.

XX WO2003040369-A2.

XX 15-MAY-2003.

XX 17-SEP-2002; 2002WO-IB004219.

XX 17-SEP-2001; 2001FR-00011981.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-441574/41.

PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.

XX Disclosure; Page 741; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies

CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.

XX SQ Sequence 17 BP; 3 A; 9 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1717 GTACGGAGATGGAGAT 1732
17 GGATGGGAGATGGAGAT 2

Db 1717 GTACGGAGATGGAGAT 1732
17 GGATGGGAGATGGAGAT 2

RESULT 790
ADB45372

ID ADB45372 standard; DNA; 17 BP.

AC ADB45372;

DT 18-DEC-2003 (first entry)

DE Tumour suppression/reversion associated nucleotide #5695.

KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.

OS Homo sapiens.

XX WO2003040369-A2.

XX 15-MAY-2003.

XX 17-SEP-2002; 2002WO-IB004219.

XX 17-SEP-2001; 2001FR-00011981.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-441574/41.

PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.

XX Disclosure; Page 697; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies

(Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia). Analysis of the expression of the nucleotides can be used for diagnosis CC and/or prognosis of these diseases. The nucleotides and polypeptides can CC also be used to screen for their specific interactive molecules, CC potentially useful for treating diseases associated with abnormal CC expression of the nucleotides.

XX Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other; 0;
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCAGGCTTACAG 1670
 Db 2 ATCACAGGCTTACAG 17

RESULT 791
 ADB4458/c
 ID ADB4458 standard; DNA; 17 BP.
 XX AC ADB4458;
 XX DT 18-DEC-2003 (first entry)
 XX DE Tumour suppression/reversion associated nucleotide #5181.
 XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX OS Homo sapiens.
 XX PN WO2003040369-A2.
 XX PD 15-MAY-2003.
 XX PF 17-SEP-2002; 2002WO-IB004219.
 XX PR 17-SEP-2001; 2001FR-00011981.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX DR WPI; 2003-441574/41.
 XX PT New nucleic acid encoding human prostate membrane-specific antigen,
 XX useful e.g. for treatment of tumours and viral infection, also related
 XX polypeptide and antibodies.
 XX PS Disclosure; Page 637; 771pp; French.
 XX CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis

CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

XX Sequence 17 BP; 4 A; 4 C; 1 G; 8 T; 0 U; 0 Other;
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1723 AGATGGAGATTGGTC 1738
 Db 16 AATGGAAATTGGATC 1

RESULT 792
 ADB4800/c
 ID ADB4800 standard; DNA; 17 BP.
 XX AC ADB4800;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human NOVX reverse PCR primer SEQ ID NO:362.
 XX KW human; cardiant; antiarteriosclerotic; hypotensive; immunosuppressive;
 KW dermatological; anorectic; cytostatic; antidiabetic; haemostatic;
 KW anti-HIV; antiasthmatic; antibacterial; virucide; neuroprotective;
 KW nootropic; antiparkinsonian; antilipaemic; gene therapy; vaccine; PCR;
 KW primer; ss.
 XX OS Homo sapiens.
 XX PN WO2003076642-A2.
 XX PD 18-SEP-2003.
 XX PF 02-AUG-2002; 2002WO-US024459.
 XX PR 02-AUG-2001; 2001US-0309501P.
 XX PR 03-AUG-2001; 2001US-0310291P.
 XX PR 08-AUG-2001; 2001US-0310951P.
 XX PR 09-AUG-2001; 2001US-0311322P.
 XX PR 13-AUG-2001; 2001US-0311979P.
 XX PR 14-AUG-2001; 2001US-0312203P.
 XX PR 17-AUG-2001; 2001US-0313156P.
 XX PR 17-AUG-2001; 2001US-0313201P.
 XX PR 20-AUG-2001; 2001US-0313702P.
 XX PR 21-AUG-2001; 2001US-0314031P.
 XX PR 23-AUG-2001; 2001US-0314466P.
 XX PR 28-AUG-2001; 2001US-0315403P.
 XX PR 29-AUG-2001; 2001US-0315853P.
 XX PR 31-AUG-2001; 2001US-0316508P.
 XX PR 21-SEP-2001; 2001US-0323936P.
 XX PR 03-DEC-2001; 2001US-0338078P.
 XX PR 05-FEB-2002; 2002US-0354655P.
 XX PR 05-MAR-2002; 2002US-0361764P.
 XX PR 19-APR-2002; 2002US-0373825P.
 XX PR 15-MAY-2002; 2002US-0380971P.
 XX PR 15-MAY-2002; 2002US-0380980P.
 XX PR 16-MAY-2002; 2002US-0381039P.
 XX PR 28-MAY-2002; 2002US-0383761P.
 XX PR 29-MAY-2002; 2002US-0383887P.
 XX PR 01-AUG-2002; 2002US-00210130.
 XX (CURA-) CURAGEN CORP.
 XX Zerkusen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK;
 XX Pena CBA, Shimkets RA, Li L, Berghs C, Zhong M, Casman SJ, Voss EZ;
 XX Boldog FL, Padigaru M, Smithson G, Shenoy SG, Ji W, Gorman L;
 XX Vernet CAM, Leite MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;
 XX Burgess CE, Khramtsov NV, Ort T, Ellerman K, Rastelli L, Agee ML;

PI Chaudhuri A, Chant JS, Dipippo VA, Edinger SR, Eisen A, Gangolli EA;
PI Giot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjal T, Liu X;
PI Taupier RJ, Catterton E;
XX
XX
XX
XX WPI; 2003-779062/73.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes,
PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
PT or pharmacogenomics.
XX
XX Example 49; SEQ ID NO 362; 562pp; English.
XX
XX The invention relates to a novel (NOVX) human polypeptide. A polypeptide
CC of the invention has cardiant, antiarteriosclerotic, hypotensive,
CC immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,
CC haemostatic, anti-HIV, antiasthmatic, antibacterial, virucide,
CC neuroprotective, nootropic, antiparkinsonian, and antilipaeamic activity.
CC A polynucleotide encoding a polypeptide of the invention may have a use
CC in gene therapy, and as a vaccine. A polypeptide of the invention is
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, the disease selected from a pathology
CC associated with the polypeptide. These may also be used in diagnosing,
CC treating or preventing NOVX-associated disorders such as cardiomyopathy,
CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,
CC haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,
CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,
CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's
CC disease), haematopoietic disorders, dyslipidaemias and other wasting
CC disorders associated with chronic diseases. The nucleic acids are also
CC used as hybridisation probes, in chromosome mapping, tissue typing,
CC preventive medicine, and pharmacogenomics. The polypeptides are also
CC useful as vaccines. The present sequence represents a PCR primer used in
CC the invention.
XX
XX SQ Sequence 17 BP; 2 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. NO. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1719 ACCGAGATGGAGATTG 1734
DB 16 ACCGAGCTGGAGTGG 1
RESULT 793
AAA92575/c
ID AAA92575 standard; DNA; 18 BP.
XX
XX AAA92575;
XX
XX 04-JAN-2001 (first entry)
XX
XX Antisense oligonucleotide ISIS# 30285.
XX
XX Human, SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;
KW SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.
XX
XX Synthetic.
XX
XX US6107092-A.
XX
XX 22-AUG-2000.
XX
XX 29-MAR-1999; 99US-00280409.
XX
XX 29-MAR-1999; 99US-00280409.
XX
XX (ISIS-) ISIS PHARM INC.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX
XX Cowsert LM, Bennett CF, O'malley BW;
PI

XX
DR WPI; 2000-586211/55.
XX
PT Antisense compounds targeted to steroid receptor RNA activator useful for
PT diagnosis, prophylaxis and treatment of diseases associated with the
PT steroid activator, such as infection, inflammation or tumor formation.
XX
PS Claim 3; Col 41; 47pp; English.
XX
CC The present sequence is one of a large number of antisense
CC oligonucleotides which is directed against one of four human steroid
CC receptor RNA activator (SRA) nucleic acid sequences. Two series of
CC antisense oligonucleotides were synthesised. The first series comprised 8
CC -30 oligodeoxynucleotides with a phosphorothioate backbone. The second
CC series comprised chimeric oligonucleotides composed of a central gap
CC region, consisting of ten 2'-deoxynucleotides, which was flanked on both
CC sides by four-nucleotide wings. The wings were composed of 2'-
CC methoxyethyl (2'-MOE) nucleotides. Both series contained the same
CC nucleotide sequences. The antisense compounds are useful for research,
CC diagnosis, treatment and prophylaxis to prevent or delay infection,
CC inflammation or tumour formation. Therapeutically the oligonucleotides
CC are highly safe and are effectively administered to humans
XX
XX SQ Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. NO. 5.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1658 ACCAGGCTTCACAGC*G 1673
DB 16 ACCAGGCTTCACAGC 1
RESULT 794
AAC58274/c
ID AAC58274 standard; DNA; 19 BP.
XX
XX AAC58274;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human PRO212 reverse PCR primer SEQ ID NO:93.
XX
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; PCR primer;
KW hybridisation; probe; cytostatic; nootropic; neuroprotective;
KW antiinflammatory; immunosuppressive; immunostimulant; angiogenic;
KW leukaemia; lymphoid malignancy; neuronal disorder; glial disorder;
KW astrocytal disorder; hypothalamic disorder; glandular disorder;
KW macrophagal disorder; epithelial disorder; stromal disorder;
KW blastocoeic disorder; inflammatory disorder; angiogenic;
KW immunologic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200053755-A2.
XX
XX 14-SEP-2000.
XX
XX 06-JAN-2000; 2000WO-US000376.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 07-JUL-1999; 99US-0143048P.
XX 26-JUL-1999; 99US-0145698P.
XX 30-NOV-1999; 99WO-US028313.
XX 20-DEC-1999; 99WO-US039311.
XX 05-JAN-2000; 2000WO-US000219.
XX
XX (GETH) GENENTECH INC.
XX

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KU, Roy MA;
PI Watanabe CK, Wood WI;
XX WPI; 2000-572270/53.
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer.
XX
PS Example 23; Page 133; 286pp; English.
XX
CC The present invention describes an isolated antibody that binds to one of
CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,
CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,
CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,
CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR
CC PRO2199. PRO antagonists can be used to inhibit tumour cell growth. The
CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis
CC and prevention of cancer. The antibodies and other anti-tumour compounds
CC may be used to treat various conditions, including those characterised by
CC overexpression and/or activation of the amplified PRO genes. Exemplary
CC conditions or disorders to be treated with such antibodies and other
CC compounds include benign or malignant tumours (e.g., renal, liver,
CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,
CC glioblastomas, and various head and neck tumours), leukaemias and
CC lymphoid malignancies, other disorders such as neuronal, glial,
CC astrocytal, hypothalamic and other glandular, macrophagal, epithelial,
CC stromal and blastocoele disorders, and inflammatory, angiogenic and
CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and
CC hybridisation probes used in the isolation of the human PRO sequences.
CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO
CC polynucleotide and protein sequences given in the exemplification of the
CC present invention
XX
SQ Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 5.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1655 AGCACGACGCTCACAG 1670
Db 17 AGCACGACGGTACAG 2
RESULT 795
ADB6783/C
ID ADB66783 standard; DNA; 20 BP.
XX
AC ADB66783;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human E2A-Pbx1 antisense phosphorothioate oligonucleotide ISIS No. 16123.
XX
DE Human; E2A-Pbx1; antisense; phosphorothioate;
KW pre-B-cell acute lymphocytic leukaemia; sarcomatous cancer; E2A-HLA;
KW E2A-HLF; cytostatic; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod base= OTHER
FT /note= "phosphorothioate internucleotide linkages"
XX
XX US6607915-B1.
XX 19-AUG-2003.
XX
XX 25-JUL-2000; 2000US-00624945.

XX 30-SEP-1999; 99US-0156836P.
PR
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wancewicz E;
XX
DR WPI; 2003-707866/67.
XX
PT New antisense compounds targeted to nucleic acids encoding E2A-Pbx1,
PT useful for inhibiting the expression of E2A-Pbx1, and for treating or
PT diagnosing a disease associated with overexpression of E2A-Pbx1, e.g.
PT sarcomatous cancer.
XX
PS Example 2; Col 24; 20pp; English.
XX
CC The present invention relates to antisense compounds targeted to
CC polynucleotide sequences encoding human E2A-Pbx1. The antisense compounds
CC comprise antisense phosphorothioate oligonucleotides. The antisense
CC compounds are useful for inhibiting the expression of E2A-Pbx1, and for
CC treating or diagnosing a disease or condition associated with the
CC overexpression or constitutive activation of E2A-Pbx1, e.g. pre-B-cell
CC acute lymphocytic leukaemia or sarcomatous cancer. The compounds are also
CC useful as research reagents and tools, e.g. for detecting and determining
CC the role of E2-Pbx1 in various cell functions and physiological
CC processes. The present sequence represents a human E2A-Pbx1 antisense
CC phosphorothioate oligonucleotide.
XX
SQ Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 20;
Best Local Similarity 81.2%; Pred. No. 6.3e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1668 CAGCTGGAAACCTGGT 1683
Db 16 CAGCTGTCAGCCTGGT 1
RESULT 796
ABV69782
ID ABV69782 standard; cDNA; 11 BP.
XX
AC ABV69782;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7568.
XX
DE Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENKEL) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX

PS Claim 24; Page 239; 1345pp; German.

CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

XX SQ Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1681 GGTCGTCCTC 1691
 |||||
 Db 1 GGTCGTCCTC 11

RESULT 797

ABV62361
 ID ABV62361 standard; cDNA; 11 BP.

XX AC ABV62361;

XX DT 21-OCT-2002 (first entry)

XX DE Human skin EST 147.

XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO200253774-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-EP015179.

XX PR 03-JAN-2001; 2001DE-01000127.

XX PA (HENK) HENKEL KGAA.

XX PI Petersohn D, Conradt M, Hofmann K;

XX WPI; 2002-590638/63.

DR In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX PS Disclosure; Page 30; 1345pp; German.

CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag

CC (EST) of the invention

XX SQ Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1681 GGTCGTCCTC 1691
 |||||
 Db 1 GGTCGTCCTC 11

RESULT 798

ABI08693
 ID ABI08693 standard; DNA; 12 BP.

XX AC ABI08693;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 308666 for detecting SNP TSC0023148.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB00713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 308666; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 1 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1746 CTCCTATCCT 1756
 |||||
 Db 1 CTCCTATCCT 11

```

RESULT 799
ABI58915/C
ID ABI58915 standard; DNA; 12 BP.
XX
XX AC ABI58915;
XX
XX DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 358888 for detecting SNP TSC0051363.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 358888; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1746 CTCCTATCCT 1756
Db 12 CTCCTATCCT 2

RESULT 800
ABI01113
ID ABI01113 standard; DNA; 12 BP.
XX
XX AC ABI01113;
XX
XX DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 301086 for detecting SNP TSC0019345.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```

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XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 301086; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1737 TCCCACTCCT 1747
Db 2 TCCCACTCCT 12

RESULT 801
ABI53626
ID ABI53626 standard; DNA; 12 BP.
XX
XX AC ABI53626;
XX
XX DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 353599 for detecting SNP TSC0048610.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
```

PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 333599; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1703 AAGTTGGGTTA 1713
DB 1 AAGTTGGGTTA 11
RESULT 802
ABI65852/c
ID ABI65852 standard; DNA; 12 BP.
XX
AC ABI65852;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 365825 for detecting SNP TSC0055375.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 365825; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1703 AAGTTGGGTTA 1713
DB 1 AAGTTGGGTTA 11
RESULT 803
ABI33606/c
ID ABI33606 standard; DNA; 12 BP.
XX
AC ABI33606;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 333579 for detecting SNP TSC0037611.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 333579; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
XX
Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1747 TCCTATCCTA 1757
DB 11 TCCTATCCTA 1
RESULT 803
ABI33606/c
ID ABI33606 standard; DNA; 12 BP.
XX
AC ABI33606;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 333579 for detecting SNP TSC0037611.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 333579; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
XX
Query Match 7.9%; Score 11; DB 1; Length 12;

```

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 1747 TCCTATCCTA 1757
Db 12 TCCTATCCTA 2
|||||

RESULT 804
AB181002/c
ID AB181002 standard; DNA; 12 BP.
XX
AC AB181002;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 380975 for detecting SNP TSC0064086.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 380975; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1724 GATGGAGATTG 1734
Db 12 GATGGAGATTG 2
|||||

RESULT 805
AB168036
ID AB168036 standard; DNA; 12 BP.
XX
XX AB168036;
AC

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 1724 GATGGAGATTG 1734
Db 12 GATGGAGATTG 2
|||||

RESULT 806
AB159814
ID AB159814 standard; DNA; 12 BP.
XX
XX AB159814;
AC

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1724 GATGGAGATTG 1734
Db 1 GATGGAGATTG 11
|||||

RESULT 806
AB159814
ID AB159814 standard; DNA; 12 BP.
XX
XX AB159814;
AC

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1724 GATGGAGATTG 1734
Db 12 GATGGAGATTG 2
|||||

RESULT 805
AB168036
ID AB168036 standard; DNA; 12 BP.
XX
XX AB168036;
AC

Oligonucleotide primer SEQ ID NO 368009 for detecting SNP TSC0056696.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 368009; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1724 GATGGAGATTG 1734
Db 1 GATGGAGATTG 11
|||||

RESULT 806
AB159814
ID AB159814 standard; DNA; 12 BP.
XX
XX AB159814;
AC

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1724 GATGGAGATTG 1734
Db 12 GATGGAGATTG 2
|||||

RESULT 805
AB168036
ID AB168036 standard; DNA; 12 BP.
XX
XX AB168036;
AC

Oligonucleotide primer SEQ ID NO 359787 for detecting SNP TSC0051760.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.

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PD XX 18-OCT-2001.
PF XX
PR XX 06-APR-2001; 2001WO-IB000713.
PR XX 07-APR-2000; 2000DE-01019173.
PR XX (EPIG-) EPIGENOMICS AG.
PR XX
PI XX Olek A, Piepenbrock C, Berlin K;
PI XX
DR XX WPI; 2001-657177/75.
DR XX
PT XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT XX designed to detect single-nucleotide polymorphisms and cytosine
PT XX methylation status.
PT XX
PS XX Claim 1; SEQ ID NO 359787; 29pp + Sequence Listing; German.
PS XX
CC XX This invention describes novel oligonucleotide primers or peptide nucleic
CC XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC XX and cytosine methylation status in chemically pretreated genomic DNA. The
CC XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC XX range of diseases including immune system, gastrointestinal, respiratory,
CC XX central nervous system, cardiovascular and metabolic disorders. The
CC XX oligomers are also used for detecting cell type differentiation. ABC00010
CC XX -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC XX represent the oligomers described in the invention. NOTE: The sequence
CC XX data for this patent did not form part of the printed specification, but
CC XX was obtained in electronic format from WIPO at
CC XX ftp.wipo.int/pub/published_pct_sequences
CC XX
SQ XX Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;
SQ XX
Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1721 GGAGTGGAGA 1731
DB 1 GGAGTGGAGA 11
|||||
RESULT 807
ABI77791/c
ID ABI77791 standard; DNA; 12 BP.
XX
AC ABI77791;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 377764 for detecting SNP TSC0007286.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF Oligonucleotide primer SEQ ID NO 377764 for detecting SNP TSC0007286.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
PR XX
PA (EPIG-) EPIGENOMICS AG.
PI XX Olek A, Piepenbrock C, Berlin K;
PI XX
DR WPI; 2001-657177/75.
DR XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT XX designed to detect single-nucleotide polymorphisms and cytosine
PT XX methylation status.
PT XX
PS Claim 1; SEQ ID NO 359787; 29pp + Sequence Listing; German.
PS XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1704 AGTTCGGTTAG 1714
DB 11 AGTTCGGTTAG 1
|||||
RESULT 808
ABH98049
ID ABH98049 standard; DNA; 12 BP.
XX
AC ABH98049;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 298042 for detecting SNP TSC0017887.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
PR XX
PA (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
PI
DR WPI; 2001-657177/75.
DR
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
PS Claim 1; SEQ ID NO 298042; 29pp + Sequence Listing; German.
PS
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1704 AGTTCGGTTAG 1714
DB 11 AGTTCGGTTAG 1
|||||

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CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1698 GGTGGAAGTTG 1708
|||||
Db 2 GGTGGAAGTTG 12

RESULT 809
ABH74564
ID ABH74564 standard; DNA; 12 BP.

XX AC ABH74564;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 274549 for detecting SNP TSC0003590.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PI WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

XX PS Claim 1; SEQ ID NO 274549; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABJ00010-ABJ82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1704 AGTTCGGTTAG 1714
|||||

Db 2 AGTTCGGTTAG 12

RESULT 810
ABI40118

XX ID ABI40118 standard; DNA; 12 BP.

XX AC ABI40118;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 340091 for detecting SNP TSC0041342.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PI WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

XX PS Claim 1; SEQ ID NO 340091; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABJ00010-ABJ82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1708 GGGTTAGGAGT 1718
|||||
Db 1 GGGTTAGGAGT 11

RESULT 811
ABC37623

XX ID ABC37623 standard; DNA; 13 BP.

XX AC ABC37623;

XX DT 20-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 37640 for detecting SNP TSC0011712.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 37640; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 1 A; 8 C; 0 G; 3 T; 0 U; 1 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1745 CCTCCCTATCC 1755
Db 2 CCTCCCTATCC 12
RESULT 812
ABF99563
ID ABF99563 standard; DNA; 13 BP.
AC ABF99563;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 198560 for detecting SNP TSC0048863.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 198560; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1749 CCTATCCTCTAAA 1759
Db 1 CCTATCCTCTAAA 11
RESULT 813
ABH01585
ID ABH01585 standard; DNA; 13 BP.
AC ABH01585;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 201562 for detecting SNP TSC0049571.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 201562; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX
 SQ Sequence 13 BP; 2 A; 8 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 CTCCCAACTCC 1746
 Db 3 CTCCCAACTCC 13
 RESULT 814
 ABH30529/c
 ID ABH30529 standard; DNA; 13 BP.
 XX
 AC ABH30529;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 230506 for detecting SNP TSC0056222.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 230506; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 13 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 1 Other;
 Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 4.1e+02;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1724 GATGGAGATTGCC 1736
 Db 13 GATGGAGATTGGY 1
 RESULT 815
 ABC21702
 ID ABC21702 standard; DNA; 13 BP.
 XX
 AC ABC21702;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 21719 for detecting SNP TSC0004349.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 21719; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 1 Other;
 Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 4.1e+02;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1721 GGAGATGGAGATT 1733
 Db 1 GGAGTTGGAGATY 13
 RESULT 816
 ABF22699

ID ABF22699 standard; DNA; 13 BP.
 AC ABF22699;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 122696 for detecting SNP TSC0030668.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 122696; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF22699, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 0 A; 8 C; 0 G; 4 T; 0 U; 1 Other;
 CC
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF22699, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 0 A; 8 C; 0 G; 4 T; 0 U; 1 Other;
 CC
 CC Query Match 7.9%; Score 11; DB 1; Length 13;
 CC Best Local Similarity 84.6%; Pred. No. 4.1e+02;
 CC Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1742 ACTCTCTCCCTATC 1754
 Db :|||||||
 1 RCTCTCCCTCTC 13
 RESULT 817
 ABF22699/c
 ID ABF22699 standard; DNA; 13 BP.
 AC ABF22699;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 122697 for detecting SNP TSC0032287.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.

XX WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 128973; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF22699, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 1 C; 7 G; 3 T; 0 U; 0 Other;
 CC
 CC Query Match 7.9%; Score 11; DB 1; Length 13;
 CC Best Local Similarity 107.0%; Pred. No. 4.1e+02;
 CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 GCTCCCACTC 1745
 Db :|||||||
 12 GCTCCCACTC 2
 RESULT 818
 ABH01584/c
 ID ABH01584 standard; DNA; 13 BP.
 AC ABH01584;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 201561 for detecting SNP TSC0049571.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX

```

DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 201561; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 CTCCTCAACTCC 1746
Db 11 CTCCTCAACTCC 1
|||||
RESULT 819
ABH31314/c
ID ABH31314 standard; DNA; 13 BP.
XX
AC ABH31314;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 231291 for detecting SNP TSC0056398.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 231291; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 CTCCTCAACTCC 1746
Db 11 CTCCTCAACTCC 1
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RESULT 820
ABH08492
ID ABH08492 standard; DNA; 13 BP.
XX
AC ABH08492;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 208469 for detecting SNP TSC0050942.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
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PT methylation status.
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CC central nervous system, cardiovascular and metabolic disorders. The
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XX
SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1748 CCTATATCCTAA 1758
Db 12 CCTATATCCTAA 2
|||||

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CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
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SQ Sequence 13 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 1 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1748 CCTATATCCTAA 1758
Db 12 CCTATATCCTAA 2
|||||
RESULT 820
ABH08492
ID ABH08492 standard; DNA; 13 BP.
XX
AC ABH08492;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 208469 for detecting SNP TSC0050942.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
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PR 07-APR-2000; 2000DE-01019173.
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PI Olek A, Piepenbrock C, Berlin K;
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DR WPI; 2001-657177/75.
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PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 208469; 29pp + Sequence Listing; German.
XX
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CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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CC central nervous system, cardiovascular and metabolic disorders. The
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CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1698 GGTGGAGTTG 1708
 Db 1 GGTGGAGTTG 11
 RESULT 821
 ABH22016
 ID ABH22016 standard; DNA; 13 BP.
 AC ABH22016;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 221993 for detecting SNP TSC0054021.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 AC
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 221993 for detecting SNP TSC0054021.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 AC
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 221993 for detecting SNP TSC0054021.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 AC
 XX
 DT 22-FEB-2002 (first entry)
 XX

QY 1700 TGGAGTTGGTT 1712
 Db 1 TGGAGTTGGTT 13
 RESULT 822
 ABH35639/c
 ID ABH35639 standard; DNA; 13 BP.
 AC ABH35639;
 XX
 DT 22-FEB-2002 (first entry)
 XX

QY 1707 TGGGTTAGGAG 1717
 Db 13 TGGGTTAGGAG 3
 RESULT 823
 ABF86040
 ID ABF86040 standard; DNA; 13 BP.
 AC ABF86040;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 186037 for detecting SNP TSC0045841.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 AC
 XX
 DT 18-OCT-2001.
 XX

QY 1707 TGGGTTAGGAG 1717
 Db 13 TGGGTTAGGAG 3
 RESULT 823
 ABF86040
 ID ABF86040 standard; DNA; 13 BP.
 AC ABF86040;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 186037 for detecting SNP TSC0045841.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 AC
 XX
 DT 18-OCT-2001.
 XX

XX Oligonucleotide SEQ ID NO 235616 for detecting SNP TSC0057525.
 DE
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 AC
 XX
 DT 18-OCT-2001.
 XX
 DE 06-APR-2001; 2001WO-IB000713.
 XX
 KW 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 235616; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
 Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0;
 QY 1707 TGGGTTAGGAG 1717
 Db 13 TGGGTTAGGAG 3
 RESULT 823
 ABF86040
 ID ABF86040 standard; DNA; 13 BP.
 AC ABF86040;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 186037 for detecting SNP TSC0045841.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 AC
 XX
 DT 18-OCT-2001.
 XX

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PF 06-APR-2001; 2001WO-IB000713.
XX
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 186037; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX range of diseases including immune system, gastrointestinal, respiratory,
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XX -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 3 A; 1 C; 7 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred.No. 4.1e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1714 GGAGTACGGAG 1724
XX
XX Db 13 GGAGTACGGAG 3
XX
XX RESULT 824
XX ABC82521
XX ID ABC82521 standard; DNA; 13 BP.
XX
XX AC ABC82521;
XX
XX XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 82538 for detecting SNP TSC0020824.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX XX
XX PN WO200177384-A2.
XX
XX XX
XX PD 18-OCT-2001.
XX
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
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XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
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XX XX
XX DR WPI; 2001-657177/75.
XX
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 82538; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX range of diseases including immune system, gastrointestinal, respiratory,
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XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 3 A; 1 C; 7 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred.No. 4.1e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1714 GGAGTACGGAG 1724
XX
XX Db 1 GGAGTACGGAG 11
XX
XX RESULT 824
XX ABF86041/C
XX ID ABF86041 standard; DNA; 13 BP.
XX
XX AC ABF86041;
XX
XX XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 186038 for detecting SNP TSC0045841.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX XX
XX PN WO200177384-A2.
XX
XX XX
XX PD 18-OCT-2001.
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XX PI Olek A, Piepenbrock C, Berlin K;
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XX XX
XX DR WPI; 2001-657177/75.
XX
XX XX
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XX
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CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;

  Query Match      7.9%; Score 11; DB 1; Length 13;
  Best Local Similarity 84.6%; Pred. No. 4.1e+02;
  Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1741 AACTCTCTCCCTAT 1753
Db      :|||||
        1 RACTCTCTACCTAT 13

RESULT 826
ABF35842
ID ABF35842 standard; DNA; 13 BP.
XX
AC ABF35842;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 135839 for detecting SNP TSC0033923.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
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PR 07-APR-2000; 2000DE-01019173.
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PI Olek A, Piepenbrock C, Berlin K;
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DR WO200177384-A2.
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PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 135839; 29pp + Sequence Listing; German.
XX
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CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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CC central nervous system, cardiovascular and metabolic disorders. The
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CC -ABF35842, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
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  Query Match      7.9%; Score 11; DB 1; Length 13;
  Best Local Similarity 84.6%; Pred. No. 4.1e+02;
  Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1721 GGAGATCGAGATT 1733
Db      :|||||
        1 GGAGATCGAGATY 13

RESULT 828
ABH31315
ID ABH31315 standard; DNA; 13 BP.
XX
AC ABH31315;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 231292 for detecting SNP TSC0056398.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```


Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
Claim 1; SEQ ID NO 82537; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIFO at ftp.wipo.int/pub/published_pct_sequences

Sequence 13 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 1 Other;

Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 4.1e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 1741 AACTCCTCCCTAT 1753
:|||||
Dd 13 RACTCTACCTAT 1

RESULT 830
ABF15181/C
ID 1 ABF15181 standard; DNA; 13 BP.
AC ABF15181;
XX XX
XX XX
DT 21-FEB-2002 (first entry)
XX XX
DE Oligonucleotide SEQ ID NO 115178 for detecting SNP TSC0028862.
XX XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
FN
XX
PD 18-OCT-2001.
PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
FA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
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PT
XX Claim 1; SEQ ID NO 115178; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIFO at ftp.wipo.int/pub/published_pct_sequences

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 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
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 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
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 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1697 TGGTGGAGATT 1707
 Db 11 TGGTGGAGATT 1

RESULT 831
 ABC33136
 ID ABC33136 standard; DNA; 13 BP.
 XX
 AC ABC33136;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 33153 for detecting SNP TSC0010569.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
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 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
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 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 33153; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
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 CC and cytosine methylation status in chemically pretreated genomic DNA. The
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 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
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 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1697 TGGTGGAGATT 1707
 Db 11 TGGTGGAGATT 1

RESULT 831
 ABF35843/C
 ID ABF35843 standard; DNA; 13 BP.
 XX
 AC ABF35843;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 115177 for detecting SNP TSC0028862.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 115177; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1722 GAGATGGAGAT 1732
 Db 2 GAGATGGAGAT 12

RESULT 832
 ABF15180
 ID ABF15180 standard; DNA; 13 BP.
 XX
 AC ABF15180;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 115177 for detecting SNP TSC0028862.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
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 PA (EPIG-) EPIGENOMICS AG.
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 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
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 PT designed to detect single-nucleotide polymorphisms and cytosine
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 CC central nervous system, cardiovascular and metabolic disorders. The
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 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
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 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1697 TGGTGGAGATT 1707
 Db 3 TGGTGGAGATT 13

RESULT 833
 ABF35843/C
 ID ABF35843 standard; DNA; 13 BP.
 XX
 AC ABF35843;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 115177 for detecting SNP TSC0028862.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
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 PF 06-APR-2001; 2001WO-IB000713.
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 PR 07-APR-2000; 2000DE-01019173.
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 PI Olek A, Piepenbrock C, Berlin K;
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 DR WPI; 2001-657177/75.
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 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 115177; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

AC ABF35843;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 135840 for detecting SNP TSC0033923.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 135840; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 1 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
CC Best Local Similarity 84.6%; Pred. No. 4.1e+02;
CC Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1721 GGAGATGGAGATT 1733
DB 13 GGAGATCGAGATY 1
XX
RESULT 834
ABF46427/c
ID ABF46427 standard; DNA; 13 BP.
XX
AC ABF46427;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 146424 for detecting SNP TSC0036912.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.

XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 146424; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
CC Best Local Similarity 100.0%; Pred. No. 4.1e+02;
CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1722 GAGATGGAGAT 1732
DB 12 GAGATGGAGAT 2
XX
RESULT 835
ABH05407/c
ID ABH05407 standard; DNA; 13 BP.
XX
AC ABH05407;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 205384 for detecting SNP TSC0050352.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 205384; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 7 C; 1 G; 1 T; 0 U; 1 Other;

Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 4.1e+02;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1694 GCGTGGTGAAGT 1706

Db 13 GCGTGGTGTAGY 1

RESULT 836

ABH35638
 ID ABH35638 standard; DNA; 13 BP.

XX AC ABH35638;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 235615 for detecting SNP TSC0057525.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 235615; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 1 Other;

Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1707 TCGGTAGGAG 1717

Db 1 TCGGTAGGAG 11

RESULT 837

ABC46634/C
 ID ABC46634 standard; DNA; 13 BP.

XX AC ABC46634;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 46651 for detecting SNP TSC0013461.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 46651; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1741 AACTCCTCCT 1751

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Db      13 AACTCCTCCT 3
|||||
RESULT 838
ABC21703/c
ID ABC21703 standard; DNA; 13 BP.
XX
XX
AC ABC21703;
XX
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 21720 for detecting SNP TSC0004349.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 21720 for detecting SNP TSC0004349.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 21720; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1721 GGAGTGGAGATT 1733
|||||
Db 13 GGAGTGGAGATT 1
|||||
RESULT 839
ABC37622/c
ID ABC37622 standard; DNA; 13 BP.
XX
XX
AC ABC37622;
XX
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 37639 for detecting SNP TSC0011712.

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XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
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XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
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PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 37639; 29pp + Sequence Listing; German.
XX
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CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
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CC central nervous system, cardiovascular and metabolic disorders. The
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CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1745 CCTCCTATCC 1755
|||||
Db 12 CCTCCTATCC 2
|||||
RESULT 840
ABF35840
ID ABF35840 standard; DNA; 13 BP.
XX
XX
AC ABF35840;
XX
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 135837 for detecting SNP TSC0033923.
XX
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX

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XX SQ Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGA 1731
|||||
Db 13 GGAGATGGAGA 3

RESULT 843
ABH19250
ID ABH19250 standard; DNA; 13 BP.
AC ABH19250;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 219227 for detecting SNP TSC0053301.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPITG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 219227; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
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XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1715 GAGTACGGAGA 1725
|||||
Db 2 GAGTACGGAGA 12

RESULT 844
ABF98562/c
ID ABF98562 standard; DNA; 13 BP.
AC ABF98562;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 198559 for detecting SNP TSC0048863.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
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OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 198559; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1749 CCTATCCTAAA 1759
Db 13 CCTATCCTAAA 3
RESULT 846
ABF84271/C
ID ABF84271 standard; DNA; 13 BP.
AC ABF84271;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 184268 for detecting SNP TSC0006682.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 146423; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
SQ
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1723 AGATGGAGATT 1733
Db 11 AGATGGAGATT 1
RESULT 847
ABF46426
ID ABF46426 standard; DNA; 13 BP.
AC ABF46426;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 146423 for detecting SNP TSC0036912.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IE000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 146423; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
```


CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1722 GAGATGGAGAT 1732
 DB 2 GAGATGGAGAT 12
 RESULT 848
 ABF15421/C
 ID ABF15421 standard; DNA; 13 BP.
 XX
 AC ABF15421;
 XX
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 115418 for detecting SNP TSC0028927.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB0000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 115418; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 1 Other;
 Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1737 TCCCAACTCCT 1747
 DB 3 TCCCAACTCCT 13
 RESULT 850
 ABH05406
 ID ABH05406 standard; DNA; 13 BP.
 XX
 AC ABH05406;
 XX

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1694 GCCTGGTGGAA 1704
 DB 13 GCCTGGTGGAA 3
 RESULT 849
 ABH21129
 ID ABH21129 standard; DNA; 13 BP.
 XX
 AC ABH21129;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 221106 for detecting SNP TSC0053805.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB0000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 221106; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
 Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1737 TCCCAACTCCT 1747
 DB 3 TCCCAACTCCT 13
 RESULT 850
 ABH05406
 ID ABH05406 standard; DNA; 13 BP.
 XX
 AC ABH05406;
 XX

[illegible]

PT methylation status.
PS Claim 1; SEQ ID NO 184267; 29pp + Sequence Listing; German.
XX
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1723 AGATGGAGATT 1733
Db 3 AGATGGAGATT 13
RESULT 853
ABC61028
ID ABC61028 standard; DNA; 13 BP.
XX
AC ABC61028;
XX
XX 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 61045 for detecting SNP TSC0016265.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 61045; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1721 GGAGATGGAGA 1731
Db 1 GGAGATGGAGA 11
RESULT 854
ABF22698/c
ID ABF22698 standard; DNA; 13 BP.
XX
AC ABF22698;
XX
XX 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 122695 for detecting SNP TSC0030668.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 122695; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 8 G; 0 T; 0 U; 1 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 4.1e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1742 ACTCCTCCCTATC 1754
Db 13 RCTCCTCCCTCTC 1

```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 46652; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1741 AACTCCTCCCT 1751
XX Db 1 AACTCCTCCCT 11
XX
XX RESULT 857
XX ABF28977
XX ID ABF28977 standard; DNA; 13 BP.
XX
XX AC ABF28977;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 128974 for detecting SNP TSC0032287.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 135838; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1721 GGAGATGGAGATT 1733
XX Db 13 GGAGATTGAGATY 1
XX
XX RESULT 856
XX ABC46635
XX ID ABC46635 standard; DNA; 13 BP.
XX
XX AC ABC46635;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 46652 for detecting SNP TSC0013461.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

```

PA (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 128974; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 GCTCCCACTC 1745
 DB |||||
 2 GCTCCCACTC 12
 RESULT 858
 ABF15420
 ID ABF15420 standard; DNA; 13 BP.
 AC
 AC ABF15420;
 XX
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 115417 for detecting SNP TSC0028927.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 115417; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 1 Other;
 Query Match 7.9%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1694 GCGTGGTGGA 1704
 DB |||||
 1 GCGTGGTGGA 11
 RESULT 859
 ABH19251/C
 ID ABH19251 standard; DNA; 13 BP.
 AC
 AC ABH19251;
 XX
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 219228 for detecting SNP TSC0053301.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 219228; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

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XX AC AAF29395;
XX DT 27-APR-2001 (first entry)
XX DE Oligonucleotide primer 2 DNA sequence.
XX KW Selective base pair; steric hindrance; static repulsion; ss.
XX OS Synthetic.
XX PN WO200105801-A1.
XX PD 25-JAN-2001.
XX PF 14-JUL-2000; 2000WO-JP04720.
XX PR 15-JUL-1999; 99JP-00201450.
XX PR 02-MAY-2000; 2000JP-00133519.
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PI Hirao I, Ishikawa M, Fujiwara T, Yokoyama S;
XX DR WPI; 2001-147320/15.
XX XX Non-natural nucleic acid base pair recognised by polymerases for
PT production of artificial genes for treatment of genetic disorders.
XX PS Disclosure; Page 14; 64pp; Japanese.
XX CC This invention relates to a non-natural selective base pair for nucleic
CC acids produced by introducing to a nucleic acid base a group imparting
CC steric hindrance to pairing with the counter-base, static repulsion and a
CC stacking effect. The non-natural selective base pair can be used in the
CC production of non-natural genes and their use in the production of nucleic
CC proteins containing non-natural amino acids. The production of nucleic
CC acids for treatment of genetic disorders. Oligonucleotides AAF29385 -
CC AAF29398 represent template and primer sequences used in an example
CC illustrating the invention
XX SQ Sequence 14 BP; 5 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
XX Query Match 7.9%; Score 11; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 4.5e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTAT 1753
Db 13 CTCCTCCCTAT 3

RESULT 862
AAV31919
ID AAV31919 standard; DNA; 15 BP.
XX AC AAV31919;
XX DT 21-AUG-1998 (first entry)
XX DE Peptide nucleic acid probe 62.
XX KW Peptide nucleic acid; PNA; probe; hybridisation; mycobacteria;
XX KW ribosomal nucleic acid; rRNA; drug-resistant strain; mutation; ss.
XX OS Synthetic.
XX OS Mycobacterium sp.
XX FH Key Location/Qualifiers
XX modified_base 1..15
XX FT /*tag= a
XX FT /note= "This sequence contains a polyamide backbone
XX FT instead of a deoxyribose backbone"

Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1715 GAGTACGGAGA 1725
Db 12 GAGTACGGAGA 2

RESULT 860
ABH22017/c
ID ABH22017 standard; DNA; 13 BP.
XX AC ABH22017;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 221994 for detecting SNP TSC0054021.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 221994; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI02073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1700 TGGAGTGGGTT 1712
Db 13 TGGAGTGGGTT 1

RESULT 861
AAF29395/c
ID AAF29395 standard; DNA; 14 BP.

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XX PN WO9815648-A1.
XX PD 16-APR-1998.
XX PF 03-OCT-1997; 97WO-DK000425.
XX PR 04-OCT-1996; 96DK-00001096.
XX PR 18-OCT-1996; 96DK-00001156.
XX PR 05-MAY-1997; 97DK-00000512.
XX PA (DAKO-) DAKO AS.
XX PI Stender H, Lund K, Mollerup TA;
XX DR WPI; 1998-240831/21.
XX PT Peptide nucleic acid probes for detection of ribosomal nucleic acid of
XX PT mycobacteria - allow differentiation between species of tuberculosis
XX PT complex and others and can penetrate cell membranes without pretreatment.
XX PS Claim 22; Page 66; 106pp; English.
XX SQ This is the nucleotide sequence of the peptide nucleic acid (PNA) probe
XX used in the method of the invention, to detect ribosomal nucleic acid of
XX mycobacteria. The probes are used, in situ or in vitro, for detection of
XX the Mycobacterium tuberculosis complex (MTC), specifically M.
XX tuberculosis, and especially in sputum samples, but also in other body
XX fluids, biopsy specimens, foods, soil, air and water. Particularly, they
XX are used to diagnose, stage or monitor infection, or for identification
XX of drug-resistant strains (which generally have mutations in rRNA)
XX SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1759 AGGCCCACTGG 1769
Db |||||
4 AGGCCCACTGG 14

RESULT 863
AAAX31800
ID AAAX31800 standard; DNA; 15 BP.
AC AAAX31800;
XX
XX 21-MAY-1999 (first entry)
XX Transcript tag sequence increased in pancreatic and colorectal cancer.
DE Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.
KW Homo sapiens.
XX WO9853319-A2.
XX 26-NOV-1998.
XX 20-MAY-1998.
XX 20-MAY-1998; 98WO-US010277.
XX 21-MAY-1997; 97US-0047352P.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1999-070161/06.
XX Use of isolated gene transcripts - useful for developing products for the
XX level of at least one transcript in a first sample of a tissue to a

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PT diagnosis, prognosis and treatment of cancers, particularly colon and
PT pancreatic cancer.
XX Disclosure; Page 79; 120pp; English.
XX
XX AAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the
XX tag to a gen data base member, or by using the tag sequences as probes to
XX isolate unidentified genes from cDNA libraries. The tag sequences can
XX also be used in a method for diagnosing colon or pancreatic cancer in a
XX sample suspected of being neoplastic. The method comprises comparing the
XX level of at least one transcript in a first sample of a tissue to a
XX second sample, where the first sample is a colonic tissue suspected of
XX being neoplastic and the second sample is a normal human colonic tissue.
XX The transcript is identified by a tag selected from AAX30947-31815. The
XX methods of the invention can be used in the diagnosis, prognosis and
XX treatment of cancer
XX SQ Sequence 15 BP; 4 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 TGGAACCTCTGG 1682
Db |||||
3 TGGAACCTCTGG 13

RESULT 864
AAAX31164
ID AAAX31164 standard; DNA; 15 BP.
AC AAAX31164;
XX
XX 21-MAY-1999 (first entry)
XX Tag sequence of a transcript increased in colorectal cancer.
DE Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.
KW Homo sapiens.
XX WO9853319-A2.
XX 26-NOV-1998.
XX 20-MAY-1998; 98WO-US010277.
XX 21-MAY-1997; 97US-0047352P.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1999-070161/06.
XX Use of isolated gene transcripts - useful for developing products for the
XX diagnosis, prognosis and treatment of cancers, particularly colon and
XX pancreatic cancer.
XX Claim 2; Page 33; 120pp; English.
XX
XX AAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the
XX tag to a gen data base member, or by using the tag sequences as probes to
XX isolate unidentified genes from cDNA libraries. The tag sequences can
XX also be used in a method for diagnosing colon or pancreatic cancer in a
XX sample suspected of being neoplastic. The method comprises comparing the
XX level of at least one transcript in a first sample of a tissue to a

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CC second sample, where the first sample is a colonic tissue suspected of
 CC being neoplastic and the second sample is a normal human colonic tissue.
 CC The transcript is identified by a tag selected from AAX30947-31815. The
 CC methods of the invention can be used in the diagnosis, prognosis and
 CC treatment of cancer

XX CC
 SQ Sequence 15 BP; 4 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 TGGAAACCTGG 1682

Db 3 TGGAAACCTGG 13

RESULT 865

AAI67293/C
 ID AAI67293 standard; DNA; 15 BP.

XX AC AAI67293;

XX DT 11-FEB-2002 (first entry)

XX XX Human FKBP8 allele-specific oligonucleotide (ASO) probe.

XX KW FKBP8-binding protein 8; FKBP8; haplotyping; polymorphism; cancer; ss;
 KW immunosuppression; human; allele-specific oligonucleotide; ASO; probe.

XX OS Homo sapiens.

XX PN WO200172965-A2.

XX PD 04-OCT-2001.

XX PF 26-MAR-2001; 2001WO-US009718.

XX PR 24-MAR-2000; 2000US-0192125P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Anastasio AE, Bentivegna SC, Choi JY, Klien SE, Koshy B;
 PI Stephens JC;

XX DR WPI; 2001-626261/72.

XX XX New haplotypes of the FKBP8-binding protein 8 gene, useful for genotyping
 PT that gene in individual and to design new therapy for associated disease
 PT such as immunosuppression and cancer.

XX PS Claim 15; Page 13; 98pp; English.

XX XX The invention relates to haplotyping the FKBP8-binding protein 8 (38kD)
 CC (FKBP8) gene in an individual. The method involves determining the
 CC identity of the nucleotide pair at one or more polymorphic sites, selected
 CC from P1 to P26 (described in the specification). The invention is useful
 CC to improve the efficiency and reliability of several steps in the
 CC discovery and development of drugs for treating diseases associated with
 CC FKBP8 activity, for example immunosuppression and cancer. Sequences
 CC AAI67274-299 represent allele-specific oligonucleotide (ASO) probes for
 CC detecting FKBP8 gene polymorphisms

XX SQ Sequence 15 BP; 2 A; 7 C; 4 G; 1 T; 0 U; 1 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 4.9e+02;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1673 GGAACCTGGTGT 1685

Db 15 GGCACCCCGGTGT 3

RESULT 866

AAFS0722
 ID AAF50722 standard; DNA; 15 BP.

XX AC AAF50722;

XX DT 30-MAR-2001 (first entry)

XX XX IGF-I oligonucleotide #1682.

XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX PS Example 8; Page 71; 201pp; English.

XX XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 6 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAC 1677

Db 4 ACAGCTGGAAC 14

RESULT 867

AAFS0724
 ID AAF50724 standard; DNA; 15 BP.


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XX AC AAF50724;
XX XX
XX DT 30-MAR-2001 (first entry)
XX DE
XX DE IGF-I oligonucleotide #1684.
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200078341-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PF 21-JUN-2000; 2000WO-AU000693.
XX XX
XX PR 21-JUN-1999; 99US-0140345P.
XX XX
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX XX
XX PI Wright CJ, Werther GA, Edmondson SR;
XX XX WPI; 2001-041421/05.
XX DR
XX PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX XX
XX PS Example 8; Page 71; 201pp; English.
XX CC
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX XX
XX SQ Sequence 15 BP; 6 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 4.9e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1667 ACAGCTGGAAC 1677
XX Db |||||
XX 2 ACAGCTGGAAC 12
XX
XX RESULT 868
XX AAF50721
XX ID AAF50721 standard; DNA; 15 BP.
XX XX
XX AC AAF50721;
XX XX
XX DT 30-MAR-2001 (first entry)
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

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XX DE IGF-I oligonucleotide #1681.
XX XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200078341-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PF 21-JUN-2000; 2000WO-AU000693.
XX XX
XX PR 21-JUN-1999; 99US-0140345P.
XX XX
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX XX
XX PI Wright CJ, Werther GA, Edmondson SR;
XX XX WPI; 2001-041421/05.
XX DR
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX XX
XX PS Example 8; Page 71; 201pp; English.
XX CC
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX XX
XX SQ Sequence 15 BP; 5 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 4.9e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1667 ACAGCTGGAAC 1677
XX Db |||||
XX 5 ACAGCTGGAAC 15
XX
XX RESULT 869
XX AAF50725
XX ID AAF50725 standard; DNA; 15 BP.
XX XX
XX AC AAF50725;
XX XX
XX DT 30-MAR-2001 (first entry)
XX DE
XX DE IGF-I oligonucleotide #1685.
XX XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

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KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO2000078341-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 XX
 XX 21-JUN-1999; 99US-0140345P.
 PF
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PR
 XX Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 PA
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 XX inhibits or reduces growth factor mediated cell proliferation and/or
 XX inflammation.
 XX Example 8; Page 71; 201pp; English.
 PS
 XX The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 XX inhibiting or reducing growth factor mediated cell proliferation,
 XX inflammation and/or other disorders. The present sequence is an
 XX oligonucleotide which can be used to design the antisense
 XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
 XX F45161). The method is useful for ameliorating the effects of psoriasis,
 XX ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
 XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 XX hyperneovascular condition such as a neovascular condition of the retina,
 XX brain or skin, growth factor-mediated malignancies, other sclerotic
 XX disease, kidney disease, hyperproliferation of the inside of blood
 XX vessels or any other hyperplasia
 XX Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 SQ

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO2000078341-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 XX
 XX 21-JUN-1999; 99US-0140345P.
 PF
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PR
 XX Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 PA
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 XX inhibits or reduces growth factor mediated cell proliferation and/or
 XX inflammation.
 XX Example 8; Page 71; 201pp; English.
 PS
 XX The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 XX inhibiting or reducing growth factor mediated cell proliferation,
 XX inflammation and/or other disorders. The present sequence is an
 XX oligonucleotide which can be used to design the antisense
 XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
 XX F45161). The method is useful for ameliorating the effects of psoriasis,
 XX ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
 XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 XX hyperneovascular condition such as a neovascular condition of the retina,
 XX brain or skin, growth factor-mediated malignancies, other sclerotic
 XX disease, kidney disease, hyperproliferation of the inside of blood
 XX vessels or any other hyperplasia
 XX Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 7.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.9e-02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAAC 1677
 DB 1 ACAGCTGGAAC 13
 RESULT 871
 AAS98658/c
 ID AAS98658 standard; DNA; 15 BP.
 XX AAS98658;
 AC
 XX 26-MAR-2002 (first entry)
 DT
 XX Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #24.
 DE
 XX Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
 KW cytosolic; gene therapy; malignant histiocytosis; isogene;
 KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
 KW genotype; human; allele specific oligonucleotide; ASO; probe; ss.
 XX Homo sapiens.
 OS
 XX WO200179225-A2.
 PN
 XX

Query Match 7.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.9e-02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAAC 1677
 DB 3 ACAGCTGGAAC 13
 RESULT 871
 AAS98658/c
 ID AAS98658 standard; DNA; 15 BP.
 XX AAS98658;
 AC
 XX 26-MAR-2002 (first entry)
 DT
 XX Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #24.
 DE
 XX Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
 KW cytosolic; gene therapy; malignant histiocytosis; isogene;
 KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
 KW genotype; human; allele specific oligonucleotide; ASO; probe; ss.
 XX Homo sapiens.
 OS
 XX WO200179225-A2.
 PN
 XX

Query Match 7.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.9e-02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAAC 1677
 DB 1 ACAGCTGGAAC 11
 RESULT 870
 AAF50723
 ID AAF50723 standard; DNA; 15 BP.
 XX AAF50723;
 AC
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #1683.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 KW

QY 1667 ACAGCTGGAAC 1677
 DB 1 ACAGCTGGAAC 11
 RESULT 870
 AAF50723
 ID AAF50723 standard; DNA; 15 BP.
 XX AAF50723;
 AC
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #1683.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 KW

QY 1667 ACAGCTGGAAC 1677
 DB 3 ACAGCTGGAAC 13
 RESULT 871
 AAS98658/c
 ID AAS98658 standard; DNA; 15 BP.
 XX AAS98658;
 AC
 XX 26-MAR-2002 (first entry)
 DT
 XX Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #24.
 DE
 XX Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
 KW cytosolic; gene therapy; malignant histiocytosis; isogene;
 KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
 KW genotype; human; allele specific oligonucleotide; ASO; probe; ss.
 XX Homo sapiens.
 OS
 XX WO200179225-A2.
 PN
 XX

PD 25-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US012044.
 XX
 PR 12-APR-2000; 2000US-0196411P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Choi JY, Koshy B;
 XX
 DR WPI; 2002-075058/10.
 XX
 XX Novel polymorphic variants of colony stimulating factor 1 receptor useful
 PT in studying expression and function of the protein, useful for screening
 PT candidate drugs to treat diseases e.g. inflammatory disorders.
 XX
 PS Claim 15; Page 15; 164pp; English.
 XX
 CC The invention describes a novel isolated polynucleotide (I) comprising a
 CC sequence which is a polymorphic variant (PV) of a reference sequence for
 CC colony stimulating factor 1 receptor (CSF1R) gene, found on the
 CC polypeptide are useful for improving the discovery and development of
 CC drugs for treating diseases associated with CSF1R activity, e.g.,
 CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
 CC and the haplotypes can be used to validate CSF1R as a candidate target
 CC for treating a specific condition or disease predicted to be associated
 CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
 CC be used in developing diagnostic tests and therapeutic treatments. (I) is
 CC useful in studying the expression and function of CSF1R, and in
 CC expressing CSF1R protein for use in screening for candidate drugs to
 CC treat diseases related to CSF1R activity and in studying the effect of
 CC the variation on the biological activity of CSF1R as well as on the
 CC binding affinity of candidate drugs targeting CSF1R. Antibodies are
 CC useful in a variety of diagnostic and prognostic formats and therapeutic
 CC methods. A transgenic animal is useful in studying expression of the
 CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs
 CC targeted against CSF1R protein, and for testing the efficacy of
 CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
 CC are useful as probes and primers, and for assaying a polymorphism in the
 CC target region. Without requiring any a priori knowledge of the phenotypic
 CC effect of any particular CSF1R or haplotype the invention provides a
 CC method for identifying lead compounds that are more likely to show
 CC efficacy in clinical trials. This sequence is an allele specific
 CC oligonucleotide probe used for detecting CSF1R gene polymorphisms,
 CC described in the method of the invention
 XX
 SQ Sequence 15 BP; 3 A; 7 C; 1 G; 3 T; 0 U; 1 Other;
 Query Match 7.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 4.9e+02;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1673 GGAACCTGGTGT 1685
 Db |||||
 14 GGAACCTGGTGT 2
 RESULT 872
 ABK92567
 ID ABK92567 standard; DNA; 15 BP.
 XX
 AC ABK92567;
 XX
 XX 20-AUG-2002 (first entry)
 XX
 DE ASO primer #4 to detect human CHRM4 gene polymorphisms.
 XX
 KW Human; single nucleotide polymorphism; SNP; CHRM4; haplotyping;
 KW chromosome 1p12-p11.2; cholinergic receptor muscarinic 4; genotyping;
 KW Alzheimer's disease; neurological disorder;
 KW allele-specific oligonucleotide; ASO; primer; ss.
 XX
 OS Homo sapiens.

XX
 PN WO200236609-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 31-OCT-2001; 2001WO-US045709.
 XX
 PR 31-OCT-2000; 2000US-0244627P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 PA (PETE/) PETERSON N.
 PA (ROUN/) ROUNDS E.
 XX
 PI Denton RR, Duda A, Gilson CR, Kazemi A, Nandabalan K, Tirrell C;
 XX
 DR WPI; 2002-489997/52.
 XX
 XX Novel genetic variants of cholinergic receptor muscarinic 4 useful in
 PT studying expression and function of protein, and for screening drugs to
 PT treat diseases e.g. Alzheimer's disease and other neurological disorders.
 XX
 PS Claim 14; Page 13; 63pp; English.
 XX
 CC The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human cholinergic receptor, muscarinic 4 (CHRM4) gene
 CC located on chromosome 1p12-p11.2, and methods for haplotyping and/or
 CC genotyping the CHRM4 gene. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the CHRM4 gene
 CC polymorphisms. The polynucleotides and screened compounds are useful for
 CC the treatment of diseases associated with CHRM4 activity, such as
 CC Alzheimer's disease and other neurological disorders. ASK92564-ABK92575
 CC represent ASO primers for detecting human CHRM4 gene polymorphisms
 XX
 SQ Sequence 15 BP; 3 A; 5 C; 5 G; 1 T; 0 U; 1 Other;
 Query Match 7.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 4.9e+02;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1658 ACCAGGCTCACAG 1670
 Db |||||
 3 ACCAGGCTCACRG 15
 RESULT 873
 ABK92619
 ID ABK92619 standard; DNA; 15 BP.
 XX
 AC ABK92619;
 XX
 XX 20-AUG-2002 (first entry)
 XX
 DE ASO primer #17 to detect human ADORA3 gene polymorphisms.
 XX
 KW Human; single nucleotide polymorphism; SNP; ADORA3; haplotyping;
 KW chromosome 1p21-p13; adenosine A3 receptor; genotyping;
 KW pathophysiological heart condition; myocardial ischaemia;
 KW chronic heart failure; allele-specific oligonucleotide; ASO; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200236610-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 31-OCT-2001; 2001WO-US045718.
 XX
 PR 31-OCT-2000; 2000US-0244626P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Gilson CR, Kazemi A, Koshy B, Monroe G;

XX DR WPI; 2002-489998/52.

XX PT Novel genetic variants of the adenosine A3 receptor, useful

PT therapeutically and in screening for drugs to treat diseases related to

PT ADORA3 activity e.g., myocardial ischemia and chronic heart failure.

XX PS Claim 15; Page 14; 82pp; English.

XX CC The present invention relates to novel single nucleotide polymorphisms

CC (SNPs) in the human adenosine A3 receptor (ADORA3) gene located on

CC chromosome 1p21-p13, and methods for haplotyping and/or genotyping the

CC ADORA3 gene. The methods of the invention make use of allele-specific

CC oligonucleotides (ASOs) as probes and primers and/or primer-extension

CC oligonucleotides for detecting the ADORA3 gene polymorphisms. The

CC polynucleotides and screened compounds are useful for the treatment of

CC diseases associated with ADORA3 activity, such as pathophysiological

CC conditions of the heart e.g. myocardial ischemia and chronic heart

CC failure. ABK32603-ABK92628 represent ASO primers for detecting human

CC ADORA3 gene polymorphisms

XX CC Sequence 15 BP; 2 A; 6 C; 4 G; 2 T; 0 U; 1 Other;

SQ

Query Match 7.9%; Score 11; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1759 AGGCCCACTGG 1769

DB 2 AGGCCCACTGG 12

RESULT 874

ABK32117

ID ABK32117 standard; DNA; 15 BP.

XX AC ABK32117;

XX DT 23-APR-2002 (first entry)

XX DE Human colon cancer SAGE tag #218.

XX KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;

KW serial analysis of gene expression; diagnostic; prognostic; probe;

KW cancer marker; ss.

XX OS Homo sapiens.

XX PN US6333152-B1.

XX PD 25-DEC-2001.

XX PF 20-MAY-1998; 98US-00081646.

XX PR 20-MAY-1998; 98US-00081646.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;

XX DR WPI; 2002-153821/20.

XX PT New human nucleic acid containing specific SAGE tags, useful as

PT diagnostic markers for cancer, also derived probes.

XX PS Disclosure; Col 28; 161pp; English.

XX CC The invention relates to an isolated, purified human nucleic acid (I)

CC that has the same sequence as a mRNA found in humans and is a SAGE

CC (serial analysis of gene expression) tag comprising a single stranded

CC probe containing at least 10 consecutive nucleotides. SAGE tags, are

CC diagnostic and prognostic markers of cancer, especially of the colon and

CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer

XX CC SAGE tags of the invention

XX SQ Sequence 15 BP; 4 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 TGGAAACCTGG 1682

DB 3 TGGAAACCTGG 13

RESULT 876

AAL39485/c

ID AAL39485 standard; DNA; 15 BP.

XX AC AAL39485;

XX CC AAL39485;

XX CC

CC SAGE tags of the invention

XX SQ Sequence 15 BP; 4 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 TGGAAACCTGG 1682

DB 3 TGGAAACCTGG 13

RESULT 876

AAL39485/c

ID AAL39485 standard; DNA; 15 BP.

XX AC AAL39485;

XX CC AAL39485;

XX CC

```

DT XX 05-SEP-2002 (first entry)
DE XX CCBP2 detecting ASO probe SEQ ID No 12.
KW XX Chemokine binding protein 2; CCBP2; CCBP2 protein isoform; gene therapy;
KW XX polymorphic gene variant; single nucleotide polymorphism; human; probe;
XX ss.
OS XX Homo sapiens.
PN WO200232926-A2.
XX WO200232926-A2.
PD 25-APR-2002.
XX 12-OCT-2001; 2001WO-US042685.
XX 12-OCT-2000; 2000US-0239638P.
XX (GENA-) GENAISSANCE PHARM INC.
PA Armstrong B, Kazemi A, Koshy B;
PI WPI; 2002-435524/46.
DR XX
XX New genetic variants having polymorphisms in the chemokine binding
PT protein 2 (CCBP2) gene, useful for studying CCBP2 functions, and for
PT treating disorders affected by expression or function of the CCBP2
PT isogene.
XX Claim 14; Page 13; 84pp; English.
XX The invention relates to an isolated polynucleotide comprising genes and
CC haplotypes of the chemokine binding protein 2 (CCBP2) gene. Polymorphic
CC variants of the CCBP2 gene are useful in studying the expression and
CC function of CCBP2, and in expressing CCBP2 proteins for use in screening
CC candidate drugs for treating diseases associated with CCBP2 activity.
CC Polynucleotides comprising a polymorphic gene variant or fragment may be
CC used for therapeutic purposes, where a patient could benefit from
CC expression or increased expression of a particular CCBP2 protein isoform,
CC or an expression vector encoding the isoform may be administered to the
CC patient. Haplotype information is useful in improving the efficiency and
CC output of several steps in drug discovery and development process,
CC including target validation, identifying lead compounds, and early phase
CC clinical trials. The polynucleotides of the invention can be used to
CC treat disorders related to the CCBP2 gene by gene therapy. This
CC polynucleotide sequence represents a preferred ASO probe for detecting
CC CCBP2 gene polymorphisms relating to the invention
XX
SQ Sequence 15 BP; 0 A; 5 C; 5 G; 4 T; 0 U; 1 Other;
Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 4.9e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1659 CCAGGCTCAGC 1671
Db 13 CCAGGSACAGC 1
RESULT 877
AAQ89557
ID AAQ89557 standard; DNA; 16 BP.
XX
AC AAQ89557;
XX
DT 11-DEC-1995 (first entry)
XX
DE Rat CYP7 gene steroid regulatory element (-1151 to -1135).
XX
KW CYP7; cholesterol 7 alpha hydroxylase; transcription factor;
KW regulatory element; ss.
OS Rattus rattus.

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XX EP648840-A2.
XX
PD 19-APR-1995.
XX
PF 07-OCT-1994; 94BP-00115856.
XX
PR 13-OCT-1993; 93US-00135488.
PR 13-OCT-1993; 93US-00135510.
PR 13-OCT-1993; 93US-00135511.
PR 28-JAN-1994; 94US-00187453.
XX
PA (UYNE-) UNIV NORTHEASTERN OHIO.
XX
XX Chiang JYL;
XX WPI; 1995-148718/20.
XX
XX Cholesterol 7-hydroxylase (CYP7) gene regulatory elements - including
PT bile responsive elements, useful for identifying CYP7 transcription
PT factors.
XX
XX Claim 1; Page 17; 84pp; English.
XX
XX AAQ89556 and AAQ89557 are steroid regulatory elements of rat cholesterol
CC 7 alpha-hydroxylase (CYP7). CYP7 gene expression is controlled by DNA
CC regulatory elements that are located within the gene. The location of
CC these regulatory elements has been identified and they have been
CC isolated. These DNA fragments are useful in the identification of CYP7
CC transcription factors
XX
SQ Sequence 16 BP; 3 A; 8 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1740 CAACTCCTCC 1750
Db 1 CAACTCCTCC 11
RESULT 878
AAQ89026
ID AAQ89026 standard; DNA; 16 BP.
XX
AC AAQ89026;
XX
XX 26-SEP-2001 (first entry)
XX
DE Human SAPI140 exon 9-intron 9 boundary genomic sequence.
XX
KW Human; 140kDa Shc associated protein; SAPI40; tyrosine phosphatase Lyp1;
KW chromosome 9; haematopoietic; B-cell; T-cell; acute myeloid leukaemia;
KW AML; acute lymphoblastic leukaemia; ALL; hyperproliferation; cancer;
KW autoimmune disorder; apoptosis; allergic disorder; immunosuppression; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX exon 1. .7
XX /*tag= a
XX /partial
XX /number= 9
XX
XX intron 8. .16
XX /*tag= b
XX /partial
XX /number= 9
XX
XX WO200151509-A2.
XX
PD 19-JUL-2001.
XX

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PF 10-JAN-2001; 2001WO-CA000023.
XX
XX
PR 10-JAN-2000; 2000US-0175233P.
XX
XX (HOSP-) HOSPITAL FOR SICK CHILDREN.
FA
XX Roifman CM, Sharfe N;
XX
XX WPI; 2001-442133/47.
XX
XX New Shc associated protein, useful for identifying modulators for
XX treating cancer.
PT
XX
XX
XX Example 3; Fig 4B; 106pp; English.
XX
XX The present sequence represents the human SAPI140 exon 9-intron 9 boundary
XX genomic sequence. Human 140kDa Shc associated protein (SAPI140; AAU03596)
XX is a novel non-transmembrane protein which is isolated by binding to the
XX human cytoplasmic tyrosine phosphatase Lyp1. The gene encoding for SAPI140
XX maps to chromosome 9. SAPI140 is useful for identifying compounds which
XX can bind and modulate SAPI140 protein activity. Compounds which inhibit or
XX induce SAPI140 expression or activity are useful for modulating the
XX expression/activity of SAPI140 to modulate the activity of haematopoietic
XX cells, such as a B- or T-cells, preferably leukaemic cells. SAPI140 can be
XX used for the treatment of acute myeloid leukaemia (AML), acute
XX lymphoblastic leukaemia (ALL), uncontrolled T-cell diseases,
XX haematopoietic disorders (e.g. lymphomas) and hyperproliferation
XX disorders (e.g. cancer). Modulators of SAPI140 are useful in modulating
XX disorders such as neoplasia and autoimmunity, to stimulate cell death or
XX apoptosis, and to induce cell proliferation for treatment of autoimmune
XX diseases (e.g. multiple sclerosis, lupus, arthritis, diabetes) and
XX allergic disorders (e.g. asthma). Modulators of SAPI140 regulatory
XX pathways are also useful for treating a disorder which requires
XX immunosuppression such as transplantation
XX
XX Sequence 16 BP; 9 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 7.9%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1649 AAGGCAAGCAC 1659
DB 6 AAGGCAAGCAC 16
RESULT 879
AAQ74120/C
ID AAQ74120 standard; DNA; 14 BP.
XX
XX AAQ74120;
AC
XX
XX 02-FEB-1996 (first entry)
DT
XX
XX Platelet derived growth factor (PDGF-A) antisense oligonucleotide.
DE
XX
XX Platelet derived growth factor; PDGF-A; antisense oligonucleotide;
KW breast; pancreatic; carcinoma; glioma; melanoma; rheumatoid; arthritis;
KW angiogenesis inhibitor; tumours; cancer; ss.
XX
XX Synthetic.
OS
XX WO9516032-A1.
XX
XX 15-JUN-1995.
XX
XX 09-DEC-1993; 93WO-EP003461.
XX
XX 09-DEC-1993; 93WO-EP003461.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlengersiepen GF, Brysch W, Schlengersiepen R, Schlengersiepen K;
PI
10-JAN-2001; 2001WO-CA000023.
DR
XX
XX New antisense cpds. for treating diseases associated with growth factors
XX - esp. neoplasia, autoimmune diseases and pathological angiogenesis.
PT
XX
XX Claim 3; Page 12; 30pp; English.
PS
XX
XX AAQ74119-074124 are platelet derived growth factor (PDGF-A) antisense
XX oligonucleotides (DNA or RNA). They can be used to treat diseases
XX associated with growth factors, e.g. breast or pancreatic carcinoma,
XX glioma or melanoma, and rheumatoid arthritis. They can also be used to
XX inhibit angiogenesis, e.g. in tumours
XX
XX Sequence 14 BP; 3 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 7.8%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 4.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1726 TGGAGATTGGCTCC 1739
DB 14 TGGAGATTAGACTCC 1
RESULT 880
AAT98896
ID AAT98896 standard; DNA; 14 BP.
XX
XX AAT98896;
AC
XX
XX 23-MAR-1998 (first entry)
DT
XX
XX Probe 41w18 for HIV RT gene wild type E40W41.
XX
XX Reverse transcriptase gene; HIV; RT gene; antiviral drug susceptibility;
KW virus susceptibility; antiviral drug resistant viral strain; retrovirus;
KW Hepadnaviridae; HIV RT genotyping; probe; ss.
XX
XX Synthetic.
OS
XX Human immunodeficiency virus 1.
XX
XX WO9727332-A1.
XX
XX 31-JUL-1997.
XX
XX 17-JAN-1997; 97WO-EP000211.
XX
XX 26-JAN-1996; 96EP-03870005.
XX
XX 25-JUN-1996; 96EP-03870081.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Stuyver L, Louwagie J, Rossau R;
XX
XX WPI; 1997-393716/36.
XX
XX Determining susceptibility to antiviral drugs of reverse transcriptase
XX containing viruses - useful for genotyping HIV RT and detecting antiviral
XX resistant HIV.
XX
XX Claim 13; Page 36; 59pp; English.
XX
XX This sequence represents a probe for a wild type HIV reverse
XX transcriptase (RT) gene fragment. This sequence can be used in the method
XX of the invention for determining the susceptibility to antiviral drugs of
XX viruses which contain RT genes and are present in a biological sample. It
XX comprises: (1) releasing, isolating or concentrating the polynucleic
XX acids present in a sample; (2) amplifying the relevant part of the RT
XX genes present with at least one suitable primer pair; (3) hybridising the
XX polynucleic acids of step (1) or (2) with at least two RT gene probes,
XX the probes being applied to known locations on a solid support, and are
XX capable of simultaneously hybridising to their respective target regions
XX

```

under appropriate hybridisation and wash condition allowing the detection of homologous targets, or with the probes hybridising specifically with a sequence complementary to any of the target sequences; (4) detecting the hybrids formed in step (3); and (4) inferring the nucleotide sequence at the codons of interest (codons 38-44, 47-53, 65-72, 73-77, 148-154, 180-187, 212-216, and 217-220), and/or the amino acids of the codons of interest and/or antiviral drug resistance spectrum, and possible the type of viral isolates involved from the differential hybridisation signals obtained in step (4). The method is specifically used to detect antiviral drug resistant strains of viruses containing RT genes, especially HIV retroviruses and Hepadnaviridae. The method can also be used for genotyping HIV RT

Sequence 14 BP; 7 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 7.8%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 4.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1718 TACGAGATGGAGA 1731
|||||
Db 1 TACAGATGGAAA 14

RESULT 881
AA55199
ID AAX55199 standard; DNA; 14 BP.
XX
AC AAX55199;
XX
DT 05-JUL-1999 (first entry)
XX
DE Multiple antisense oligonucleotide 20.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN W09913886-A1.
XX
XX 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
XX
FR 09-JUN-1998; 98US-00093972.
XX

(UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction.
XX
XX Disclosure; Page 74; 120pp; English.
XX

The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases,

conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer

Sequence 14 BP; 0 A; 9 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 7.8%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 4.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1733 TGGCTCCCACTCC 1746
|||||
Db 1 TGGCTCCCCCTCC 14

RESULT 882
AAX14792
ID AAX14792 standard; DNA; 14 BP.
XX
AC AAX14792;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix forming nucleotides 727-740 of Hepatitis B virus.
XX
KW Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.
XX
OS Hepatitis B virus.
XX
PN US5861244-A.
XX
XX 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX

(PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
XX Hepburn AG, Wang C;
XX
XX WPI; 1999-130384/11.
XX
XX Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria.
XX
XX Disclosure; Col 19-20; 168pp; English.

The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and a reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in

CC clinical samples, but also detection of oncogenes and Hepatitis B virus
 XX
 SQ Sequence 14 BP; 0 A; 7 C; 0 G; 7 T; 0 U; 0 Other;
 Query Match 7.8%; Score 10.8; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 4.9e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1743 CTCCTCCCTATCCT 1756
 Db 1 CTCCTCCCTTTCCT 14
 RESULT 883
 AAA34646
 ID AAA34646 standard; DNA; 14 BP.
 XX
 AC AAA34646;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2335.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; hypotensive; cytotatic;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US017712.
 XX
 PR 03-AUG-1998; 98US-0095212P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-205971/18.
 XX
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Disclosure; Page 557; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present

CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 14 BP; 0 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 7.8%; Score 10.8; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 4.9e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1733 TGGCTCCCACTCC 1746
 Db 1 TGGCTCCCACTCC 14
 RESULT 884
 AAP20768
 ID AAP20768 standard; DNA; 14 BP.
 XX
 AC AAP20768;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human multiple target antisense (MTA) oligonucleotide #2335.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2000062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 PS Claim 14; Page 625; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and

CC chemokines, endogenously produced specific and non-specific enzymes.
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides and (I) can be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention

SQ Sequence 14 BP; 0 A; 9 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 4.9e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1733 TGGCTCCCAACTCC 1746

Db 1 TGGCTCCCTCCCTCC 14

RESULT 885

AAF21471

ID AAF21471 standard; DNA; 14 BP.

AC AAF21471;

DT 14-MAR-2001 (first entry)

XX Human multiple target antisense (MTA) oligonucleotide #3038.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary obstruction; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.

PS Disclosure; Page 297; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with the
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention

SQ Sequence 14 BP; 0 A; 9 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 14;

Best Local Similarity 85.7%; Pred. No. 4.9e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1733 TGGCTCCCAACTCC 1746

Db 1 TGGCTCCCTCCCTCC 14

RESULT 886

ABZ96462

ID ABZ96462 standard; DNA; 14 BP.

AC ABZ96462;

DT 17-OCT-2003 (first entry)

XX Human nucleic acid sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI	Miller S, Tang L, Shahabuddin S;	XX
XX	WPI; 2003-229219/22.	XX
DR	Pharmaceutical composition for treating ailments associated with impaired	XX
XX	respiration, has oligo(s) antisense to specific gene(s) or its	XX
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or	XX
PT	ubiquinone.	XX
PT	Disclosure; SEQ ID NO 11704; 872pp; English.	XX
XX	The invention relates to a novel pharmaceutical composition, which has a	XX
XX	first active agent comprising an oligonucleotide antisense to the	XX
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,	XX
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of	XX
CC	junctions of genes encoding a polypeptide associated with lung and/or	XX
CC	nasal airway dysfunction and a second active agent comprising an	XX
CC	antiinflammatory steroid and ubiquinone. A composition of the invention	XX
CC	has antiinflammatory, antiasthmatic, antiallergic, hypotensive,	XX
CC	immunosuppressive, and cytostatic activity. The composition may have a	XX
CC	use in antisense gene therapy. The composition is useful for treating or	XX
CC	preventing a respiratory, lung or malignant disease or condition, also	XX
CC	for enhancing the prophylactic or therapeutic respiratory effect of an	XX
CC	antiinflammatory steroid in a subject, for reducing or depleting levels	XX
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine	XX
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or	XX
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,	XX
CC	lung inflammation, lung allergies, or a respiratory disease or condition.	XX
CC	Note: The sequence data for this patent is not represented in the printed	XX
CC	specification, but was obtained in electronic format directly from WIPO	XX
CC	at ftp.wipo.int/pub/published_pct_sequences	XX
XX	Sequence 14 BP; 0 A; 9 C; 2 G; 3 T; 0 U; 0 Other;	XX
XX	Query Match 7.8%; Score 10.8; DB 1; Length 14;	XX
XX	Best Local Similarity 85.7%; Pred. No. 4.9e+02;	XX
XX	Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	XX
QY	1733 TGGCTCCCACTCC 1746	XX
DB	1 TGGCTCCCACTCC 14	XX
RESULT 887		XX
ABZ97165		XX
ID	ABZ97165 standard; DNA; 14 BP.	XX
XX	ABZ97165;	XX
XX	17-OCT-2003 (first entry)	XX
DT	Human MTA oligonucleotide.	XX
DE	Human; antisense; lung dysfunction; nasal airway dysfunction;	XX
XX	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;	XX
KW	antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;	XX
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;	XX
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;	XX
KW	lung inflammation; respiratory disease; ds.	XX
OS	Homo sapiens.	XX
XX	WO200285308-A2.	XX
FN	31-OCT-2002.	XX
XX	23-APR-2002; 2002WO-US013135.	XX
PD	24-APR-2001; 2001US-0286137P.	XX
PF	(EPIG-) EPIGENESIS PHARM INC.	XX
XX	Nvce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;	XX
PA		XX
PI		XX

XX PS Claim 1; Page 13; 13pp; English.

XX CC The DNA probes represented in AAQ22441-76 are 15 nucleotide sequences

CC wherein 8 nucleotides of each sequence are G, 3 are T, 1 is C, 1 is A and

CC 2 are N, except that the nucleotide sequence is not the M13 consensus

CC sequence GAGGGTGGGNGTCT. The probes can detect hyper- variable regions

CC (HVRs) in genomic DNA with such precision as to enable individuals to be

CC identified or fingerprinted by reference to variations in their DNA in

CC these regions. The DNA probes can be used in paternity and maternity

CC testing, zygosity testing in twins, cell chimerism studies, e.g.

CC detection of donor versus recipient cells after bone marrow

CC transplantation, forensic medicine, family sp. verification, tests for

CC inbreeding, pedigree analysis, identification of loci or genetic

CC diseases, animal or plant breeding and pedigree analysis authentication,

CC quality control of cell lines and analysis. Preparation: The M13 sequence

CC was initially randomised manually by the method of random sampling

CC without replacement to produce random sequences. Later a computer

CC programme was written that implemented an algorithm that produced a

CC random sequence by sampling without replacement. Several of the random

CC sequences that were obtd. were synthesised, labelled and used as DNA

CC probes

XX SQ Sequence 15 BP; 2 A; 1 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 5.4e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 CTCCTCACTCTCTCC 1749

Db | | | | | | | | | | | | | | | |

15 CCCACACTCTCTCC 2

RESULT 889

AAQ45774

ID AAQ45774 standard; DNA; 15 BP.

XX AC AAQ45774;

XX DT 25-MAR-2003 (revised)

DT 08-DEC-1993 (first entry)

XX Human prostate transglutaminase gene PCR primer ZC4048.

XX Degenerate; polymerase chain reaction; enzyme; inter alia;

KW therapeutic wound repair; skin graft closure; food prepn; preparation;

KW stabilising; marker; identifying agent; agonists; antagonists;

KW cellular apoptosis; ss.

XX OS Synthetic.

XX WO9313207-A2.

XX PD 08-JUL-1993.

XX PF 30-DEC-1992; 92WO-US011353.

XX PR 31-DEC-1991; 91US-00816284.

XX PA (ZYMO) ZYMOGENETICS INC.

XX Ohara PV, Grant FJ, Sheppard PO;

XX WPI; 1993-227323/28.

XX Isolated polynucleotide molecule, for stabilising good prepn. - utilised

PT for coding human prostatic or placental trans glutaminase(s) and DNA, for

PT repairing wounds, ulcerated lesions, skin grafts, and cellular markers.

XX Example; Page 43; 48pp; English.

XX The sequence is that of oligonucleotide ZC4048 which was used in a PCR to

CC confirm the presence of additional 5' sequences, as part of the

CC generation of a full-length human prostate transglutaminase cDNA clone.

CC It was designed to hybridise to the antisense lambda sequences near the

CC EcoRI site of the lambda-gt11 vector. (Updated on 25-MAR-2003 to correct

CC PN field.)

XX SQ Sequence 15 BP; 3 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 5.4e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGAA 1676

Db | | | | | | | | | | | | | | | |

1 GCGCTCAGCTGAA 14

RESULT 890

AAQ88720

ID AAQ88720 standard; DNA; 15 BP.

XX AC AAQ88720;

XX DT 27-FEB-1996 (first entry)

XX c-Ha-ras modified antisense oligonucleotide.

DE antisense; analogue; non-terminal pyrimidine; phosphorothioate; backbone;

XX treatment; HIV; human immunodeficiency virus; HSV; herpes simplex virus;

KW cancer; integrin; cell adhesion receptor; infection; diagnosis;

KW nuclease resistance; ss.

XX OS Homo sapiens.

XX EP653439-A2.

XX PD 17-MAY-1995.

XX PF 07-NOV-1994; 94EP-00117513.

XX PR 12-NOV-1993; 93DE-04338704.

XX PA (FARH) HOECHST AG.

XX Peyton A, Uhlmann E, Mag M, Kretzschmar G, Helsing M, Winkler I;

PI WPI; 1995-180677/24.

DR New anti-sense oligo-nucleotide analogues - with modified non-terminal

PT pyrimidine nucleotide units, useful for treating viral infections,

PT cancer, etc.

XX Claim 1; Page 23; 36pp; German.

XX The antisense oligonucleotide (ON) shown is a derivative of an equivalent

CC wild type Human c-Ha-ras ON, in which at least one, esp. 2-10, non-

CC terminal pyrimidine nucleotide(s) is/are modified. The modification may

CC be: (a) replacement of a phosphodiester linkage by: a phosphorothioate

CC (PS), -dithioate, -aramidate; borano-, alkyl-, aralkyl-phosphate; 2,2,2-

CC trichloro-1,1dimethyl-, alkyl- or aryl- phosphate linkage; or (3',-

CC thio)formacetal, methylhydroxylamine, oxime, methylenedimethylthio,

CC dimethylene sulphone or silyl linkage; (b) replacement of a sugar

CC phosphate backbone by a morpholinonucleoside, oligomer; (c) replacement

CC of beta-D-2-deoxyribose by another sugar or carbocyclic, open-chain or

CC bicyclic sugar analogue; or (c) replacement of the natural nucleoside

CC base by an analogue, e.g. 5-hydroxymethyl-uridine. The 5' and/or 3'

CC terminus may also be modified with a lipophilic gp., eg. a farnesyl. The

CC modifications increase nuclease resistance and thus improve stability and

CC activity

XX SQ Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGCAACCCG 1681
||||| |||||
Db 1 CAGCTGCAACCCAG 14

RESULT 891
AAT56203/C
ID AAT56203 standard; RNA; 15 BP.
XX AAT56203;
XX
XX 25-MAR-2003 (revised)
DT 14-MAY-1997 (first entry)
XX
XX
DE Mouse TNF-a hammerhead ribozyme target sequence (nt position 615).
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW ss.
XX
XX Mus musculus.
OS
XX
XX
XX W09523225-A2.
PN
XX
XX
PD 31-AUG-1995.
XX
XX
XX 23-FEB-1995; 95WO-IB000156.
XX
PR 23-FEB-1994; 94US-00201109.
PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321893.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX

DR WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX PS
XX Claim 2; Page 250; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha mRNA at
CC the nucleotide base position indicated in the DE line. Regions of the
CC mRNA that do not form secondary folding structures and that contain
CC potential hammerhead and hairpin ribozyme cleavage sites were identified
CC by computer analysis. Ribozymes directed against these mRNA sequences
CC were designed and synthesised with modifications that improve their
CC nuclease resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit TNF-alpha expression, making them
CC potentially useful for treating rheumatoid arthritis, septic shock and
CC other inflammatory disorders including psoriasis, as well as for
CC treatment of AIDS. (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 15 BP; 2 A; 8 C; 2 G; 0 T; 3 U; 0 Other;
Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 5.4e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1708 GCGTTAGGAGTACG 1721
||||| |||||
Db 15 GCGTGAGGAGCAG 2

RESULT 892
AAQ97685
ID AAQ97685 standard; DNA; 15 BP.
XX
XX
AC AAQ97685;
XX
XX 22-MAR-1996 (first entry)
XX
DE Biotinylated antisense oligonucleotide against c-Ha-ras.
XX
KW antisense; c-ras; antigen; monoclonal antibody; avidin; biotinylation;
KW non-viral vector; complex; Lewis Y antigen; bladder carcinoma; ss.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= 5'-biotin-C
XX
XX W09521195-A1.
XX
XX 10-AUG-1995.
XX
XX 06-FEB-1995; 95WO-US0001161.
XX
XX 07-FEB-1994; 94US-00192655.
XX
XX (RERE-) RES DEV FOUND.
XX
XX Rosenblum MG, Donato NJ;
XX
XX WPI; 1995-283733/37.
XX
XX A non-viral vector having a cell binding component - used to introduce
PT genetic material into, or to deliver a cytotoxic moiety to a specific
PT cell.
XX
XX Example 14; Page 18; 35pp; English.
XX
XX A non-viral vector comprising a cell binding component having a biotin-
CC binding element (eg. avidin or streptavidin) conjugated to a biotinylated

CC moiety is claimed. The cell binding element is a monoclonal antibody
 CC (MAB) or a ligand which binds a cell surface receptor or a nucleic acid,
 CC pref. a triplex forming oligonucleotide or an antisense oligonucleotide.
 CC A MAB (BR96) which specifically binds Lewis Y antigen on several human
 CC carcinomas was chemically conjugated to avidin. AAO97685 is complementary
 CC to the c-Ha-ras 5' flanking mRNA sequence and was synthesised with a
 CC biotinylated cytosine at the 5' terminal position. The biotinylated
 CC oligonucleotide was incubated with the BR96-Avidin and complexes of BR96-
 CC avidin:antisense c-Ha-ras were purified. The complexes were incubated
 CC with T24 bladder carcinoma cells which express Lewis Y antigen and also
 CC contain the c-Ha-ras oncogene. After incubation the product of the ras
 CC oncogene, p21, was monitored by western blotting. Cell growth was also
 CC monitored. Neutralisation of the effects of ras oncogene by intracellular
 CC delivery of antisense molecules through internalisation of the Lewis Y
 CC antigen was demonstrated
 XX
 SQ Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 5.4e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681
 Db 1 CAGCTGCAACCCAG 14

RESULT 893
 AAT44432
 ID AAT44432 standard; DNA; 15 BP.
 XX
 AC AAT44432;
 XX
 DT 27-JAN-1997 (first entry)
 XX
 DE Antisense oligonucleotide VIII against c-Ha-ras.
 XX
 KW 8-azapurine; modification; stronger complex; inhibition; ss.
 XX
 OS Synthetic.
 XX
 PN EP680969-R2.
 XX
 PD 08-NOV-1995.
 XX
 PF 26-APR-1995; 95EP-00106230.
 XX
 PR 02-MAY-1994; 94DE-04415370.
 XX
 FA (FARH) HOECHST AG.
 XX
 PI Seela F, Lampe S;
 XX
 DR WPI; 1995-375165/49.
 XX

PT New oligo:nucleotide(s) contg. 8-aza:purine base - useful as therapeutic
 PT and diagnostic agents with more stable hybridisation to target nucleic
 PT acid.
 XX
 PS Disclosure; Page 37; 51pp; German.
 XX
 CC AAT44425-54 are antisense oligonucleotides which have at least one 8-
 CC azapurine base. The presence of an 8-azapurine base results in
 CC significantly stronger complexing when hybridising to target nucleic
 CC acids. The present sequence is against c-Ha-ras
 XX
 SQ Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 5.4e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681

Db 1 CAGCTGCAACCCAG 14
 RESULT 894
 AAT44237
 ID AAT44237 standard; DNA; 15 BP.
 XX
 AC AAT44237;
 XX
 DT 22-JUL-1997 (first entry)
 XX
 DE c-Ha-ras antisense component of capped oligonucleotide.
 XX
 KW Antisense therapy; cellular ras oncogene; c-Ha-ras; guanosine;
 KW nuclease resistance; stability; ss.
 XX
 OS Synthetic.
 XX
 PN DE19502912-A1.
 XX
 PD 01-AUG-1996.
 XX
 PF 31-JAN-1995; 95DE-01002912.
 XX
 PR 31-JAN-1995; 95DE-01002912.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Peyman A, Uhlmann E;
 XX
 DR WPI; 1996-355223/36.
 XX
 PT Oligo:nucleotide(s) with series of G residues at at least one end have
 PT increased stability against nuclease and cell penetration, - are partic.
 PT anti:sense sequences for treating and diagnosing cancer, viral diseases
 PT etc.
 XX
 PS Claim 3; Page 13; 15pp; German.
 XX
 CC Ten- to 40-mer oligonucleotides which have a cap of 1-10 (esp. 4) G
 CC residues on at least one end are provided; if caps are present at both
 CC ends, they can be of the same or different lengths. A cap sequence
 CC increases nuclease resistance of the oligonucleotide and also increases
 CC cell penetration. The present sequence is that of a preferred
 CC oligonucleotide, directed against c-Ha-ras sequences, which can be capped
 CC for use in anticancer therapy
 XX
 SQ Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 5.4e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681
 Db 1 CAGCTGCAACCCAG 14

RESULT 895
 AAX33907
 ID AAX33907 standard; DNA; 15 BP.
 XX
 AC AAX33907;
 XX
 DT 30-JUN-1999 (first entry)
 XX
 DE c-Ha-ras expression inhibitor.
 XX
 KW Gene expression inhibitor; probe; nucleic acid detection; growth factor;
 KW viral infection; therapy; HSV-1; cancer; restenosis; integrin;
 KW cell-cell adhesion receptor; c-Ha-ras; ss.
 XX

Synthetic.
Homo sapiens.
AU9648028-A.
26-SEP-1996.
12-MAR-1996; 96AU-00048028.
13-MAR-1995; 95DE-01008923.
24-NOV-1995; 95DE-01043865.
(FARH) HOECHST AG.
Peyman A, Uhlmann E, Breipohl G, Wallmeier H;
WPI; 1996-455932/46.
New phosphono-mono-ester oligo-nucleotide analogues - inhibitors of gene
expression for treating viral infections, cancer, restenosis, etc.
Disclosure; Page 41; 129pp; English.
This sequence represents an inhibitor of c-Ha-ras expression, and is an
example of an oligonucleotide analogue of the invention. The
oligonucleotide analogues of the invention are used as inhibitors of gene
expression (antisense oligonucleotides, ribozymes, sense oligonucleotides
and triplex-forming oligonucleotides), as probes for the detection of
nucleic acids, and as auxiliaries in molecular biology. As gene
expression inhibitors they may be used for treating viral infections
(especially where the virus is HSV-1, HSV-2, an influenza virus, VSV,
hepatitis B or papilloma virus), cancer, restenosis, medical conditions
mediated by integrins or cell-cell adhesion receptors, and medical
conditions induced by growth factors (especially TNF-alpha)
Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1668 CAGCTGGACCCCTG 1681
||||| |||||
1 CAGCTGCAACCCAG 14
RESULT 896
AAT14843
AAT14843 standard; DNA; 15 BP.
AAT14843;
25-MAR-2003 (revised)
14-NOV-1996 (first entry)
Human prostatic transglutaminase primer ZC4048.
Human; prostatic; prostate; placental; transglutaminase; primer;
calcium dependent crosslinking; tissue adhesive; wound repair; PCR;
skin graft; food; protozoan deterioration; dried fish; meat texture;
cleavable crosslink; apoptosis; degenerative nerve disease; amplify;
hyperproliferation; factor xiii; blood; immunogenicity; stability;
half life; ss.
Synthetic.
US5514579-A.
07-MAY-1996.
30-DEC-1992; 92US-00989973.
31 MAY 1997 0815 00916294


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XX 23-DEC-1994; 94US-00363240.
XX (RIBO-) RIBOZYME PHARM INC.
XX (WARN) WARNER LAMBERT CO.
XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
XX WPI; 1996-321852/32.
XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX useful for preventing or treating initial development, progression or
XX regression of vascular diseases, esp. familial hypercholesterolaemia.
XX Claim 4; Page 32; 72pp; English.
XX AAT49608-T49863 represent target sequences for the human cholesterol
XX ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX transfer between plasma lipoproteins. The numbering of the targets refers
XX to the position of the cleavage site in full length CETP. The ribozyme
XX binds to 5 nucleotides either side of this site, provided the sequence
XX is immediately upstream. The ribozymes are able to cleave mRNA from the
XX gene encoding CETP, thereby blocking synthesis and/or expression of the
XX mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX can be inhibited (or eliminated) thereby preventing the reduction in size
XX density of the high density lipoproteins (HDL), prolonging HDL half life,
XX and therefore increasing HDL levels. The ribozymes can be used to treat
XX conditions associated with abnormal levels of CETP, specifically familial
XX hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX hyperbetalipoproteinaemia, hypopalipoproteinaemia, dyslipidaemia,
XX vascular complications of diabetes, transplant, atherectomy and
XX angioplasty restenosis. By inhibiting CETP, the levels of HDL and low
XX density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX The HH ribozymes can also be used diagnostically to study genetic drift
XX and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX ribozymes target specific regions of the CETP gene, they have low non-
XX specific activity
XX Sequence 15 BP; 3 A; 9 C; 0 G; 0 T; 3 U; 0 Other;
SQ Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 65;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1738 CCCAACTCTCTCCTTA 1752
Db 1 CCCAACUCCUCCUA 15

RESULT 35
AAT49839
ID AAT49839 standard; RNA; 15 BP.
AC AAT49839;
XX 07-MAR-1997 (first entry)
XX Human CETP HH ribozyme target sequence #1754.
XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplasty restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX Homo sapiens.
XX WO9620279-A1.
XX

PD 04-JUL-1996.
XX 11-DEC-1995; 95WO-US016000.
XX 23-DEC-1994; 94US-00363240.
XX (RIBO-) RIBOZYME PHARM INC.
XX (WARN) WARNER LAMBERT CO.
XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
XX WPI; 1996-321852/32.
XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX useful for preventing or treating initial development, progression or
XX regression of vascular diseases, esp. familial hypercholesterolaemia.
XX Claim 4; Page 32; 72pp; English.
XX AAT49608-T49863 represent target sequences for the human cholesterol
XX ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX transfer between plasma lipoproteins. The numbering of the targets refers
XX to the position of the cleavage site in full length CETP. The ribozyme
XX binds to 5 nucleotides either side of this site, provided the sequence
XX is immediately upstream. The ribozymes are able to cleave mRNA from the
XX gene encoding CETP, thereby blocking synthesis and/or expression of the
XX mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX can be inhibited (or eliminated) thereby preventing the reduction in size
XX density of the high density lipoproteins (HDL), prolonging HDL half life,
XX and therefore increasing HDL levels. The ribozymes can be used to treat
XX conditions associated with abnormal levels of CETP, specifically familial
XX hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX hyperbetalipoproteinaemia, hypopalipoproteinaemia, dyslipidaemia,
XX vascular complications of diabetes, transplant, atherectomy and
XX angioplasty restenosis. By inhibiting CETP, the levels of HDL and low
XX density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX The HH ribozymes can also be used diagnostically to study genetic drift
XX and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX ribozymes target specific regions of the CETP gene, they have low non-
XX specific activity
XX Sequence 15 BP; 4 A; 5 C; 2 G; 0 T; 4 U; 0 Other;
SQ Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 65;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1747 TCCCTATCTCTTAAGG 1761
Db 1 UCCCUAUCUUAAGG 15

RESULT 36
AAT49813
ID AAT49813 standard; RNA; 15 BP.
AC AAT49813;
XX 18-MAR-1997 (first entry)
XX Human CETP HH ribozyme target sequence #1666.
XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplasty restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX Homo sapiens.
XX

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XX PN W09620279-A1.
XX OS Homo sapiens.
XX PD 04-JUL-1996.
XX PF 11-DEC-1995; 95WO-US016000.
XX PR 23-DEC-1994; 94US-00363240.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
XX PT WPI; 1996-321852/32.
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX PT useful for preventing or treating initial development, progression or
XX PT regression of vascular diseases, esp. familial hypercholesterolaemia.
XX PS Claim 4; Page 32; 72pp; English.
XX CC AAT49608-T49863 represent target sequences for the human cholesterol
XX CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX CC transfer between plasma lipoproteins. The numbering of the targets refers
XX CC to the position of the cleavage site in full length CETP. The ribozyme
XX CC binds to 5 nucleotides either side of this site, provided the sequence UH
XX CC is immediately upstream. The ribozymes are able to cleave mRNA from the
XX CC gene encoding CETP, thereby blocking synthesis and/or expression of the
XX CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX CC can be inhibited (or eliminated) thereby preventing the reduction in size
XX CC and therefore increasing HDL levels. The ribozymes can be used to treat
XX CC conditions associated with abnormal levels of CETP, specifically familial
XX CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX CC hyperbetalipoproteinemia, hypopalipoproteinemia, dyslipidaemia,
XX CC vascular complications of diabetes, transplant, atherectomy and
XX CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
XX CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX CC The HH ribozymes can also be used diagnostically to study genetic drift
XX CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX CC ribozymes target specific regions of the CETP gene, they have low non-
XX CC specific activity
XX SQ Sequence 15 BP; 3 A; 6 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 65;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1659 CCAGGCTCACAGCTG 1673
Db 1 CCAGGCUCACAGCUG 15
|||||:|||||:
1 CCAGGCUCACAGCUG 15

RESULT 37
AAT49835
ID AAT49835 standard; RNA; 15 BP.
XX AC AAT49835;
XX DT 07-MAR-1997 (first entry)
XX DE Human CETP HH ribozyme target sequence #1748.
XX KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX KW familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinemia;
XX KW peripheral vascular disease; hyperbetalipoproteinemia; RCT; inhibitor;
XX KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;

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XX LDL; ss.
XX OS Homo sapiens.
XX PN W09620279-A1.
XX PD 04-JUL-1996.
XX PF 11-DEC-1995; 95WO-US016000.
XX PR 23-DEC-1994; 94US-00363240.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
XX PT WPI; 1996-321852/32.
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX PT useful for preventing or treating initial development, progression or
XX PT regression of vascular diseases, esp. familial hypercholesterolaemia.
XX PS Claim 4; Page 32; 72pp; English.
XX CC AAT49608-T49863 represent target sequences for the human cholesterol
XX CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX CC transfer between plasma lipoproteins. The numbering of the targets refers
XX CC to the position of the cleavage site in full length CETP. The ribozyme
XX CC binds to 5 nucleotides either side of this site, provided the sequence UH
XX CC is immediately upstream. The ribozymes are able to cleave mRNA from the
XX CC gene encoding CETP, thereby blocking synthesis and/or expression of the
XX CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX CC can be inhibited (or eliminated) thereby preventing the reduction in size
XX CC and therefore increasing HDL levels. The ribozymes can be used to treat
XX CC conditions associated with abnormal levels of CETP, specifically familial
XX CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX CC hyperbetalipoproteinemia, hypopalipoproteinemia, dyslipidaemia,
XX CC vascular complications of diabetes, transplant, atherectomy and
XX CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
XX CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX CC The HH ribozymes can also be used diagnostically to study genetic drift
XX CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX CC ribozymes target specific regions of the CETP gene, they have low non-
XX CC specific activity
XX SQ Sequence 15 BP; 3 A; 8 C; 0 G; 0 T; 4 U; 0 Other;

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 65;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 AACTCCTCCCTATCC 1755
Db 1 AACUCCUCCUUAUCC 15
|||||:|||||:
1 AACUCCUCCUUAUCC 15

RESULT 38
ABS60987/c
ID ABS60987 standard; DNA; 20 BP.
XX AC ABS60987;
XX DT 05-NOV-2002 (first entry)
XX DE Human genotyping PCR primer #140.
XX KW Human; ss; aminopeptidase P; XNPEP2; bradykinin receptor B1; primer;
XX KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
XX KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;

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CC for the gene encoding one of the proteins listed above

XX Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

SQ Query Match 10.6%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. NO. 1.1e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1669 AGCTGGACCTGGTGTC 1686

DB 19 AGCTGGACCTGGTGTC 2

RESULT 39

ABZ85226

ID ABZ85226 standard; DNA; 20 BP.

XX AC ABZ85226;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antiasthmatic gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIC-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX Claim 15; SEQ ID NO 468; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiasthmatic, antihypertensive, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC

angiotesin converting enzyme 2; ACE2; protease inhibitor 4; PI4;

KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;

KW cardiovascular disease; angina pectoris; hypertension; heart failure;

KW myocardial infarction; ventricular hypertrophy; vascular disease;

KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;

KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;

KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;

KW viral infection; bacterial infection; fungal infection; COPD;

KW Chronic obstructive pulmonary disease; enterocolitis.

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.

XX 23-JAN-2001; 2001US-0263678P.

XX 02-MAR-2001; 2001US-0273037P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PA (TSUC/) TSUCHIHASHI Z.

PA (HUI/) HUI L.

XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;

PI Swanson BN, Powell JR;

XX WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position, useful

PT for detecting, diagnosing and treating disorders such as angioedema,

PT cancer, viral, bacterial or fungal infection, cardiovascular and

PT autoimmune diseases.

XX Example 3; Page 911; 977pp; English.

XX The invention relates to an isolated nucleic acid from a human gene

CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),

CC tachykinin receptor B1 (TACR1), Cl esterase inhibitor (CINH), kallikrein

CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme

CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one

CC polymorphic position. Also included are (1) a probe that hybridises to a

CC polymorphic position as provided in the detailed summary of single

CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic

CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the

CC nucleic acid sequence at one or more polymorphic positions in a gene

CC encoding a protein selected from the group above; (3) constructing (M2)

CC haplotypes using the genes comprising grouping at least two nucleic acids

CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor

CC ; (4) identifying (M3) an individual at risk of developing a disorder

CC using the polymorphic data; (5) a library of nucleic acids, each of which

CC comprises one or more polymorphic positions within a gene encoding a

CC human protein selected from the group above; and (6) genotyping (M4) an

CC individual comprising obtaining a nucleic acid sample, determining the

CC nucleotide present in at least one polymorphic position, and comparing at

CC least one position with a known data set. The genes (M1, M2, M3 and M4)

CC and compositions are useful for detecting, diagnosing, treating,

CC preventing various disorders such as angioedema and diseases which

CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's

CC disease, trachomas, and cardiovascular diseases like angina pectoris,

CC hypertension, heart failure, myocardial infarction, ventricular

CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary

CC artery disease, arteriosclerosis and/or atherosclerosis, and

CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory

CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic

CC obstructive pulmonary disease (COPD) and enterocolitis (many other

CC diseases and disorders are listed in the specification). The

CC polynucleotides are also useful for chromosome identification. Antibodies

CC against the proteins may be utilised for immunophenotyping of cell lines

CC and biological samples. The present sequence is a genotyping PCR primer

CC

CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

QQ Query Match 10.6%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 1.1e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAAACCTGGT 1683

DB 2 CAAAGCTGGATCCCTGGT 19

RESULT 40

AAA11514/c

ID AAA11514 standard; DNA; 21 BP.

XX AC AAA11514;

XX AC AAA11514;

XX 30-JUN-2000 (first entry)

XX Human dysferlin PCR primer #159.

XX Dysferlin; anti-dystrophic; gene therapy; muscular dystrophy; human;

XX skeletal muscle cell; hereditary; Miyoshi myopathy; diagnosis;

XX limb girdle muscular dystrophy-2B; brain-specific; PCR primer; ss.

XX Homo sapiens.

XX WO200011157-A1.

XX 02-MAR-2000.

XX 25-AUG-1999; 99WO-US019395.

XX 25-AUG-1998; 98US-0097927P.

XX (GEO) GEN HOSPITAL CORP.

XX Brown RH, Liu J, Aoki M, Ho MF, Matsuda-Asada C;

XX WPI; 2000-237646/20.

XX Novel dysferlin genes and related proteins useful for diagnosis, risk

XX identification and treatment of hereditary muscular dystrophies and other

XX dysferlin related disorders.

XX Claim 8; Page 137; 146pp; English.

XX This invention describes a novel human dysferlin nucleic acid (I) and its

XX encoding protein (II), which has anti-dystrophic activity and can be used

XX for gene therapy. Introduction of (I), a vector comprising (I) or

XX dysferlin into a cell of a mammal can be used to decrease the symptoms of

XX muscular dystrophy. The dysferlin gene is normally expressed in skeletal

XX muscle cells and is selectively mutated in several families with the

XX hereditary muscular dystrophies, e.g. Miyoshi myopathy and limb girdle

XX muscular dystrophy-2B. The primers and oligonucleotides derived from (I)

XX can be used in diagnosis of or risk identification for dysferlin-related

XX disorders in patients, fetus, or pre-embryos. Expression of brain-

XX specific dysferlin may be important as a marker for normal neural

XX development. Dysferlin DNA or subgenomic coding sequences can be used for

XX therapy of the hereditary muscular dystrophies. AAX82919-X82945 represent

XX PCR primers used in the method of the invention

XX Sequence 21 BP; 4 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

XX Query Match 10.5%; Score 14.6; DB 1; Length 21;

XX Best Local Similarity 81.0%; Pred. No. 1.3e+02;

XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1677 CCTGTGTCTCTCCAGCGT 1697

DB 21 CCGTGGGTCCCTCCAGCAT 1

RESULT 41

AAA36969/c

ID AAA36969 standard; DNA; 21 BP.

XX AC AAA36969;

XX 03-AUG-2000 (first entry)

XX Human dysferlin exon amplification primer SEQ ID NO:231.

XX Human; dysferlin; mutant; identification; chromosome 2p12-14; detection;

XX muscular dystrophy; diagnosis; hereditary muscular dystrophy;

XX Miyoshi myopathy; limb girdle muscular dystrophy; primer; amplification;

XX screening; ss.

XX Homo sapiens.

XX WO200011016-A1.

XX 02-MAR-2000.

XX 25-AUG-1999; 99WO-US019394.

XX 25-AUG-1998; 98US-0097930P.

XX (GEO) GEN HOSPITAL CORP.

XX (UYPI-) UNIV PITTSBURGH.

XX Brown RH, Liu J, Hoffman E, Chou F;

XX WPI; 2000-246531/21.

XX Dysferlin polynucleotide, its mutant form useful for diagnosis and

XX treatment of hereditary muscular dystrophies e.g. Miyoshi myopathy and

XX limb girdle muscular dystrophy.

XX Disclosure; Page 34; 136pp; English.

XX The present invention describes an isolated dysferlin DNA of 20-25

XX nucleotides in length, comprising a nucleotide sequence specifically

XX selected from nucleotides 911-913, 929-948, 1019-1038, 1392-1411, 1424-

XX 1443, 1484-1503, 1499-1518, 1543-1565, 1715-1734, 1714-1759, 2241-2260,

XX 2864-2883, 2978-2997, 3057-3076, 3198-3217, 3252-3271, 4356-4375, 4665-

XX 4684, 5015-5034, 5610-5629, 5726-5735, 6035-6054, 6179-6198, 6243-6263

XX and 6529-6548 of the human dysferlin nucleotide sequence given in

XX AAA36744. Dysferlin nucleotide sequences containing specific mutations

XX can be used for diagnosing a patient, a fetus or a pre-embryo at risk of

XX developing a dysferlin associated disorder by detecting mutations in the

XX dysferlin gene in biological samples from patients. Alternatively, the

XX biological sample containing genomic DNA can be incubated with a

XX restriction enzyme, preferably BstEII, BstEII, PstI, HaeI, AclI, AclI,

XX Bsp1286, NlaIV, NlaIII, BclI, BstEII, PstI, HaeI, AclI, AclI,

XX Tsp509I, SalI, HincII, TaqI, HinfI, TfiI, SfiI or PstI and the presence

XX or absence of a restriction enzyme site in the sample is detected as an

XX indication of the presence or absence of a particular mutation in the

XX sample. Dysferlin polynucleotides are useful for treating hereditary

XX muscular dystrophies such as Miyoshi myopathy (MM) and limb girdle

XX muscular dystrophy-2B (LGM2-2B). MM and LGM2-2B map to the human

XX chromosome 2p12-14 region between the genetic markers D2S292 and D2S286.

XX The present sequence represents a primer for human dysferlin

XX Sequence 21 BP; 4 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

XX Query Match 10.5%; Score 14.6; DB 1; Length 21;

XX Best Local Similarity 81.0%; Pred. No. 1.3e+02;

XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1677 CCTGTGTCTCTCCAGCGT 1697

DB 21 CCGTGGGTCCCTCCAGCAT 1

Mon Aug 30 09:26:45 2004

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XX OS Synthetic.
XX PN JP2002233380-A.
XX PD 20-AUG-2002.
XX PF 08-FEB-2001; 2001JP-00031958.
XX PR 08-FEB-2001; 2001JP-00031958.
XX PA (CHCC ) CHISSO CORP.
XX DR WPI; 2002-736476/80.
XX PT A nucleic acid molecule derived from a plasmid of Streptomyces albus.
XX PS Example 3; Page 4; 17pp; Japanese.
XX CC The invention relates to a DNA molecule which is derived from plasmid
XX CC pNO33 of Streptomyces albus. In the scope of the invention, a microbe
XX CC host may be transformed by the vector. The vector is used for the
XX CC preparation of epsilon-polylysine. The current sequence represents an S.
XX CC albus plasmid pNO33 related PCR primer sequence
XX SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 10.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1636 GGGCTTGTAGCAGAG 1651
DB 17 GGGCTTGTAGCAGATG 2
RESULT 44
ABZ31506
ID ABZ31506 standard; DNA; 20 BP.
XX AC ABZ31506;
XX DT 30-JAN-2003 (first entry)
XX DB Candida albicans GRACE strain PCR primer SEQ ID NO 5725.
XX KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
XX KW signal transduction; RNA replication; cell division; growth;
XX KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX OS Candida albicans.
XX PN WO200253728-A2.
XX PD 11-JUL-2002.
XX PF 26-DEC-2001; 2001WO-US049486.
XX PR 29-DEC-2000; 2000US-0259128P.
XX PR 20-FEB-2001; 2001US-00792024.
XX PR 22-AUG-2001; 2001US-0314050P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX DR WPI; 2002-566694/60.
XX CC Constructing strains for identifying gene products as effective targets
XX CC for therapeutic intervention, by inactivating in the strain one allele of
XX CC a gene and placing other allele of the gene under conditional expression.
XX PS Claim 36; SEQ ID NO 5725; 167pp + Sequence Listing; English.

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XX OS Synthetic.
XX PN ABL58444 standard; DNA; 18 BP.
XX PD 30-JUL-2002 (first entry)
XX PF Cyp-C probe generating primer.
XX PR Embryoid body; stem cell; MAMA; gynecological; medicine; RT-PCR; primer;
XX PA galactin-3; cyp-C; ss.
XX DR Synthetic.
XX PT WO200165928-A1.
XX PS 13-SEP-2001.
XX CC 09-MAR-2000; 2000WO-IB000246.
XX PR 09-MAR-2000; 2000WO-IB000246.
XX PA (CHIC/) CHICHEPORTICHE Y.
XX PI Chicportiche Y, Ody C;
XX DR WPI; 2002-055092/07.
XX CC Promoting (M1) the success rate of in vitro production of embryoid bodies
XX CC from mammalian embryonic stem cells useful for regenerative medicine
XX CC comprises increasing the quantity of MAMA.
XX PS Disclosure; Page 14; 32pp; English.
XX CC The invention relates to a method of promoting the success rate of in
XX CC vitro production of embryoid bodies from mammalian embryonic stem cells
XX CC by increasing the quantity of MAMA or its homologues. MAMA is useful as
XX CC an agent of differentiation in an in vitro culture medium of mammalian
XX CC embryonic stem cells. An in vitro culture medium which contain MAMA and
XX CC the methods are useful for promoting the success rate of in vitro
XX CC production of embryoid bodies from embryonic stem cells which contain
XX CC MAMA. MAMA, cultures and vectors containing MAMA and the methods may be
XX CC used for regenerative medicine. MAMA may be used as a promoter of the
XX CC implantation of eggs obtained in vitro and to promote the successful
XX CC attachment of in vitro-fertilized eggs to the uterine membrane. The
XX CC present sequence represents a primer used for generating cyp-C specific
XX CC probes by RT-PCR, for northern hybridisation analysis of MAMA, galactin-3
XX CC and cyp-C mRNAs in transfected embryonic stem cells
XX SQ Sequence 18 BP; 1 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 10.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1672 TGGAGCCCTGGTGTCT 1687
DB 2 TGGAGCCCTGGTGTCT 17
RESULT 43
ABV73609/C
ID ABV73609 standard; DNA; 20 BP.
XX AC ABV73609;
XX DT 10-JAN-2003 (first entry)
XX DE S. albus plasmid pNO33 related primer #1.
XX KW Plasmid; epsilon-polylysine; pNO33; PCR; primer; ss.

```

XX The invention relates to constructing (M1) a strain of diploid fungal
 CC cells in which both alleles of a gene are modified, comprising
 CC one allele by insertion or replacement by a cassette having an
 CC expressible selectable marker and modifying other allele by
 CC recombination, of a promoter replacement fragment with a heterologous
 CC promoter, so that expression of the second allele is regulated by the
 CC promoter. (M1) is useful for constructing a strain of diploid fungal
 CC cells in which both alleles of a gene are modified. The diploid fungal
 CC cells having both alleles modified are useful for identifying a gene that
 CC is essential to the survival or growth of a fungus, a gene that
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene that
 CC that contributes to the resistance of a diploid fungus to an antifungal
 CC agent, an antifungal agent that inhibits the growth of a diploid fungus
 CC and for identifying a therapeutic agent for treatment of a diploid fungus
 CC disease. (M1) is useful for identifying a compound which modulates the
 CC activity of a gene product, preferably enzymatic activity, carbon
 CC compound catabolism, biosynthetic, transporter, transcriptional,
 CC translational, signal transduction, DNA replication and cell division
 CC activity. The method is useful for identifying a compound having the
 CC ability to inhibit growth or proliferation of *C. albicans* cells and for
 CC treating infection by *C. albicans*. The present sequence is that of a PCR
 CC primer used in the method of the invention. Note: The sequence data for
 CC this patent is not represented in the printed specification but is based
 CC on sequence information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 20 BP; 4 A; 9 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 10.4%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1737 TCCCACTCTCCCTA 1752
 Db 1 TCCCACTCTCCCAA 16
 |||||

RESULT 45
 ABI93783/c
 ID ABI93783 standard; DNA; 20 BP.
 AC ABI93783;
 DT 16-FEB-2002 (first entry)
 DE Capture oligonucleotide Zip ID#870 oligo #9.
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX Synthetic.

OS
 XX WO200179548-A2.
 XX
 XX 25-OCT-2001.
 XX
 XX 04-APR-2001; 2001WO-US010958.
 XX
 XX 14-APR-2000; 2000US-0197271P.
 XX
 XX (CORR) CORNELL RES FOUND INC.
 XX
 XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX WPI; 2002-034366/04.
 XX
 XX Designing capture oligonucleotide probes for use on a support to which
 XX complementary oligonucleotides hybridize with little mismatch.
 XX Example 5; Fig 29; 300pp; English.

PS

XX The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. *Salmonella*, *Listeria* monocytogenes and *Haemophilus influenzae*, fungal
 CC infectious agents e.g. *Cryptococcus neoformans*, *Candida albicans* and
 CC *Aspergillus fumigatus*, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from *Onchocerca volvulus*, *Entamoeba histolytica* and *Dracunculus*
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABI82074 to
 CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention
 XX

SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 10.4%; Score 14.4; DB 1; Length 20;
 Best Local Similarity 93.8%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1728 GAGATTGGCTCCCAAC 1743
 Db 18 GAGATTGGCTCCCAAC 3
 |||||

RESULT 46
 ABQ93591/c
 ID ABQ93591 standard; DNA; 21 BP.
 AC ABQ93591;
 XX
 XX 16-OCT-2002 (first entry)
 DT
 XX Human DISC1/DISC2 PCR primer disc09 fl.
 DE
 XX Human; Disrupted In Schizophrenia 1; DISC1; neuroleptic; gene therapy;
 KW neuropsychiatric disorder; schizoaffective disorder; bipolar disorder;
 KW unipolar affective disorder; adolescent conduct disorder; schizophrenia;
 KW PCR; primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200258637-A2.
 XX
 XX 01-AUG-2002.
 XX
 XX 23-JAN-2002; 2002WO-US002186.
 XX
 XX 24-JAN-2001; 2001US-00770107.
 XX
 XX (MILL-) MILLENIUM PHARM INC.
 XX
 XX Meyer JM, Barrington-Martin R, Parker A, Barnes GT;
 XX WPI; 2002-590791/63.
 XX
 XX New human Disrupted-In-Schizophrenia (DISC) 1 and DISC2 genes containing
 PT single nucleotide polymorphisms, useful for preventing or treating
 PT neuropsychiatric disorders e.g. schizophrenia.
 XX
 XX Claim 17; Fig 4; 169pp; English.

esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting gene expression. They may also be used for the treatment of liver disease, as hormone regulation agents and as hydrolysis reagents for the detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAGTGG 1673
| | | | | | | | | | | | | | | | | | | | | |
DB 19 AACACCCGGCTCACAGATG 1

RESULT 48
AAQ080880/c
ID AAQ080880 standard; DNA; 20 BP.
XX
AC AAQ080880;
XX
DT 25-MAR-2003 (revised)
DT 30-AUG-1995 (first entry)
XX
DE Europium (III) texaphyrin (EuTx) DNA conjugate 9B.
XX
KW Europium (III) texaphyrin (EuTx) DNA conjugate 9B; liver disease;
KW targeted intracellular mRNA hydrolysis; gene expression inhibition;
KW hormone regulation; hydrolysis reagents; alkyl phosphate esters;
KW detoxification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /note= "EuTx-NH(CH2)6-PO4-cytosine"
XX
PN WO9429316-A2.
XX
PD 22-DEC-1994.
XX
PF 09-JUN-1994; 94WO-US006284.
XX
PR 09-JUN-1993; 93US-00075123.
PR 14-APR-1994; 94US-00227370.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (PHAR-) PHARMACYCLICS INC.
XX
PI Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;
PI Kral VA, Iverson B, Mody T, Miller RA, Magda D;
XX
DR WPI; 1995-036382/05.
XX
PT Texaphyrin metal complex mediated ester hydrolysis - esp. useful for
PT targeted intracellular hydrolysis of mRNA and for inhibiting gene
PT expression.
XX
PS Example 7; Fig 9; 125pp; English.
XX
CC AAQ080879-Q80892 are texaphyrin lanthanide metal DNA conjugates, which are
CC esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting
CC gene expression. They may also be used for the treatment of liver disease,
CC as hormone regulation agents and as hydrolysis reagents for the
CC detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

The invention relates to a novel Disrupted-In-Schizophrenia (DISC) 1 allelic variant polynucleotide. The polypeptides of the invention have neuroleptic activity. The polynucleotides may have a use in gene therapy. DISC1 or DISC2 nucleic acid molecules are useful for diagnosing or treating a subject having a disease or disorder associated with specific DISC1 or DISC2 alleles and/or aberrant DISC1 expression or activity e.g. neuropsychiatric disorder such as schizoaffective, bipolar, unipolar affective or adolescent conduct disorder or schizophrenia. Similarly, the compound that inhibits DISC1 protein activity may be used in the method for treating such neuropsychiatric disorders. The sequences shown in CC ABQ93575-ABQ93658 represent the PCR primers used in the invention to CC amplify the sequences of DISC2 and DISC2

Sequence 21 BP; 3 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 10.4%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1640 TTGTAGCAGAGGCAA 1655
| | | | | | | | | | | | | | | | | | | | | |
DB 19 TTGCAGCAGAGGCAA 4

RESULT 47
AAQ080879/c
ID AAQ080879 standard; DNA; 20 BP.
XX
AC AAQ080879;
XX
DT 25-MAR-2003 (revised)
DT 30-AUG-1995 (first entry)
XX
DE Europium (III) texaphyrin (EuTx) DNA conjugate 9A.
XX
KW Europium (III) texaphyrin (EuTx) DNA conjugate 9A; liver disease;
KW targeted intracellular mRNA hydrolysis; gene expression inhibition;
KW hormone regulation; hydrolysis reagents; alkyl phosphate esters;
KW detoxification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 7 /*tag= a
FT /*mod_base= OTHER
FT /note= "EuTx-NH(CH2)6 alkylamidated thymidine"
XX
PN WO9429316-A2.
XX
PD 22-DEC-1994.
XX
PF 09-JUN-1994; 94WO-US006284.
XX
PR 09-JUN-1993; 93US-00075123.
PR 14-APR-1994; 94US-00227370.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (PHAR-) PHARMACYCLICS INC.
XX
PI Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;
PI Kral VA, Iverson B, Mody T, Miller RA, Magda D;
XX
DR WPI; 1995-036382/05.
XX
PT Texaphyrin metal complex mediated ester hydrolysis - esp. useful for
PT targeted intracellular hydrolysis of mRNA and for inhibiting gene
PT expression.
XX
PS Example 7; Fig 9; 125pp; English.
XX
CC AAQ080879-Q80892 are texaphyrin lanthanide metal DNA conjugates, which are

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Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAGCTG 1673
DB 19 AACACCGCGCTCACAGATG 1

RESULT 49
AAQ91455/c
ID AAQ91455 standard; DNA; 20 BP.
XX
AC AAQ91455;
XX
DT 25-MAR-2003 (revised)
XX
DT 30-AUG-1995 (first entry)
XX
DE Dysprosium (III) texaphyrin (DyTx) DNA conjugate.
XX
XX Dysprosium (III) texaphyrin (DyTx) DNA conjugate; liver disease;
KW targeted intracellular mRNA hydrolysis; gene expression inhibition;
KW hormone regulation; hydrolysis reagents; alkyl phosphate esters;
KW detoxification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "DyTx-NH(CH2)6-P04-cytosine"
XX
XX WO9429316-A2.
XX
PD 22-DEC-1994.
XX
PF 09-JUN-1994; 94WO-05006284.
XX
PR 09-JUN-1993; 93US-00075123.
PR 14-APR-1994; 94US-00227370.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
PA (PHAR-) PHARMACYCLICS INC.
XX
XX Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;
PI Kral VA, Iverson B, Mody T, Miller RA, Magda D;
XX
XX WPI; 1995-036382/05.
XX
XX Texaphyrin metal complex mediated ester hydrolysis - esp. useful for
FT targeted intracellular hydrolysis of mRNA and for inhibiting gene
FT expression.
XX
XX Disclosure; Fig 21; 125pp; English.
XX
XX AAQ91451-Q91457 are texaphyrin lanthanide metal DNA conjugates, which are
CC esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting
CC gene expression. They may also be used for the treatment of liver disease,
CC as hormone regulation agents and as hydrolysis reagents for the
CC detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAGCTG 1673
DB 19 AACACCGCGCTCACAGATG 1

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RESULT 50
AAQ81567/c
ID AAQ81567 standard; DNA; 20 BP.
XX
AC AAQ81567;
XX
DT 04-SEP-1995 (first entry)
XX
DE Hepatitis B virus polypeptide cDNA PCR primer p142.
XX
XX Hepatitis B virus; HBV; polypeptide; diagnosis and detection;
KW PCR primer p142; ss.
XX
OS Synthetic.
XX
PN JP06321991-A.
XX
PD 22-NOV-1994.
XX
XX 14-MAY-1993; 93JP-00113136.
PF 14-MAY-1993; 93JP-00113136.
PR 14-MAY-1993; 93JP-00113136.
XX
XX (MITU ) MITSUBISHI KASEI CORP.
PA
XX
XX WPI; 1995-041293/06.
XX
XX Polypeptide derived from type B hepatitis virus and gene to code it -
PT used in diagnosis of type B hepatitis virus.
XX
XX Example 2; Page 5; 13pp; Japanese.
XX
CC AAQ81567 and AAQ81568 are a pair of primers for the PCR amplification of
CC the cDNAs encoding the hepatitis B virus (HBV) polypeptides described in
CC AAR68865-R68871. The polypeptides or their fragments can be used in the
CC diagnosis and detection of HBV
XX
XX Sequence 20 BP; 4 A; 1 C; 12 G; 3 T; 0 U; 0 Other;

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 CTCCTCACTCTCTCCATC 1754
DB 19 CCCCCCACTCTCTCCAGTC 1

RESULT 51
AAT08224/c
ID AAT08224 standard; DNA; 20 BP.
XX
AC AAT08224;
XX
DT 23-MAY-1996 (first entry)
XX
DE p142, PCR primer used for isolation of antisense HBV strain X region.
XX Hepatitis B virus; X region; antisense; antibody; vector; diagnosis;
KW hepatoma; hepatitis; antiviral; anticancer; transcription; ss.
XX
OS Synthetic.
XX
XX WO9527788-A1.
XX
PD 19-OCT-1995.
XX
PF 10-APR-1995; 95WO-JP000700.
XX
XX 11-APR-1994; 94JP-00095458.
XX
XX (DAIN-) DAINABOT CO LTD.
PA

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Mon Aug 30 09:26:45 2004

XX Uchida T, Shikata T;
 PI WPI; 1995-366392/47.
 DR X region anti-sense DNA sequence of new hepatitis B strain, related
 PT peptide(s) and antibodies - useful for diagnosis and investigation of HBV
 PT infection.
 XX Example 2; Page 22; 61pp; Japanese.
 XX AA080224-53 are PCR primers used for the isolation and amplification of 2
 CC antisense DNA sequences derived from the X region of a new strain of
 CC hepatitis B. The DNA codes for a viral peptide ASXP. The ASXP peptide and
 CC antibodies recognising it are useful in the diagnosis of hepatitis caused
 CC by the virus, in the investigation of transcription activated and
 CC enhanced by the presence of the ASXP peptide, and in the development of
 CC effective antiviral and anticancer drugs for the treatment of hepatitis
 CC and hepatoma
 XX Sequence 20 BP; 4 A; 1 C; 12 G; 3 T; 0 U; 0 Other;
 SQ Query Match 10.2%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1736 CTCCCAACTCTCCCTATC 1754
 DB 19 CCCTCAACTCTCCCAATC 1
 RESULT 52
 AAV07290/c
 ID AAV07290 standard; DNA; 20 BP.
 XX AC AAV07290;
 XX 14-AUG-1998 (first entry)
 DT Oligonucleotide #4.
 DE Metallotexaphyrin; dysprosium; europium; conjugate; RNase H;
 KW antisense therapy; ss.
 XX Synthetic.
 OS US5763172-A.
 XX 09-JUN-1998.
 PD 07-JUN-1995; 95US-00486962.
 XX 21-JAN-1992; 92US-00822964.
 PR 09-JUN-1993; 93US-00075123.
 PR 14-APR-1994; 94US-00227370.
 PR 09-JUN-1994; 94WO-US006284.
 PR 26-MAY-1995; 95US-00452261.
 PR 07-JUN-1995; 95US-00485581.
 XX (PHAR-) PHARMACYCLICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX Sessler JL, Wright M, Miller RA, Dow WC, Magda D;
 PI WPI; 1998-347306/30.
 DR Enhancing therapeutic activity of oligo-nucleotides in cells - using
 XX conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester
 PT bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.
 XX Disclosure; Col 37-38; 34pp; English.
 XX This sequence is shown in the specification. The invention relates to
 PS the invention relates to a method of enhancing the therapeutic activity

CC of oligonucleotides in cells. It comprises contacting a targeted
 CC intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide
 CC conjugate. The contact is carried out under physiological conditions for
 CC a time sufficient to hydrolyse the phosphate ester bond of the targeted
 CC RNA. The metallotexaphyrin of the conjugate has catalytic activity for
 CC phosphate ester bond hydrolysis. The oligonucleotide of the conjugate may be
 CC complementary binding affinity to the targeted RNA. The conjugate may be
 CC used in antisense therapies for treating, e.g. cancer, viral infections,
 CC autoimmune diseases and restenosis. The conjugate may also be used as
 CC hydrolysis reagents for the detoxification of di- and trialkyl phosphate
 CC esters, which are used in solvents, insecticides and chemical nerve
 CC gases. The metallotexaphyrin complex enhances the therapeutic activity of
 CC the oligonucleotide, not only by facilitating cellular uptake of the
 CC oligonucleotide but also by hydrolysing target RNA within the cell,
 CC independent of RNase H. Attachment to the complex may also cause the
 CC oligonucleotide to take on some of the pharmacodynamic an biodistribution
 CC properties of the texaphyrin, such as selective localisation in tumours.
 CC The present oligonucleotide is shown in the specification
 XX Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;
 SQ Query Match 10.2%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1655 AGCACCCAGGCTCACAGCTG 1673
 DB 19 AACACCCCGGCTCACAGATG 1
 RESULT 53
 AAV07037/c
 ID AAV07037 standard; DNA; 20 BP.
 XX AC AAV07037;
 XX 08-JUL-1998 (first entry)
 DT Texaphyrin oligonucleotide conjugate.
 DE Texaphyrin oligonucleotide conjugate; dysprosium; metal complex;
 KW hydrolytic cleavage activity; ss.
 XX Synthetic.
 OS Key modified_base 1
 FH Location/Qualifiers
 FT /*tag= a
 FT /note= "A texaphyrin dysprosium metal complex, bound to
 FT cytosine via a linking phosphate group"
 XX WO9807733-A1.
 XX 26-FEB-1998.
 XX 20-AUG-1997; 97WO-US014682.
 XX 20-AUG-1996; 96US-0700277.
 XX (PHAR-) PHARMACYCLICS INC.
 XX Magda D, Crofts SP, Wright M;
 XX WPI; 1998-179049/16.
 XX New conjugates which have hydrolytic cleavage activity for RNA - comprise
 PT a texaphyrin metal complex bound to an internal linkage of an
 PT oligonucleotide.
 XX Example 4; Page 51; 77pp; English.
 XX This sequence is shown in the specification. The invention relates to
 XX texaphyrin oligonucleotide conjugates which have hydrolytic cleavage

CC activity for RNA. They comprise a texaphyrin metal complex bound to an
 CC internal linkage of an oligonucleotide or oligonucleotide analogue. The
 CC conjugates may be used for the destruction of retroviral RNA, messenger
 CC RNA, ribosomal RNA, RNA cofactors, transfer RNA, small nuclear RNA and
 CC small cytoplasmic RNA. They may be used for eliminating diseased or
 CC cancerous cells or tissues, in blood purification protocols (in vivo or
 CC in vitro), in antiviral treatments, or as diagnostic probes (e.g. in
 CC determination of the nucleotide sequence of RNA or to detect
 CC polymorphisms in RNA). Administration of the conjugates is, e.g., oral,
 CC topical or parenteral, especially topical or intravenous. The conjugates
 CC are especially effective under conditions where the concentration of RNA
 CC target exceeds that of available conjugate

SQ Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAGCTG 1673

DB 19 AACACCCGGCTCACAGATG 1

RESULT 54

AAV99212/c

ID AAV99212 standard; DNA; 20 BP.

AC AAV99212;

XX

XX

DT 09-MAR-1999 (first entry)

XX

XX

DE Antisense primer for intron boundary mapping of DNA Metase exon 35-36.

XX

XX

KW DNA methyltransferase; DNA Metase; antisense oligonucleotide; human;

XX

KW cellular growth; tumour growth inhibition; silenced gene activation;

XX

XX

OS beta thalassemia; sickle cell anemia; PCR primer; ss.

XX

OS Synthetic.

XX

OS Homo sapiens.

XX

PN WO9854313-A2.

XX

PD 03-DEC-1998.

XX

XX

PF 29-MAY-1998; 98WO-IB001107.

XX

XX

ER 30-MAY-1997; 97US-00866340.

XX

ER 17-DEC-1997; 97US-0069865P.

XX

XX

PA (UYMC-) UNIV MCGILL.

XX

XX

PI Szyf M, Bigey P, Ramchandani S;

XX

XX

DR WPI; 1999-059833/05.

XX

XX

PT New DNA methyltransferase nucleotide sequences - used particularly to

develop antisense oligonucleotides for diagnostic and therapeutic

purposes, particularly for inhibiting tumour growth.

Example 8; Page 32; 108pp; English.

CC PCR primers AAV99163-220 were used to map the intron boundaries of the
 CC exons of DNA methyltransferase (DNA Metase) genomic sequence. Antisense
 CC oligonucleotides which inhibit DNA Metase expression can be
 CC derived from the genomic DNA Metase sequence. The antisense
 CC oligonucleotides can be used in investigating the role of DNA Metase in
 CC cellular growth. They can be administered at different points in the cell
 CC cycle, or in conjugation with promoters or inhibitors of cell growth to
 CC determine the role of DNA Metase in the growth of the cell type of
 CC interest. The antisense oligonucleotides can also be used for inhibiting
 CC tumour growth in a mammal, or to activate silenced genes to provide a
 CC missing gene function. This ameliorates disease symptoms, e.g. in beta

CC thalassemia and sickle cell anemia. The antisense oligonucleotides can
 CC also be used as analytical and diagnostic tools and a potentiators of
 CC transgenic plant and animal studies

SQ Sequence 20 BP; 5 A; 9 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1681 GGTGTCCTCTCAGCGTGG 1699

DB 20 GGGGTCTGCTCTCGGTGG 2

RESULT 55

AAZ88439/c

ID AAZ88439 standard; DNA; 20 BP.

XX

AC AAZ88439;

XX

DT 08-MAY-2000 (first entry)

XX

DE Exemplary texaphyrin oligonucleotide conjugate SEQ ID NO:5.

XX

KW Texaphyrin; metal complex; catalytic; RNA hydrolysis; virucide;

XX

KW antibacterial; cytostatic; antiinflammatory; antitumour; antiviral; ss.

XX

OS Synthetic.

XX

PN US6022959-A.

XX

PD 08-FEB-2000.

XX

PF 20-NOV-1997; 97US-00975522.

XX

XX

PR 20-AUG-1996; 96US-0077185P.

XX

PR 20-AUG-1997; 97WO-US014682.

XX

XX

PA (PHAR-) PHARMACYCLICS INC.

XX

XX

PI Wright M, Crofts SP, Magda D;

XX

XX

DR WPI; 2000-160391/14.

XX

PT Texaphyrin metal complex derivatized ribonucleic acids possessing

XX

PT hydrolytic cleavage activity against RNA are useful as e.g. antiviral,

XX

PT antibacterial, antitumor and antiinflammatory agents.

XX

PS Example 4; Col 32; 30pp; English.

XX

XX

CC The present invention describes a conjugate with hydrolytic cleavage

XX

CC activity for ribonucleic acid (RNA), which comprises a texaphyrin metal

XX

CC complex bound to an internal linkage of an oligonucleotide or

XX

CC oligonucleotide analogue. AAZ88435 to AAZ88440 represent exemplary

texaphyrin oligonucleotide conjugates used in the exemplification of the
 present invention. The novel conjugates have virucide, antibacterial,
 cytostatic and antiinflammatory properties, and are involved in RNA
 hydrolysis. The conjugates are useful for inhibiting the expression of a
 gene by targeted intracellular mRNA (messenger ribonucleic acid)
 hydrolysis. The conjugates have applications for anti-viral and anti-
 bacterial therapy as well as cancers and inflammatory responses caused by
 overexpression of certain proteins

SQ Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAGCTG 1673

DB 19 AACACCCGGCTCACAGATG 1

Mon Aug 30 09:26:45 2004

AAD41746 standard; DNA; 20 BP.

AAD41746;
30-OCT-2002 (first entry)

RESULT 56
AAD05958
ID AAD05958 standard; DNA; 20 BP.

Human RECQL2 antisense oligonucleotide, ISIS #137526.
Antisense; RECQL2; Bloom's disorder; prophylaxis; infection; tumour;
inflammation; therapy; human; phosphorothioate; ss.

Human diacylglycerol kinase-zeta intron 18/exon 19 junction sequence.
Human; catalyst; diacylglycerol; DAG; phosphatidic acid; DAG modulator;
diacylglycerol kinase zeta; DGK; ds.

Homo sapiens.

Key Location/Qualifiers
intron 1..10
/*tag= a
/number= 18
/partial
exon 11..20
/*tag= b
/number= 19
/partial

US6221658-B1.

24-APR-2001.

25-AUG-1999; 99US-00382911.

22-APR-1996; 96US-0016210P.

22-APR-1997; 97US-00841483.

(UTAH) UNIV UTAH RES FOUND.

Prescott SM, Bunting M, Tang W, Topham M;

WPI; 2001-327248/34.

New DNAs of the human diacylglycerol kinase, useful for modulating the levels of diacylglycerol kinase in cells to catalyze the conversion of diacylglycerol to phosphatidic acid, therefore increasing phosphatidic acid levels.

Disclosure; Col 17-18; 74pp; English.

The patent discloses novel human diacylglycerol kinase (DGK) isoforms namely diacylglycerol kinase epsilon, diacylglycerol kinase zeta, diacylglycerol kinase zeta-2 and their corresponding cDNAs. Human diacylglycerol kinase DNA is useful for coding human diacylglycerol kinase, which is useful for catalysing the conversion of diacylglycerol to phosphatidic acid. In particular, the human diacylglycerol kinase and its DNA are useful for decreasing intracellular levels of diacylglycerol (DAG) and for increasing intracellular levels of phosphatidic acid in cells. The present DNA sequence is the exon/intron junction sequence of human diacylglycerol kinase (DGK) zeta gene

Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCTGTGGAA 1704

Db 2 GGCCTCCAGTGTGGAA 20

RESULT 57

AAD41746/c

Key Location/Qualifiers
modified_base 1..20
/*tag= a
/mod_base= OTHER
modified_base 1..5
/*tag= b
/mod_base= OTHER
/*note= "2'-methoxyethyl nucleotides"
modified_base 9
/*tag= d
/mod_base= m5c
modified_base 16..20
/*tag= c
/mod_base= OTHER
/*note= "2'-methoxyethyl nucleotides"
modified_base 19..20
/*tag= e
/mod_base= m5c

US6399378-B1.

04-JUN-2002.

01-MAR-2001; 2001US-00798096.

01-MAR-2001; 2001US-00798096.

(ISIS-) ISIS PHARM INC.

Ward DT, Watt AT;

WPI; 2002-535979/57.

Antisense compounds targeted to nucleic acids encoding RECQL2 associated with Bloom's disorder, for modulating RECQL2 expression and treating diseases e.g. tumors associated with expression of the RECQL2 in humans.
Example 15; Col 44; 8pp; English.
The invention relates to antisense compounds targetted to nucleic acid encoding RECQL2 (gene associated with Bloom's disorder) to inhibit the expression of RECQL2. Antisense compounds of the invention are useful for treating diseases associated with expression of RECQL2, in humans. They are useful for diagnostics, therapeutics and as research reagent, e.g. prophylactically to prevent or delay infection, inflammation or tumour formation. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human RECQL2 DNA

Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1662 GGCTCAGCTGTGAACCT 1680

Db 20 GGCTCAGCTGTGAACCT 2

RESULT 58
 ABT23628/c
 ID ABT23628 standard; DNA; 20 BP.
 XX AC ABT23628;
 XX
 DT 22-MAY-2003 (first entry)
 DE
 DE Stabilising reagent method related oligo SEQ ID No 80.
 XX
 XX Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;
 KW specific amplification; pathogenic microorganism; chimeric;
 KW genetic engineering; clinical medicine; ss.
 OS Unidentified.
 XX
 PN WO2002101042-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 12-JUN-2002; 2002WO-JP005832.
 XX
 PR 12-JUN-2001; 2001JP-00177737.
 PR 20-AUG-2001; 2001JP-00249689.
 XX
 PA (TAKI) TAKARA BIO INC.
 XX
 PI Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
 PI Shoki T, Asada K, Kato I;
 XX
 DR WPI; 2003-148805/14.
 XX
 XX Method for stabilizing and storing reaction reagents for specific
 PT amplification and detection of nucleic acids particularly in e.g.
 PT identifying pathogenic microorganisms or viruses in sample.
 XX
 PS Example 15; Page 137; 177pp; Japanese.
 XX
 CC The invention relates to a novel stabilising reaction reagent for use in
 CC the amplification and/or detection of a target nucleic acid comprising:
 CC preparing a reaction mixture with e.g. a nucleic acid as template, at
 CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
 CC defined period of time to form a reaction product during the
 CC amplification of such target nucleic acid. The method is useful for
 CC stabilising and long-term storage of reaction reagents for highly
 CC sensitive and specific amplification and detection of nucleic acids
 CC particularly in identifying pathogenic microorganisms or viruses in a
 CC sample using chimeric oligonucleotide primers, which is useful in genetic
 CC engineering and clinical medicine. This polynucleotide sequence
 CC represents an oligo relating to the novel stabilising reaction reagent
 CC method of the invention
 XX
 SQ Sequence 20 BP; 4 A; 1 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 10.2%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1736 CTCCTCACTCTCCCTATC 1754
 Db 19 CCCCCAACTCTCCCACTC 1
 RESULT 59
 ACD13735
 ID ACD13735 standard; DNA; 20 BP.
 XX AC ACD13735;
 XX
 DT 14-AUG-2003 (first entry)
 XX
 DE STS187T7 amplification primer F.

XX
 KW RIEG; ss; ophthalmological; neoplastic disorder; hyperplastic disorder;
 KW abnormal cell proliferation; umbilical artery expression; PCR; primer;
 KW Rieger's syndrome; vitelline artery expression; human; STS.
 XX
 OS Homo sapiens.
 XX
 PN US6518411-B1.
 XX
 PD 11-FEB-2003.
 XX
 PF 22-NOV-1996; 96US-00754477.
 XX
 PR 22-NOV-1996; 96US-00754477.
 XX
 PA (UNIP) UNIV IOWA.
 XX
 PI Murray JC, Semina E;
 XX
 DR WPI; 2003-465605/44.
 XX
 XX New RIEG polypeptides and nucleic acids, useful in antisense therapy, in
 PT drug screening assays, and in treating Rieger syndrome or associated
 PT conditions related to umbilical and vitelline artery expression.
 XX
 PS Example 1; Col 57; 101pp; English.
 XX
 CC The invention relates to an isolated RIEG nucleic acid. The nucleic acids
 CC are useful as probes to detect transcripts or genomic sequences encoding
 CC the same or homologous proteins, in predictive and therapeutic evaluation
 CC of allelic mutations which might be manifested in neoplastic or
 CC hyperplastic disorders or abnormal cell proliferation, in antisense
 CC therapy, in drug screening assays and in the treatment of Rieger's
 CC syndrome or associated conditions related to umbilical and vitelline
 CC artery expression. The present sequence represents a STS amplification
 CC primer
 XX
 SQ Sequence 20 BP; 3 A; 9 C; 1 G; 7 T; 0 U; 0 Other;
 Query Match 10.2%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1733 TGGCTCCCACTCCCTCCCT 1751
 Db 2 TGTCTCCCAATCTCTCACT 20
 RESULT 60
 ADB89990/c
 ID ADB89990 standard; DNA; 20 BP.
 XX AC ADB89990;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Antisense oligonucleotide targeting mouse C3 component, ISIS140078.
 XX
 KW Mouse; ss; antisense; complement component C3; inflammation;
 KW septic shock; multiple organ failure; hyperacute organ failure;
 KW autoimmune disorder; CNS inflammation; multiple sclerosis;
 KW atherosclerosis; tumour.
 XX
 OS Mus musculus.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone and all cytosines are 5
 FT -methyl cytosines"
 FT modified_base 1..5
 FT /tag= a

[illegible]

```

DE Cosmid amplification primer #11.
XX
XX ss; RGS; Solurshin; Reiger syndrome; glaucoma; pituitary disorder;
KW abdominal disorder; umbilical artery expression;
KW vitelline artery expression; cosmid; primer.
XX
XX Synthetic.
XX
XX US2003105002-A1.
XX
XX 05-JUN-2003.
XX
XX 22-MAR-2002; 2002US-00105004.
XX
XX 22-NOV-1996; 96US-00754477.
XX
XX (MURR/) MURRAY J C.
XX (SEMI/) SEMINA E.
XX
XX Murray JC, Semina E;
XX
XX WPI; 2003-678200/64.
XX
XX New nucleic acid molecule encoding an RGS polypeptide, useful for
PT suppressing the development of Reiger syndrome, which can lead to
PT glaucoma and for treating associated conditions related to umbilical and
PT vitelline artery expression.
XX
XX Example 1; Page 31; 104pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding
CC RGS/Solurshin. The nucleic acid molecule, polypeptides and methods are
CC useful for suppressing the development of Reiger syndrome, which can lead
CC to glaucoma, and for treating associated conditions including pituitary
CC and abdominal disorders related to umbilical and vitelline artery
CC expression. The present sequence represents a cosmid amplification
CC primer.
XX
XX Sequence 20 BP; 3 A; 9 C; 1 G; 7 T; 0 U; 0 Other;
SQ
Query Match 10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1733 TGGCTCCCACTCTCCCT 1751
Db 2 TGTCTCCCAATCTCTCACT 20
RESULT 63
ID ADD13897
AC ADD13897 standard; DNA; 21 BP.
XX
XX ADD13897;
XX
XX 01-JAN-2004 (first entry)
XX
XX Human vH PCR primer vH3-11.
XX
XX library; transfection; humanized monoclonal antibody; antigen;
KW T cell receptor; primer; ss; PCR; vH.
XX
XX Homo sapiens.
XX
XX EF1298207-A1.
XX
XX 02-APR-2003.
XX
XX 01-OCT-2001; 2001EP-00123596.
XX
XX 01-OCT-2001; 2001EP-00123596.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
Breitling F, Moldenhauer G, Poustka A, Kuehlwein T;
WPI; 2003-383833/37.
XX
XX Preparing library of protein-producing eukaryotic cells, useful for
PT producing humanized high-affinity antibodies, comprises introducing
PT specific recombination signals into chromosomal gene loci and integrating
PT a variety of DNA sequences.
XX
XX Example 5; Fig 14C; 75pp; German.
XX
XX This invention describes a novel method of preparing a library of protein
CC -producing eukaryotic cells comprising (a) introducing specific
CC recombination signals into one or two chromosomal gene loci, (b)
CC Expanding at least one of the modified cells, (c) Transfecting many
CC different DNA sequences, each flanked by recombination signals, into the
CC expanded cells and (d) Integrating the DNA sequences into the gene loci
CC on the basis of the recombination signals and the appropriate
CC recombinease. The resulting cells express different proteins, each from an
CC integrated DNA sequence and the proteins are bound to the cell surface.
CC The method is particularly used to produce libraries of humanized
CC monoclonal antibodies, for selection of those with affinity for
CC particular antigens and useful for diagnostic or therapeutic use.
CC Libraries of T cell receptors may also be prepared. The method produces
CC libraries of high diversity; provides easy, quick and automatable
CC selection from a large number of proteins, allows relatively simple
CC alteration of the expressed gene (e.g. fusion to other protein-coding
CC sequences), is suitable for large scale protein production and allows
CC simple verification and characterization of selected cell lines. The
CC method does not require incorporation of a resistance marker. This
CC sequence represents a PCR primer used to amplify the genes of the
CC invention.
XX
XX Sequence 21 BP; 1 A; 12 C; 3 G; 5 T; 0 U; 0 Other;
SQ
Query Match 10.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1679 CTGGTGTCCTCTCCAGCGT 1697
Db 1 CTGCCCTCTCTCCAGCGT 19
RESULT 64
AAAS58421
ID AAA58421 standard; DNA; 20 BP.
XX
XX AAA58421;
XX
XX 11-OCT-2000 (first entry)
XX
XX Oct-4 transcript RT-PCR primer #2.
XX
XX Human embryonic stem cell; oct-4 expression; development;
KW transplantation; drug screening; drug discovery; RT-PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WC200027995-A1.
XX
XX 18-MAY-2000.
XX
XX 09-NOV-1999; 99WO-AU000990.
XX
XX 09-NOV-1998; 98AU-00007009.
XX
XX 15-SEP-1999; 99AU-00002852.
XX
XX (MONU ) UNIV MONASH.
XX (UYSI-) UNIV SINGAPORE NAT.
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX

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PI Reubinoff BE, Pera MF, Yee PC, Trounson AO, Bongso A;
 XX WPI; 2000-376517/32.
 XX
 XX Novel undifferentiated human embryonic stem cells which are useful as a
 PT source of novel gene products.
 XX
 XX Disclosure; Page 31; 56pp; English.
 XX
 XX The present sequence is a RT-PCR primer for the human oct-4 transcript.
 CC It was used to measure oct-4 expression in differentiated and
 CC undifferentiated cells. These were all derived from human embryonic stem
 CC cells. Stem cells can be used to treat inherited diseases, to study the
 CC cellular and molecular biology of early human development, in functional
 CC genomics, to identify novel growth factors and to generate differentiated
 CC cells to use in transplantation, drug screening or drug discovery in
 CC vitro
 XX
 XX Sequence 20 BP; 4 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 10.1%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1656 GCACGAGGCTCACA 1669
 DB 7 GCACGAGGCTCACA 20
 RESULT 65
 AAV91006/c
 ID AAV91006 standard; RNA; 17 BP.
 XX
 XX AAV91006;
 XX
 XX 18-FEB-1999 (first entry)
 XX Human C-raf target site nucleotide position 581.
 XX
 XX Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO9850530-A2.
 XX
 XX 12-NOV-1998.
 XX
 XX 05-MAY-1998; 98WO-US009249.
 XX
 XX 09-MAY-1997; 97US-0046059P.
 XX 09-JUN-1997; 97US-0049002P.
 XX 03-JUL-1997; 97US-0051718P.
 XX 22-AUG-1997; 97US-0056808P.
 XX 02-OCT-1997; 97US-0061324P.
 XX 02-OCT-1997; 97US-0061324P.
 XX 05-NOV-1997; 97US-0064866P.
 XX 19-DEC-1997; 97US-0068212P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX WPI; 1999-009494/01.
 XX
 XX Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer,
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates

PT used as antiviral agents and synthons.
 XX
 XX Claim 177; Page 147; 259pp; English.
 XX
 XX A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACS
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACS that can be used in the
 CC method, specifically for modulating the expression of a Raf gene
 XX
 XX Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
 SQ
 Query Match 9.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1641 TGTACGAGGCAAGC 1657
 DB 17 TGTACGAGGCAAGC 1
 RESULT 66
 AAV91005/c
 ID AAV91005 standard; RNA; 17 BP.
 XX
 XX AAV91005;
 XX
 XX 18-FEB-1999 (first entry)
 XX Human C-raf target site nucleotide position 576.
 XX
 XX Human; C-raf; A-raf; E-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO9850530-A2.
 XX
 XX 12-NOV-1998.
 XX
 XX 05-MAY-1998; 98WO-US009249.
 XX
 XX 09-MAY-1997; 97US-0046059P.
 XX 09-JUN-1997; 97US-0049002P.
 XX 03-JUL-1997; 97US-0051718P.
 XX 22-AUG-1997; 97US-0056808P.
 XX 02-OCT-1997; 97US-0061321P.
 XX 02-OCT-1997; 97US-0061324P.
 XX 05-NOV-1997; 97US-0064866P.
 XX 19-DEC-1997; 97US-0068212P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;

```
XX WPI; 1999-009494/01.
XX
XX Identifying new catalytic nucleic acid that modulates selected processes
XX - especially ribozymes that cleave Raf RNA for treating cancer,
XX restenosis, and also new ribozymes and modified nucleoside triphosphates
XX used as antiviral agents and synthons.
XX
XX Claim 177; Page 147; 259pp; English.
XX
XX A method has been developed for the identification of a nucleic acid
XX capable of modulating a process in a biological system. The method
XX comprises: (a) introducing into the system a random library of nucleic
XX acid catalysts (NAC) having a substrate binding domain (SBD), comprising
XX a random sequence, and a catalytic domain (CD); and (b) identifying NAC
XX in systems where modulation has occurred and/or determining the sequence
XX of at least part of the SBDs in such systems. Nucleic acid molecules with
XX endonuclease activity and catalytic activity, from the present invention,
XX are used to modulate gene expression in plant and mammalian cells and to
XX cleave target nucleic acid, particularly for treating systemic diseases
XX caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
XX ascites and infection. They may also be used to detect genetic drift and
XX mutations in diseased cells and to determine c-raf RNA. Specifically NACs
XX with RNA-cleaving activity that modulate expression of the Raf gene, are
XX used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX generally any condition associated with the level of c-raf. Introduction
XX of sugar/phosphate modifications increases stability against nuclease and
XX activity. AA90922 to AA93877 represent NACs that can be used in the
XX method, specifically for modulating the expression of a Raf gene
XX
XX Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 9.9%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1646 CAGAGGCGACGACACG 1662
XX |||||
XX Db 17 CAGAGGCGAGCTTCAG 1
XX
XX RESULT 67
XX ACD50855
XX ID ACD50855 standard; RNA; 17 BP.
XX AC ACD50855;
XX XX
XX DT 23-SEP-2003 (first entry)
XX XX
XX DE HBV hammerhead ribozyme substrate sequence #270.
XX XX
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
XX amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX
XX OS Hepatitis B virus.
XX
XX PN WO200281494-A1.
XX XX
XX PD 17-OCT-2002.
XX
XX XX
XX PF 26-MAR-2002; 2002WO-US009187.
XX
XX PR 26-MAR-2001; 2001US-00817879.
XX
XX PR 08-JUN-2001; 2001US-00877478.
XX
XX PR 08-JUN-2001; 2001US-0296876P.
XX
XX PR 24-OCT-2001; 2001US-0335059P.
XX
XX PR 05-DEC-2001; 2001US-0337055P.
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XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MACE/) MACEJAK D.
XX (MCSW/) MCSWIGGEN J.
XX (MORR/) MORRISSEY D.
XX (PAVC/) PAVCO P.
XX (LEEP/) LEE P.
XX (DRAP/) DRAPER K.
XX (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
XX Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
XX hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.
XX
XX Example 1; Page 141; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
XX inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules, and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HBV
XX ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberyne sequences
XX disclosed in the present invention
XX
XX SQ Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 9.9%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 64.7%; Pred. No. 1.5e+02;
XX Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1673 GGAACCCCTGGTGCTCC 1689
XX ||||| : ||:|:|
XX Db 1 GGAACCCUUGUGUCUCC 17
XX
XX RESULT 68
XX ACD55655/c
XX ID ACD55655 standard; RNA; 17 BP.
XX AC ACD55655;
XX XX
XX DT 23-SEP-2003 (first entry)
XX
XX DE HBV amberyne substrate sequence #165.
XX
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
XX amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX
XX OS Hepatitis B virus.
```

PN WO200281494-A1.
 XX 17-OCT-2002.
 XX 26-MAR-2002; 2002WO-US009187.
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 DR Novel compound useful for treating cirrhosis, liver failure,
 XX hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 PT Example 1; Page 206; 387pp; English.
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
 CC disclosed in the present invention
 XX Sequence 17 BP; 3 A; 0 C; 11 G; 0 T; 3 U; 0 Other;
 SQ Query Match 9.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1738 CCCAACTCTCCCTATC 1754
 DB 17 CCCAACTCTCCCACTC 1
 RESULT 69
 ACD50854
 ID ACD50854 standard; RNA; 17 BP.
 XX AC ACD50854;
 XX 23-SEP-2003 (first entry)
 DT HBV hammerhead ribozyme substrate sequence #269.
 DE
 XX

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyze; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX Hepatitis B virus.
 OS WO200281494-A1.
 XX 17-OCT-2002.
 XX 26-MAR-2002; 2002WO-US009187.
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX (RIBO-) RIBOZYME PHARM INC.
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 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 DR Novel compound useful for treating cirrhosis, liver failure,
 XX hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 PT Example 1; Page 141; 387pp; English.
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 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
 CC disclosed in the present invention
 XX Sequence 17 BP; 2 A; 4 C; 4 G; 0 T; 7 U; 0 Other;
 SQ Query Match 9.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 58.8%; Pred. No. 1.5e+02;
 Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1672 TGGAACTCTGCTCTC 1688
 DB 1 UGGAACTCTGCTCTC 17

RESULT 70
 ACDS3478
 ID ACDS3478 standard; RNA; 17 BP.
 XX
 AC ACDS3478;
 XX
 DT 24-SEP-2003 (first entry)
 XX
 DE HBV G-cleaver substrate sequence #166.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-0087478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
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 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEB/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Example 1; Page 168; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberyne sequences
 CC disclosed in the present invention

XX
 SQ Sequence 17 BP; 2 A; 5 C; 3 G; 0 T; 7 U; 0 Other;
 Query Match 9.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 58.8%; Pred. No. 1.5e+02;
 Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1674 GAACCTGGTGTCTCTCT 1690
 DB 1 GAACCUUGUGUCUCU 17
 RESULT 71
 AAX28045
 ID AAX28045 standard; DNA; 18 BP.
 XX
 AC AAX28045;
 XX
 DT 10-JUN-1999 (first entry)
 XX
 DE PCR primer for human GDNF promoter sequence.
 XX
 KW GDNF promoter; human; glial cell line-derived neurotrophic factor;
 KW neurodegenerative disease; Parkinson's disease; renal disease; therapy;
 KW urogenital disease; gastrointestinal disease; physical nerve trauma;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9907843-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-EP004620.
 XX
 PR 05-AUG-1997; 97US-0054812P.
 PR 14-APR-1998; 98US-0081751P.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Baecker PA, Johnson RM, Lee WH, Verity AN;
 XX
 DR WPI; 1998-180491/15.
 XX
 PT New human glial cell line-derived neurotrophic factor promoters - useful
 PT in the treatment of neurodegenerative conditions including Parkinson's
 PT disease.
 XX
 PS Example 1; Page 34; 100pp; English.
 XX
 CC This sequence is a primer for a human glial cell line-derived
 CC neurotrophic factor (hGDNF) promoter. The promoters can be used to
 CC identify hGDNF modulators. hGDNF modulators are used to treat a mammal
 CC exhibiting neurodegenerative disease-like symptoms, particularly,
 CC Parkinson's disease, as well as renal, urogenital, and gastrointestinal
 CC diseases, and neurodegenerative sequelae of physical nerve trauma. The
 CC hGDNF modulator has anti-neurodegenerative activity and the promoters
 CC regulate GDNF expression. GDNF has a developmental role in survival of
 CC mid-brain dopaminergic neurons, cerebellar Purkinje neurons, and cranial
 CC and spinal cord motor neurons. In the peripheral nervous system, GDNF
 CC supports the development of multiple neuronal populations, including
 CC sympathetic, parasympathetic, sensory, and autonomic neurons. Delivery of
 CC a small molecule GDNF expression modulator is less pulsatile and less
 CC invasive than prior art treatment involving intraparenchymal, ICV, or
 CC intrathecal injection of GDNF
 XX
 SQ Sequence 18 BP; 6 A; 7 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 9.9%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAGC 1671
 Db 2 AGCACCAGGCTCACAGC 18

RESULT 72
 ADEL15603/c
 ID ADEL15603 standard; DNA; 19 BP.
 AC ADEL15603;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 XX Tricyclic dextrocannabinoids related primer, mouse SOCS-3 reverse.

KW non-psychoactive cannabinoid derivative; pro-inflammatory mediator;
 KW anti-inflammatory cytokine; anti-inflammatory; analgesic; antiallergic;
 KW vasotropic; antitubercular; tuberculostatic; antiarteriosclerotic;
 KW antirheumatic; antiarthritic; antiasthmatic; dermatological; cytostatic;
 KW neuroprotective; nootropic; antiparkinsonian; antibacterial;
 KW antiparasitic; virucide; immunosuppressive; nephrotropic; antidiabetic;
 KW hepatotropic; cardiant; anti-HIV; anticonvulsant; osteopathic;
 KW inflammatory; immune disorder; demyelinating;
 KW chronic degenerative disease; cardiovascular protection; primer;
 KW tricyclic dextrocannabinoid; ss; mouse; murine.

XX Mus sp.
 OS
 XX WO2003077832-A2.
 PN
 XX 25-SEP-2003.
 PD
 XX 16-MAR-2003; 2003WO-IL000223.
 PF
 XX 18-MAR-2002; 2002IL-00148736.
 PR
 XX (PHAR-) PHARMOS CORP.
 PA
 XX Garzon A, Avraham A, Fink G;
 PI
 XX WPI; 2003-779073/73.
 DR
 XX Use of non-psychoactive cannabinoid derivative for decreasing the
 PT transcription of at least one pro-inflammatory mediator cyclooxygenase-2
 PT or increasing the transcription of at least one antiinflammatory cytokine
 PT interleukin-10.

XX Example 1; Page 29; 81pp; English.

XX The invention relates to the novel use of a composition comprising non-
 CC psychoactive cannabinoid derivative, its salt, ester or solvate used for
 CC decreasing the transcription of at least one pro-inflammatory mediator or
 CC increasing the transcription of at least one anti-inflammatory cytokine.
 CC The novel composition has the following activities: antiinflammatory,
 CC analgesic, antiallergic, vasotropic, antitubercular, tuberculostatic,
 CC antiarteriosclerotic, antirheumatic, antiarthritic, antiasthmatic,
 CC dermatological, cytostatic, neuroprotective, nootropic, antiparkinsonian,
 CC antibacterial, antiparasitic, virucide, immunosuppressive, nephrotropic,
 CC antidiabetic, hepatotropic, cardiant, anti-HIV, anticonvulsant, and
 CC osteopathic. The novel non-psychoactive cannabinoid derivative
 CC composition can be used in the preparation of a medicament for
 CC preventing, alleviating or treating a disease or disorder by regulating
 CC pro and anti-inflammatory mediators. The diseases/disorders include:
 CC inflammatory and immune disorders, pain, allergic inflammation, diseases
 CC caused by monocyte infiltration (e.g. sarcoidosis, Wegener's
 CC granulomatosis and tuberculosis), atherosclerosis, rheumatoid arthritis,
 CC aschma, interstitial lung disorders, inflammatory pulmonary diseases,
 CC diseases, osseous inflammation, pancreatitis, inflammatory skin
 CC diseases involving immune-mediated or post-traumatic inflammation,
 CC inflammatory demyelinating neuropathies, multiple sclerosis,
 CC neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's
 CC disease, bacterial, parasitic or viral infections, sepsis, renal

CC disorders, diabetic nephropathy and liver disorders), postoperative
 CC complications in cardiovascular surgery, in transplants or organs or
 CC tissue replacements and in prosthetic implants and transplant rejection.
 CC The diseases/disorders can also be used for treating demyelinating
 CC disorders and chronic degenerative diseases (e.g. AIDS dementia,
 CC Huntington's chorea, amyotrophic lateral sclerosis, Kennedy's syndrome,
 CC motor neuron disease and prion-associated neurodegeneration) and are also
 CC useful in cardiovascular protection and treatment of atheroma,
 CC restenosis, angioplasty, myocardial ischaemia and myocardial infarction.
 CC This polynucleotide sequence represents a primer used in the method to
 CC test the impact of tricyclic dextrocannabinoids on gene expression
 CC relating to the invention.

XX SQ Sequence 19 BP; 5 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 9.9%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1683 TGCTCTCCCTCCAGCGGG 1699
 Db 19 TCTCTCTCCCAACGGG 3

RESULT 73
 AAV26436
 ID AAV26436 standard; DNA; 20 BP.
 XX
 AC AAV26436;
 XX
 DT 30-JUL-1998 (first entry)
 XX
 DE PCR primer "A gamma-globin" gene.
 XX
 KW Beta-globin; adeno-associated virus vector; therapeutic; liver;
 KW hepatic disease; ss; PCR; primer; amplification.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9809524-A1.
 PN
 XX 12-MAR-1998.
 PD
 XX 02-SEP-1997; 97WO-US015453.
 PF
 XX 06-SEP-1996; 96US-0025616P.
 PR 11-SEP-1996; 96US-0025649P.
 XX
 XX (CHIR) CHIRON CORP.
 PA (INDV) UNIV INDIANA.
 XX
 PI Srivastava A, Ponnazhagan S, Chloemer RH, Wang X, Yoder MC;
 PI Zhou S, Escobedo J, Dwarki V;
 XX WPI; 1998-193255/17.
 DR
 XX Novel adeno-associated viral vectors - for liver specific delivery of
 PT therapeutic molecule.
 PT
 XX Example 2; Page 20; 32pp; English.

XX The human beta-globin promoter- A gamma-globin gene-specific primers
 CC (AAV26435 and 26436) were used to amplify and detect the human A gamma-
 CC globin gene which had been injected into C57Bl/6 mice using a recombinant
 CC adeno-associated virus (AAV) vector. This confirmed the adeno-associated
 CC virus vector can be used to deliver a therapeutic molecule to the liver
 CC of a mammal. This can be used for the expression of therapeutic molecules
 CC such as secretory proteins, antisense molecules or ribozymes, in the
 CC liver, especially to treat hepatic diseases

XX SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
 SQ

```

XX Query Match          9.9%; Score 13.8; DB 1; Length 20;
KW Best Local Similarity 88.2%; Pred. No. 1.8e+02;
KW Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTGTCCTCCACGGT 1697
DB 2 GGTTTCTCCTCCAGCAT 18

RESULT 74
AAH78641
ID AAC65593 standard; DNA; 20 BP.
XX AC AAC65593;
XX DT 14-FEB-2001 (first entry)
XX DE Human uteroglobin SNP PCR primer HUG38R.
XX KW Mouse; uteroglobin; immunoglobulin A mediated disease; IGA nephropathy;
KW autoimmunity disorder; pulmonary inflammation; Wegener's granulomatosis;
KW Goodpasture's disease; diabetic glomerulosclerosis; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200062795-A2.
XX PD 26-OCT-2000.
XX PF 13-APR-2000; 2000WO-US009979.
XX PR 21-APR-1999; 99US-0130434P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Mukherjee AB, Zheng F, Zhang Z;
XX WPI; 2000-687100/67.
XX DR Use of a composition comprising uteroglobin (or a fragment, derivative,
XX mimetic or variant), for inhibiting or treating an immunoglobulin-A
XX mediated autoimmune disorders, e.g. diabetic glomerulosclerosis and
XX pulmonary inflammation.
XX PS Example 12; Page 43; 60pp; English.
XX CC The present invention describes the use of uteroglobin in the diagnosis
XX and prevention of IGA mediated diseases, such as IGA nephropathy,
XX Wegener's granulomatosis, Goodpasture's disease and diabetic
XX glomerulosclerosis. This is possible as uteroglobin binds to fibronectin,
XX preventing the complexing of fibronectin with IGA and the deposition of
XX immune complexes in the kidney
XX SQ Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match          9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1722 GAGATGGAGATTGGTCTC 1738
DB 20 GAGATGGAGTTTCGCTC 4

RESULT 75
AAH78641
ID AAH78641 standard; DNA; 20 BP.
XX AC AAH78641;
XX DT 10-DEC-2001 (first entry)
XX DE Probe for mechanically sensitive potassium channel gene fragment.

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XX Human; mechanically sensitive potassium channel; riluzole; TWICK;
KW polyunsaturated fatty acid; arachidonic acid; hTRAAC; chromosome 11q13;
KW neuronal excitation; muscle excitation; cardiac rhythm; anoxia;
KW hormone secretion; cardiac disease; vascular disease; ischemia;
KW nervous system disorder; endocrinal disease; muscle disease;
KW retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration; probe;
KW ss.
XX OS Homo sapiens.
XX PN WO200168670-A2.
XX PD 20-SEP-2001.
XX PF 14-MAR-2001; 2001WO-FR000758.
XX PR 14-MAR-2000; 2000FR-00003264.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX PI Lazdunski M, Lesage F, Maingret F;
XX WPI; 2001-590037/66.
XX DR New mechanically sensitive potassium channel, useful for treating
XX cardiovascular diseases and in drug screening, is activated by
XX polyunsaturated fatty acids.
XX PS Disclosure; Page 15; 37pp; French.
XX CC The present probe was used to detect a gene fragment of the human
XX mechanically sensitive potassium channel gene. The channel is activated
XX by polyunsaturated fatty acids (particularly arachidonic acid (AA)) and
XX by riluzole. The polypeptide is designated human TWICK-related AA-
XX activated potassium channel (hTRAAC). The hTRAAC gene is located on
XX chromosome 11q13. hTRAAC is involved in regulation of neuronal and muscle
XX excitation, cardiac rhythm and secretion of hormones. Cells that express
XX hTRAAC, designated to screen for modulators of hTRAAC activity. Such
XX modulators are potentially useful for prevention or treatment, in humans
XX and animals, of: cardiac and/or vascular disease; nervous system
XX disorders associated with ischemia and anoxia; endocrinal diseases; and
XX associated with anomalous hormone secretion or muscle diseases; and
XX retinal diseases. Typical examples are epilepsy, cardiac arrhythmia and
XX neurodegeneration
XX SQ Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Query Match          9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGCTGGA 1675
DB 1 CCAGGCTGCCAGCTGGA 17

RESULT 76
AAD19416/c
ID AAD19416 standard; DNA; 20 BP.
XX AC AAD19416;
XX DT 18-DEC-2001 (first entry)
XX DE Human delta-6-desaturase (h6D-1) amplifying PCR primer #1.
XX KW Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;
KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;
KW cardiovascular disease; Crohn's disease; congenital liver disease;
KW schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;

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KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;
 KW autoimmune disorder; hypercholesterolaemia; atopic disorder; hb6D-1;
 KW gene therapy; human; PCR primer; ss.
 XX Homo sapiens.
 XX WO200170993-A2.
 XX 27-SEP-2001.
 XX 26-MAR-2001; 2001WO-CA000398.
 XX 24-MAR-2000; 2000CA-02301158.
 XX (SCOT-) SCOTIA HOLDINGS PLC.
 XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;
 XX WPI; 2001-611507/70.
 XX Nucleic acid encoding delta-6-desaturase gene useful for treating atopic
 PT eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome, and
 PT gastrointestinal disorders, viral infections and post viral fatigue.
 XX Example 4; Page 69; 164pp; English.
 XX The invention relates to polynucleotides that control delta-6 desaturase
 CC genes (d6D) and methods useful for identifying compounds which inhibit or
 CC promote the activity of mammalian d6D. Compounds which modulate d6D gene
 CC segments are useful for treating lipid metabolism disorders e.g. atopic
 CC eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,
 CC gastrointestinal disorders, viral infections and post viral fatigue, pre-
 CC menstrual syndrome, endometriosis, cystic fibrosis, alcoholism, cancer,
 CC Alzheimer's syndrome, cardiovascular disease, Crohn's disease, congenital
 CC liver disease, schizophrenia, diabetes and diabetic
 CC complications including diabetic neuropathy, nephropathy and retinopathy.
 CC Compounds of the invention are also useful for inhibiting progressive and
 CC acute disorders such as arterial hypertension, atherosclerosis, chronic
 CC inflammatory and autoimmune disorders, hypercholesterolaemia and other
 CC atopic disorders. d6D genes are useful in gene therapy. The present
 CC sequence is a PCR primer used to amplify human delta-6-desaturase (hb6D-
 CC 1) sequence
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 9.9%; Score 13.8; DB 1; Length 20;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1685 TCTCTCCAGCGGTGGT 1701
 DB 19 TCTCTCCAGCGGTAGT 3
 RESULT 77
 AAD22845/C
 ID AAD22845 standard; DNA; 20 BP.
 XX
 AC AAD22845;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE CD34 cell marker DNA amplifying RT-PCR up primer.
 XX Cell marker; CD34; vulnervary; cosmetic; uropathic; cardiant; osteopathic;
 KW myocardial infarction; dermatological; gastroesophageal reflux; weakness;
 KW aesthetic; muscular; medicament; heart failure; gene therapy; myofiber;
 KW urinary incontinence; faecal incontinence; muscle tissue dysfunction;
 KW muscle-derived progenitor cell; MDC; vesico-ureteral reflux;
 KW RT-PCR primer; ss.
 XX Unidentified.
 OS
 XX

PN WO200178754-A2.
 XX 25-OCT-2001.
 XX 12-APR-2001; 2001WO-US012084.
 XX 14-APR-2000; 2000US-00349937.
 XX (UUPI-) UNIV PITTSBURGH.
 XX Chancellor MB, Huard J, Capelli CC, Qu Z;
 XX WPI; 2002-025967/03.
 XX Use of a composition comprising isolated muscle-derived progenitor cells
 PT expressing cell markers having at least desmin, and having long-term
 PT survivability in situ for augmenting muscle or non-muscle soft tissue.
 XX Example 9; Page 48; 92pp; English.
 XX The invention relates to the use of a composition comprising isolated
 CC muscle-derived progenitor cells (MDC) expressing cell markers of desmin,
 CC CD34, Bcl-2, Sca-1 and Flk-1, and having long-term survivability in situ.
 CC The invention is useful for the manufacture of a medicament for
 CC augmenting and bulking muscle or non-muscle soft tissue in a mammal,
 CC where MDC do not express CD45 and c-kit cell markers. The invention is
 CC also useful in the treatment of a defect or void in non-muscle soft
 CC tissue, weakness or dysfunction in muscle tissue in a mammal, an
 CC aesthetic defect or a cosmetic defect, restoring or improving
 CC contractility of smooth muscle tissue and producing new myofibers such
 CC that the cells comprising the composition migrate to the sites of the
 CC basal lamina of myofibers and develop into satellite cells to produce new
 CC myofibers in the mammal. The invention further provides treatments and
 CC amelioration for dermatological conditions, gastroesophageal reflux,
 CC vesico-ureteral reflux, urinary incontinence, faecal incontinence, heart
 CC failure and myocardial infarction. The invention also relates to a method
 CC for genetically modifying the cells for gene transfer therapy. The
 CC present DNA sequence is a RT (reverse transcriptase)-PCR primer which is
 CC used for amplifying CD34 cell marker DNA related to the invention. The
 CC CD34 marker DNA is used for the muscle-derived progenitor cells (MDC)
 CC treatment of bone defects
 XX
 SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
 Query Match 9.9%; Score 13.8; DB 1; Length 20;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1640 TTGTAGCAGAGGCAAG 1656
 DB 20 TGTAGCAGAGTCAAG 4
 RESULT 78
 ABX78257/C
 ID ABX78257 standard; DNA; 20 BP.
 XX
 AC ABX78257;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE Human bifunctional apoptosis regulator antisense oligo ISIS NO 143788.
 XX Human; bifunctional apoptosis regulator; antisense; phosphorothioate;
 KW cytosstatic; antiinflammatory; inhibitor; infection; inflammation; tumour;
 KW ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER

FT /note= "phosphorothioate backbone, nucleotides 1-5 and 16
FT -20 are 2'-methoxyethoxy (MOE) nucleotides, nucleotides 7
FT -14 are 2'-deoxy- nucleotides, all C nucleotides are 5-
FT methyl cytosines"
PN US6468796-B1.
XX
XX
PD 22-OCT-2002.
XX
XX 27-APR-2001; 2001US-00844525.
XX
XX 27-APR-2001; 2001US-00844525.
XX (ISIS-) ISIS PHARM INC.
XX
PI Watt AT;
XX
XX WPI; 2003-196749/19.
XX
XX New antisense compounds targeted to nucleic acids encoding human
PT bifunctional apoptosis regulator, for modulating expression of the
PT regulator and treating diseases associated with expression of the
PT regulator in humans.
XX
XX Example 15; Col 45-46; 42pp; English.
XX
XX This invention describes a novel compound, 17-50 nucleobases in length
CC which specifically hybridizes with a nucleic acid encoding human
CC bifunctional apoptosis regulator (BAR) and inhibits the expression of
CC human BAR. The products of the invention have cytostatic and
CC antiinflammatory activity and can be used to inhibit human BAR expression
CC during antisense therapy, useful for inhibiting the expression of human
CC BAR in cells or tissues and for treating diseases associated with
CC expression of BAR in an animal, particularly a human suspected of having
CC or being prone to a disease or condition associated with expression of
CC human BAR. In addition the antisense oligonucleotides are useful for
CC diagnostics, therapeutics and as research reagent, e.g. prophylactically
CC to prevent or delay infection, inflammation or tumor formation. The
CC oligonucleotides described in the invention have 2'-methoxyethyl (2'-MOE)
CC wings and a deoxy gap. This sequence represents a human BAR antisense
CC oligonucleotide described in the disclosure of the invention
XX
XX Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1662 GGCTCAGCTGGACCC 1678
DB 17 GGCTCAGCTGGATCC 1
RESULT 79
ABZ92121
ID ABZ92121 standard; DNA; 20 BP.
XX
XX ABZ92121;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PN

XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 7363; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
SQ
Query Match 9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1636 GGGCTTGTAGCAGAGG 1652
DB 4 GGGCTTGTAGCAGATGG 20
RESULT 80
ABX10328/C
ID ABX10328 standard; DNA; 20 BP.
XX
XX ABX10328;
AC
XX
XX 28-JAN-2003 (first entry)
DT
XX
XX Coryneform bacterium PCR primer #30.
DE
XX
XX Coryneform bacterium; signal peptide domain; food processing; medicine;
KW cosmetic; transglutaminase; human epithelial growth factor; primer; ss;
KW PCR.
XX
XX Synthetic.
OS
XX WO200281694-A1.
PN
XX 17-OCT-2002.
PD
XX

XX PD 15-MAY-2003.
XX CC
XX PF 04-NOV-2002; 2002WO-US035323.
XX CC
XX PR 08-NOV-2001; 2001US-00006911.
XX CC
XX PA (ISIS-) ISIS PHARM INC.
XX CC
XX PI Gaarde WA, Watt AT;
XX CC
XX DR WPI; 2003-449447/42.
XX CC
XX PT New compound, having a sequence targeted to a nucleic acid encoding human
XX PT collapsin response mediator protein 2, useful for preparing a composition
XX PT for treating neurodegenerative disease, e.g., Alzheimer's disease.
XX CC
XX PS Claim 3; SEQ ID NO 59; 102pp; English.
XX CC
XX CC The invention relates to a new compound having a sequence comprising 8-50
XX CC bp targeted to a nucleic acid encoding human collapsin response mediator
XX CC protein 2 which specifically hybridizes with the nucleic acid encoding
XX CC human collapsin response mediator protein 2 and inhibits its expression.
XX CC The compound is useful for preparing a composition for treating
XX CC neurodegenerative disease, e.g., Alzheimer's disease, Down syndrome or
XX CC schizophrenia. This sequence represents the human collapsin response
XX CC mediator protein 2 gene intron 1 sequence against which the antisense
XX CC oligonucleotides may be targeted.
XX CC
XX SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
XX CC
XX CC Query Match 9.9%; Score 13.8; DB 1; Length 20;
XX CC Best Local Similarity 88.2%; Pred. No. 1.8e+02;
XX CC Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX CC
XX QY 1649 AAGGCAAGCACCAGGCT 1665
XX CC |||||
XX DB 17 AAGGCAAGGAGGAGGCT 1
XX CC
XX CC RESULT 83
XX CC AAA94234/C
XX ID AAA94234 standard; DNA; 21 BP.
XX AC
XX AA AAA94234;
XX CC
XX DT 12-JAN-2001 (first entry)
XX CC
XX DE Human testosterone-repressed prostate message-2 antisense oligo #10.
XX CC
XX KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
XX KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX OS Homo sapiens.
XX CC
XX PN WO200049937-A2.
XX PD
XX PD 31-AUG-2000.
XX CC
XX PF 25-FEB-2000; 2000WO-US004875.
XX CC
XX PR 26-FEB-1999; 99US-0121726P.
XX CC
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX CC
XX PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX CC
XX DR WPI; 2000-533132/48.
XX CC
XX PT Treating prostatic tumors and renal cancers by antisense inhibition of
XX PT the testosterone-repressed prostate messenger-2 gene.
XX CC
XX PS Example 5; Page 38; 38pp; English.

XX CC The present sequence is an antisense oligonucleotide directed at the
XX CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
XX CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX CC promote the regression of tumours, and oligonucleotides directed at human
XX CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
XX CC gene. These include prostate cancer, renal cell cancer and some breast
XX CC cancer cells. In addition to this, they also increase the
XX CC chemosensitivity of the cells, meaning that conventional chemotherapy is
XX CC more effective
XX CC
XX SQ Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;
XX CC
XX CC Query Match 9.9%; Score 13.8; DB 1; Length 21;
XX CC Best Local Similarity 88.2%; Pred. No. 2e+02;
XX CC Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX CC
XX QY 1734 GGCTCCCAACTCTCTCC 1750
XX CC |||||
XX DB 20 GGCCCCCAACTCCGCC 4
XX CC
XX CC RESULT 84
XX CC AAD57821
XX ID AAD57821 standard; DNA; 21 BP.
XX AC
XX AA AAD57821;
XX CC
XX DT 20-NOV-2003 (first entry)
XX CC
XX DE Reverse PCR primer to amplify human TCRBV22 gene.
XX CC
XX KW Human; T-cell receptor V gene; TCG; autoimmune disease; Crohn's disease;
XX KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
XX KW psoriasis; diabetes; malignancy; leukaemia; inflammatory bowel disease;
XX KW lymphoma; T cell receptor beta chain variable region; TCRBV; PCR; primer;
XX KW ss.
XX CC
XX OS Homo sapiens.
XX CC
XX PN WO2003059155-A2.
XX CC
XX PD 24-JUL-2003.
XX CC
XX PF 08-JAN-2003; 2003WO-US000882.
XX CC
XX PR 09-JAN-2002; 2002HK-00100156.
XX CC
XX PA (MAXX-) MAXX GENETECH CO LTD.
XX CC
XX PI Zang Y, Cheng S;
XX CC
XX DR WPI; 2003-689456/65.
XX CC
XX PT Detection of over-expression of specific T-cell receptor genes for
XX PT detecting autoimmune diseases and malignancies, involves extracting RNAs,
XX PT preparing labeled cDNAs with array and identifying positions having
XX PT elevated signals.
XX CC
XX PS Claim 8; Page 6; 18pp; English.
XX CC
XX CC The invention relates to over-expression of certain T-cell receptor V
XX CC genes (TCG) in sample which is detected by extracting RNAs from the
XX CC sample using a TCG array containing substrate with numerous positions
XX CC having immobilised nucleic acids complementary to fragments of TCG
XX CC families, preparing labelled cDNAs with the array under conditions which
XX CC hybridise complementary sequences and identifying positions having
XX CC elevated signals compared with other position. The invention is used for
XX CC detecting autoimmune diseases such as multiple sclerosis, rheumatoid
XX CC arthritis, insulin-dependent diabetes mellitus, type I diabetes,
XX CC inflammatory bowel disease, psoriasis, systemic lupus erythematosus or
XX CC Crohn's disease, or T cell associated malignancies such as T cell
XX CC leukaemia or T cell lymphoma. The present sequence is a PCR primer used

CC in the amplification of human T cell receptor beta chain variable region
 CC (TCRBV) DNA
 SQ Sequence 21 BP; 2 A; 7 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 9.9%; Score 13.8; DB 1; Length 21;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1687 TCCTCCAGCGTGGGGA 1703
 Db 2 TCCTCCAGCTTGTGGA 18

RESULT 85
 ACF36406/c
 ID ACF36406 standard; DNA; 21 BP.

XX AC ACF36406;

XX 18-DEC-2003 (first entry)

XX TRPM-2 antisense oligonucleotide #12.

XX TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;
 XX prostate cancer; anti-apoptotic protein; antisense; ss.

XX Synthetic.

XX Homo sapiens.

XX WO2003072591-A1.

XX 04-SEP-2003.

XX 20-FEB-2003; 2003WO-US0005305.

XX 22-FEB-2002; 2002US-00080794.

XX (UVR-) UNIV BRITISH COLUMBIA.

XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;

XX WPI; 2003-689981/65.

XX New modified antisense oligonucleotide, useful particularly for treating
 XX prostatic cancer, inhibits the testosterone-repressed prostate message-2.

XX Example 5; Page 42; 44pp; English.

XX The invention relates to a compound consisting of an oligonucleotide with
 XX a phosphorothioate backbone throughout, in which: (a) sugars on
 XX nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
 XX remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
 XX positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
 XX ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
 XX prostatic cancer cells to the androgen-independent state, in vivo or in
 XX vitro; (b) to treat prostatic cancer (after initially withdrawing
 XX androgens to induce apoptosis); and (c) to increase sensitivity of cancer
 XX cells (prostatic, renal, non-small cell lung, urothelial transitional,
 XX ovarian and some breast cancer cells) that express abnormal levels of
 XX TRPM-2 to chemotherapy or radiation. The modifications present in (I)
 XX increase stability in vivo and activity (both in vivo or in vitro) and
 XX result in a synergistic increase in effect when (I) is used with
 XX chemotherapeutic agents or other antisense oligonucleotides directed
 XX against other antiapoptotic genes. Sequences ACF36399-406 represent
 XX antisense oligonucleotides targeted against human anti-apoptotic protein
 XX TRPM-2 (testosterone-repressed prostate message-2) gene

XX Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 9.9%; Score 13.8; DB 1; Length 21;
 Best Local Similarity 88.2%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 GGCTCCCACTCTCTCC 1750
 Db 20 GGCCCCCACTCCGCC 4

RESULT 86
 AAQ46059
 ID AAQ46059 standard; DNA; 20 BP.

XX AC AAQ46059;

XX 25-MAR-2003 (revised)

XX 08-FEB-1994 (first entry)

XX Sequence of PCR primer L04 for the amplification of hly virulence factor.

XX Virulence factor; Listeria detection; food poisoning; hly; PCR; primer;

XX ss.

XX Synthetic.

XX CH682156-A5.

XX 30-JUL-1993.

XX 28-JUN-1990; 90CH-00002190.

XX 28-JUN-1990; 90CH-00002190.

XX (CAND/) CANDRIAN U.

XX (FURR/) FURRER B.

XX (HOEF/) HOEFELIN C.

XX (LUET/) LUETHY J.

XX Candrian U, Furrer B, Hoefelein C, Luethy J;

XX WPI; 1993-265174/34.

XX Listeria monocytogenes detection by enzymatic nucleic acid amplification
 XX - using oligo-nucleotide(s) derived from alpha-haemolysin and/or beta-
 XX haemo-lysin virulence factors in polymerase chain reactions.

XX Claim 2; Page 2; 2pp; German.

XX Oligos L01, L02, L03 and L04 are used for the amplification of hly (alphy
 XX -haemolysin) virulence factor; and oligos AD07, AD08 and AD09 are used
 XX for the amplification of iap (beta-haemolysin) virulence factor. They are
 XX used in a detection method for Listeria monocytogenes in food samples
 XX which is faster and more sensitive than the classical bacteriological
 XX methods. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 9.8%; Score 13.6; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1688 CCTCCAGCGTGGGAGTT 1707
 Db 1 CCTCCAGAGTGATCGATGTT 20

RESULT 87

AA42248

ID AAT42248 standard; DNA; 20 BP.

XX AC AAT42248;

XX 20-FEB-1997 (first entry)

XX Primer derived from hlyA gene used in modified PCR method.

KW Detection; PCR; polymerase chain reaction; hybrid; antibody;
 KW immunochemical detection; ss.
 XX Synthetic.

XX CA2139070-A.

XX 24-JUN-1996.

XX 23-DEC-1994; 94CA-02139070.

XX 23-DEC-1994; 94CA-02139070.

XX (BLAI/) BLAIS B W.

XX Blais BW;

XX WPI; 1996-413110/42.

XX Detection of nucleic acid sequences - by polymerase chain reaction
 PT amplification, transcription using RNA polymerase and detection of
 PT RNA:DNA hybrids using antibodies.
 XX Example 1; Page 16; 31pp; English.

XX A new method for the detection of nucleic acids comprises (a) amplifying
 CC a DNA by PCR using primers to which an appropriate RNA polymerase
 CC promoter has been appended; (b) transcribing the amplified DNA into RNA
 CC using an RNA polymerase; (c) forming RNA:DNA hybrids; and (d)
 CC immunochimically detecting the RNA:DNA hybrids using antibodies directed
 CC to RNA:DNA hybrids. Two primers (AA742247, AA742248) were selected from
 CC the hlyA gene and spanned a 730 base pair region of the gene from
 CC nucleotides 602-1332. For further use in the invention, the primer
 CC described in AA742247 had an additional 26 nucleotides added to it
 CC corresponding to T7 RNA polymerase promoter sequence. The resulting
 CC primer is described in AA742249

XX SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 9.8%; Score 13.6; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1684 GTCTCCTCCAGCGTGGTGA 1703

Db 1 GTATCCTCCAGAGTCATCGA 20

RESULT 88

AA742249

ID AA742249 standard; DNA; 20 BP.

XX AA742249;

XX 25-MAR-2003 (revised)

DT 18-JUN-1997 (first entry)

XX Plasmidogen activator/urokinase gene repeat sequence primer #1.

XX Polymorphism; repeat sequence; genetic marker; primer; amplification;
 KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
 KW linkage analysis; genetic disease; animal; plant; breeding; locus;
 KW hybridisation; chromosome; ds.

XX Synthetic.

XX US5582979-A.

XX 10-DEC-1996.

XX 04-APR-1994; 94US-00222177.

XX 21-APR-1989; 89US-00341562.

PR 05-SEP-1991; 91US-00754351.

XX (MARS-) MARSHFIELD CLINIC.

XX Weber JL;

XX WPI; 1997-042299/04.

XX Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
 PT using novel nucleic acid mols. as primers.

XX Example 9; Col 59-60; 186pp; English.

XX The invention relates to the isolation of polymorphic repeat sequences
 CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
 CC markers. Primers based on these sequences can be used to detect these
 CC repeats, especially for use in e.g paternity or maternity testing, human
 CC genetic analysis such as linkage analysis of genetic disease, commercial
 CC animal or plant breeding or pedigree analysis. The sequences AAT66084-
 CC 166107 represent repeat sequences of low informativeness found in
 CC specific human genes. The primers AAT66085-6 were used to amplify a 111
 CC bp fragment of the plasminogen activator/urokinase gene which contains
 CC the repeat sequence of AAT66084. (Updated on 25-MAR-2003 to correct PF
 CC field.)

XX SQ Sequence 20 BP; 5 A; 1 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 9.8%; Score 13.6; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1713 AGGAGTACGAGATCGAGAT 1732

Db 1 AGGAGTTAGGAGCTGGAGGT 20

RESULT 89

AAV62008

ID AAV62008 standard; DNA; 20 BP.

XX AAV62008;

XX 25-MAR-2003 (revised)

DT 11-JAN-1999 (first entry)

XX L monocytogenes hlyA gene PCR primer B.

XX Detection; pathogen; amplification; RNA enhancement product; PCR primer;
 KW DNA/RNA hybrid; Listeria sp; Streptococcus sp; Lactobacillus sp;
 KW Lactococcus sp; Micrococcus sp; Enterococcus sp; Staphylococcus sp;
 KW Bacillus sp; Pseudomonas sp; Escherichia coli; Salmonella typhimurium;
 KW Yersinia enterocolitica; ss.

XX Synthetic.

XX Listeria monocytogenes.

XX US5827661-A.

XX 27-OCT-1998.

XX 23-SEP-1996; 96US-00718596.

XX 23-DEC-1994; 94CA-02137070.

XX 30-DEC-1994; 94US-00366619.

XX (KALY-) KALYX BIOSCIENCES INC.

XX Blais BW;

XX WPI; 1998-593985/50.

XX Enhanced detection by nucleic acid amplification, especially of Listeria
 PT - uses formation of DNA-RNA hybrids after amplification, and then


```
XX SQ Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 U; 0 Other;
Query Match          9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1709 GGTAGGAGTACGGAGTGG 1728
Db 20 GGTGGGAATGCTGTGATGG 1

RESULT 92
AAX78426
ID AAX78426 standard; cDNA; 20 BP.
XX
AC AAX78426;
XX
DT 26-AUG-1999 (first entry)
XX
DE Rat GAPDH primer 35.
XX
KW GAPDH; glyceraldehyde-phosphate dehydrogenase; cytokine; rat; PCR;
KW primer; ds.
XX
OS Synthetic.
OS Rattus sp.
XX
PN JPI1155600-A.
XX
PD 15-JUN-1999.
XX
PF 28-NOV-1997; 97JP-00328171.
XX
PR 28-NOV-1997; 97JP-00328171.
XX
PA (SHIS ) SHISEIDO CO LTD.
XX
WPI; 1999-398081/34.
XX
Measuring expression of cytokine gene in sample cell - by extracting RNA
and amplifying cDNA.
XX
Claim 9; Page 15; 21pp; Japanese.
XX
This invention describes a novel method for measuring the expression of a
specific cytokine gene in a sample cell group. AAX78387-X78392 and
CC AAX78398-X78427 represent primers used to amplify the rat glyceraldehyde-
CC 2-phosphate dehydrogenase (GAPDH) gene which is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
Query Match          9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1721 GGAGATGGAGATTGGCTCCC 1740
Db 1 GAAGATGGTGGTGGCTTCC 20

RESULT 93
AAX25929
ID AAX25929 standard; DNA; 20 BP.
XX
AC AAX25929;
XX
DT 08-JUN-1999 (first entry)
XX
DE GAPDH reverse primer corresponds to bases 252-271.
XX
KW Evaluation; allergy; PCR; amplification; primer; probe; hybridisation;

gene expression; cytokine; immune response; GAPDH; ss;
glyceraldehyde-3-phosphate dehydrogenase.
Synthetic.
JPI0304880-A.
17-NOV-1998.
09-OCT-1997; 97JP-00277580.
07-MAR-1997; 97JP-00053528.
(SHIS ) SHISEIDO CO LTD.
WPI; 1999-232451/20.
Determination of a nucleic acid and a reagent for it - useful for
evaluating allergic properties of a chemical substance.
Claim 5; Page 3; 20pp; Japanese.
The invention relates to a test method for evaluating the allergic
properties of a chemical substance by PCR amplifying and determining the
levels of expression of cytokine genes involved with allergic immune
responses. Primers and probe AAX25928-X25930 are used to determine
glyceraldehyde-3-phosphate dehydrogenase (GAPDH) expression. This primer
is targeted to nucleotides 252-271 of the GAPDH gene
XX
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
Query Match          9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1721 GGAGATGGAGATTGGCTCCC 1740
Db 1 GAAGATGGTGGTGGCTTCC 20

RESULT 94
AAX97388/c
ID AAX97388 standard; DNA; 20 BP.
XX
AC AAX97388;
XX
DT 13-SEP-1999 (first entry)
XX
DE Primer used to amplify Chlamydia pneumoniae polynucleotides.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
WPI; 1999-357842/30.
03-JUN-1999.
20-NOV-1998; 98WO-IB001890.
21-NOV-1997; 97FR-00014673.
04-NOV-1998; 98US-0107078P.
(GEST ) GENSET.
XX
PI Griffais R;
XX
WPI; 1999-357842/30.
Genome sequence of Chlamydia pneumoniae.
PT
```

```

XX
PS Page 1900; Disclosure; 1912pp; English.
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match          9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1720 CGGAGATGGAGATTGGCTCC 1739
Db      ||||| ||||| ||||| |||||
      20 CGGATAGGGAGACTGGCTGC 1

RESULT 95
AAX97331/C
ID AAX97331 standard; DNA; 20 BP.
XX
AC AAX97331;
XX
DT 13-SEP-1999 (first entry)
DE
DE Primer used to amplify Chlamydia pneumoniae polynucleotides.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydothila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1999; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae.
XX
PS Page 1896; Disclosure; 1912pp; English.
CC
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match          9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1720 CGGAGATGGAGATTGGCTCC 1739
Db      ||||| ||||| ||||| |||||
      20 CGGATAGGGAGACTGGCTGC 1

RESULT 95
AAX97331/C
ID AAX97331 standard; DNA; 20 BP.
XX
AC AAX97331;
XX
DT 13-SEP-1999 (first entry)
DE
DE Human genome; biallelic marker; high density disequilibrium map;
DE genomic map; haplotype; phenotype; polymorphic base; genotyping;
DE haplotyping; hybridisation; identification; characterisation;
DE amplification; single nucleotide polymorphism; SNP; PCR primer;
DE diagnosis; ss.
XX
XX Homo sapiens.
XX
OS
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
PS Claim 9; Page 2448; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention
XX have a variety of uses: they can be used for high density mapping of the
XX human genome, and in complex association studies and haplotyping studies
XX which are useful in determining the genetic basis for disease states.
XX Compositions and methods of the invention can also be useful for the
XX identification of the targets for the development of pharmaceutical
XX agents and diagnostic methods, as well as the characterisation of the
XX differential efficacious responses to and side effects from
XX pharmaceutical agents acting on a disease as well as other treatment.
XX N.B. The SEQ ID Nos 2852, 2913, 2974, 3036, 3096, 3157, 3227, 3297 and
XX 3367, are not actually given a sequence in the Sequence Listing from the
XX present invention
XX
SQ Sequence 20 BP; 6 A; 0 C; 11 G; 3 T; 0 U; 0 Other;

Query Match          5.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1746 CTCCTATCTCTAAAGGCCCA 1765

```

```
Db          1737 TCCCAACTCTCCCTATCCT 1756
            |||||
            20 TCCCAACTCTCCCTATCCT 1
            |||||

RESULT 97
AAH38150/C
ID AAH38150 standard; DNA; 20 BP.
XX AC AAH38150;
XX DT 14-AUG-2001 (first entry)
XX DE SNP specific lower PCR primer SEQ ID 946.
XX KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
XX KW Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX OS Homo sapiens.
XX FH modified_base 1..20
XX PN WO200129262-A2.
XX DT 26-APR-2001.
XX PF 13-OCT-2000; 2000WO-US028436.
XX PP 15-OCT-1999; 99US-0160096P.
XX PR (ORCH-) ORCHID BIOSCIENCES INC.
XX PA Picoult-Newburg L, Pohl M;
XX PI WPI; 2001-290930/30.
XX DR New genotyping oligonucleotide, useful for detecting the presence,
XX PT absence or identity of single polynucleotide polymorphism in a nucleic
XX PT acid sample.
XX PS Claim 1; Page 54; 83pp; English.
XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX CC primer extension (SNPE) primers, and the sequences of regions flanking
XX CC sites of single nucleotide polymorphisms SNPs. The present invention
XX CC includes kits for determining the presence or absence of a SNP, using the
XX CC oligonucleotides of the invention. The PCR primers are used to amplify a
XX CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX CC The oligonucleotides are useful for genotyping a nucleic acid sample by
XX CC performing a single-nucleotide primer extension reaction. The
XX CC oligonucleotides are useful for determining the presence, absence or
XX CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX CC assess by association analysis the genotype of an individual or group of
XX CC individuals, having a pathological phenotypic trait suspected of being
XX CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX CC agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
XX CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX CC traits also include symptoms of or susceptibility to multifactorial
XX CC disease of which a component is or may be genetic such as autoimmune
XX CC diseases, including, rheumatoid arthritis, multiple sclerosis,
XX CC inflammation, cancer, nervous system diseases and infection by pathogenic
XX CC microorganism. The method is also useful in forensic investigations and
XX CC paternity analysis. The present sequence represents a PCR primer specific
XX CC for a human SNP containing DNA sequence
XX SQ Sequence 20 BP; 7 A; 1 C; 10 G; 2 T; 0 U; 0 Other;
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db          1737 TCCCAACTCTCCCTATCCT 1756
            |||||
            20 TCCCAACTCTCCCTATCCT 1
            |||||

RESULT 98
AAH20719
ID AAH20719 standard; DNA; 20 BP.
XX AC AAH20719;
XX DT 13-AUG-2001 (first entry)
XX DE Human telomeric repeat binding factor 2 oligonucleotide 111447.
XX KW Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
XX KW inhibitor; premature aging; hyperproliferative disorder; cancer;
XX KW cytostatic; ss.
XX OS Homo sapiens.
XX FH modified_base 1..20
XX PN WO200143752-A1.
XX DT 21-JUN-2001.
XX PF 14-DEC-2000; 2000WO-US033954.
XX PP 17-DEC-1999; 99US-00467642.
XX PR (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Cowsert LM;
XX DR WPI; 2001-398071/42.
XX PT Antisense compounds targeted to nucleic acid encoding telomeric repeat
XX PT binding factor 2 useful for treating conditions such as premature aging
XX PT and diseases such as cancer.
XX PS Example 15; Page 81; 108pp; English.
XX CC This invention describes a novel antisense compound (I) 8-30 nucleobases
XX CC in length targeted to a polynucleotide encoding human telomeric repeat
XX CC binding factor 2 (II) which specifically hybridizes with, and inhibits
XX CC the expression of (II). (I) is useful for treating a human having a
XX CC disease or condition associated with (II) such as premature aging or a
XX CC hyperproliferative disorder especially cancer, by inhibiting the
XX CC expression of (II) in human cells or tissues. (I) is useful for
XX CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX CC The products of the invention have cytostatic activity. This sequence
XX CC represents an antisense oligonucleotide used to illustrate the method of
XX CC the invention
XX SQ Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1640 TTGTAGCAGAGGCAAGCAC 1659
Db      1 TTGCATCAGAGGCCAGAC 20

RESULT 99
AAH80623/c
ID      AAH80623 standard; cDNA; 20 BP.
XX
AC      AAH80623;
XX
DT      11-SEP-2003 (revised)
DT      19-SEP-2001 (first entry)
XX
XX      Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 597.
XX
XX      Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
XX      disease diagnosis; ss.
XX
XX      Human immunodeficiency virus 1.
XX
XX      US6251588-B1.
XX
XX      26-JUN-2001.
XX
XX      10-FEB-1998; 98US-00021701.
XX
XX      10-FEB-1998; 98US-00021701.
XX
XX      (AGIL-) AGILENT TECHNOLOGIES INC.
XX
XX      Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX      WPI; 2001-424456/45.
XX
XX      Predicting the potential of an oligonucleotide to hybridize to a target
XX      nucleotide sequence, useful for evaluating oligonucleotide probe
XX      sequences, by identifying a oligonucleotides based on the evaluation of
XX      parameters.
XX
XX      Example 2; Col 67; 342pp; English.
XX
XX      The present invention describes a method for predicting the potential of
XX      an oligonucleotide to hybridize to a (complementary) target nucleotide
XX      sequence, involving identifying a subset of oligonucleotides within the
XX      predetermined number of unique oligonucleotides based on the evaluation
XX      of the parameter. Oligonucleotides in the subset are identified that are
XX      clustered along a region of the nucleotide sequence that is hybridisable
XX      to the target nucleotide sequences. This is useful for evaluating
XX      oligonucleotide probe sequences. The present sequence is an
XX      oligonucleotide described in the exemplification of the invention.
XX      (Updated on 11-SEP-2003 to standardise OS field)
XX
XX      Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

Query Match      9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1701 GGAAAGTTGGTTAGGAGTAC 1720
Db      20 GGAAAGTTCAATTAGGAATAC 1

RESULT 100
ABN83384
ID      ABN83384 standard; DNA; 20 BP.
XX
XX      ABN83384;
XX
DT      15-AUG-2002 (first entry)
XX
XX      Glyceraldehyde-3-phosphate dehydrogenase, GAPDH, PCR primer #1.
```

```
XX      GAPDH; glyceraldehyde-3-phosphate dehydrogenase; PCR; primer; ss.
XX
XX      Unidentified.
XX
XX      WO200243855-A1.
XX
XX      06-JUN-2002.
XX
XX      29-NOV-2001; 2001WO-FR003780.
XX
XX      29-NOV-2000; 2000PR-00015398.
XX
XX      (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX
XX      Ugolin N, Marguerie De Rotrou G, Kortulewski T, Alibert O;
XX      Le Roux D;
XX
XX      WPI; 2002-471810/50.
XX
XX      Array of biological or chemical probes, useful e.g. for diagnosis and
XX      drug screening, fixed to a support magnetically, through a fixing vector.
XX
XX      Example 6; Page 29; 52pp; French.
XX
XX      The present invention relates to an organised array of biological or
XX      chemical probes fixed to a support by magnetic coupling, by means of a
XX      fixing vector. The arrays are useful for diagnosis and for high-
XX      throughput screening of libraries of molecules or biological samples,
XX      e.g. to identify therapeutic or diagnostic agents, also for
XX      pharmacogenomic and toxicological analysis, and for studying the
XX      structure and expression of genomes, or generally any molecular
XX      interaction. The present sequence is a PCR primer for glyceraldehyde-3-
XX      phosphate dehydrogenase (GAPDH) gene, which was used to illustrate the
XX      invention
XX
XX      Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match      5.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1679 CTCGTCTCTCCCTCCAGCGTG 1698
Db      1 CTCGTCTCTCCACCAAG 20

RESULT 101
ABZ93876/c
ID      ABZ93876 standard; DNA; 20 BP.
XX
XX      ABZ93876;
XX
XX      17-OCT-2003 (first entry)
XX
XX      Human oligonucleotide sequence.
XX
XX      Human; antisense; lung dysfunction; nasal airway dysfunction;
XX      antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
XX      antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX      antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX      adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX      lung inflammation; respiratory disease; ds.
XX
XX      Homo sapiens.
XX
XX      WO200285308-A2.
XX
XX      31-OCT-2002.
XX
XX      23-APR-2002; 2002WO-US013135.
XX
XX      24-APR-2001; 2001US-0286137P.
```


XX Measurement of the nucleic acid of uncoupling protein-1, -2 or -3, useful
PT for evaluating a reducing drug.
XX
PS Disclosure; Page 2; 21pp; Japanese.
XX
CC The invention describes measurement of an mRNA or a cDNA of uncoupling
CC protein-1, -2 or -3 by carrying out a PCR by a DNA polymerase having 5'-
CC 3' exonuclease activity by using a forward primer, a reverse primer and a
CC probe having a reporter and a quencher and hybridising with a template
CC nucleic acid in the region placed between the above both primers. The
CC method is useful as a test method for evaluating a reducing drug. This
CC sequence represents a PCR primer for amplification of the partial
CC nucleotide sequence of cDNA encoding rat glyceraldehyde-3-phosphate
CC dehydrogenase
XX
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 16; Conservative 0; Indels 4; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGGCTCC 1740
DB 1 GAAGATGGTATGGCTCC 20

RESULT 104
ADD81514/c
ID ADD81514 standard; DNA; 20 BP.
XX
AC ADD81514;
XX
DT 29-JAN-2004 (first entry)
XX
DE HIV PRT antisense derived probe #443.
XX
KW ss; oligonucleotide hybridisation potential; efficient hybridisation;
KW large array; minimum oligonucleotide synthesis; probe.
XX
OS Human immunodeficiency virus.
XX
PN US2003054346-A1.
XX
PD 20-MAR-2003.
XX
PF 15-FEB-2001; 2001US-00784674.
XX
PR 10-FEB-1998; 98US-00021701.
XX
PA (SHAN/) SHANNON K W.
PA (WOLB/) WOLBER P K.
PA (DELE/) DELENSTARR G C.
PA (WEBB/) WEBB P G.
PA (KINC/) KINCAID R H.
XX
PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX
DR WPI; 2003-743746/70.
XX
XX Predicting potential of oligonucleotides to hybridize to target
XX nucleotide sequence comprises determining and evaluating for each
PT oligonucleotide a parameter predictive of the oligonucleotides ability to
PT hybridize with target.
XX
XX Example 2; SEQ ID NO 587; 423pp; English.
XX
CC The invention relates to a method of predicting the potential of
CC oligonucleotides to hybridise to target nucleotide sequences. The method
CC is useful for predicting the potential of an oligonucleotide to hybridise
CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
CC contains chemically modified nucleotides. The method is also useful for
CC predicting the potential of the oligonucleotides to hybridise to a

CC complementary target nucleotide sequence. The method is useful to predict
CC efficient hybridisation oligonucleotides for each of multiple target
CC sequences therefore very large arrays may be constructed and tested with
CC minimum synthesis of oligonucleotides. The present sequence represents a
CC HIV PRT antisense derived probe.
XX
SQ Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 16; Conservative 0; Indels 4; Indels 0; Gaps 0;

QY 1701 GGAAGTTGGTTAGGAGTAC 1720
DB 20 GGAAGTTCAATTAGGATAC 1

RESULT 105
ACD53920/c
ID ACD53920 standard; RNA; 17 BP.
XX
AC ACD53920;
XX
DT 24-SEP-2003 (first entry)
XX
DE HBV zinzyme substrate sequence #90.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis B virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER X.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Example 1; Page 175; 337pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
CC disclosed in the present invention

XX
SQ Sequence 17 BP; 3 A; 0 C; 11 G; 0 T; 3 U; 0 Other;
Query Match 9.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 CTCCTCACTCTCTCC 1750
DB 16 CCCCACTCTCTCC 2

RESULT 106
ACC64154
ID ACC64154 standard; DNA; 17 BP.
XX
AC ACC64154;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1401.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PS (MOLE-) MOLECULAR ENGINES LAB.
XX
PA Telleran A, Amson R, Tuijnder M;
XX
PI WPI; 2003-333167/31.
XX
DR New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.

PS Disclosure; Page 194; 738pp; French.
XX
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68906), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that

CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia

XX
SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 9.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCTCTCC 1749
DB 1 GATCCCACTCTCTCC 15

RESULT 107
AAQ50940
ID AAQ50940 standard; DNA; 18 BP.
XX
AC AAQ50940;
XX
DT 25-MAR-2003 (revised)
DT 19-MAY-1994 (first entry)
XX
DE T-cell antigen receptor J-beta2.7 probe.
XX
KW RT-PCR; polymerase chain reaction; amplification; SSCP; J-domain;
KW single-strand conformation polymorphism; joining domain; subtype beta 2;
KW ss.
XX
OS Synthetic.
XX
PN WO9322455-A1.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-JP000577.
XX
PR 30-APR-1992; 92JP-00111467.
XX 31-JUL-1992; 92JP-00205054.
XX (TAIS) TAISHO PHARM CO LTD.
XX (LTTL-) LTT INST CO LTD.
XX
PI Yamamoto K, Mizushima Y, Nishioka K, Sakoda H, Ikeda Y;
XX WPI; 1993-368813/46.
XX
PT Detection of expression of T-cell antigen receptor gene - in cancer,
PT viral or immune disease patients, by polymerase chain reaction
PT amplification of the gene and SSCP analysis.
XX
PS Example 1; Page 24; 47pp; Japanese.
XX
CC Primers corresp. to DNA coding for part of the beta-chain of the T cell
CC antigen receptor (pref. the Variable region primers AAQ50905- AAQ50926)
CC are used in PCR to amplify the T cell antigen receptor gene. The
CC amplified gene is detected by the single-strand conformation polymorphism
CC method using hybridisation probes corresp. to the beta-chain J domain
CC (see AAQ50928-Q50940). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 3 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 9.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1656 GCACAGGCTCAG 1670
DB 3 GCACAGGCTCAGG 17

RESULT 108
ABL88809

```
ID ABL88809 standard; DNA; 18 BP.
XX
AC ABL88809;
XX
DT 22-MAY-2002 (first entry)
XX
DE HIV-1 related binding molecule oligonucleotide sequence SEQ ID NO:31.
XX
DE Binding molecule; HIV-1; human immunodeficiency virus type 1;
XX reverse transcriptase; binding group; ss.
XX
OS Human immunodeficiency virus 1.
XX Synthetic.
XX
PN EP1174518-A1.
XX
XX 23-JAN-2002.
XX
PF 20-JUL-2000; 2000EP-00202611.
XX
PR 20-JUL-2000; 2000EP-00202611.
XX
XX (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX
XX Loukachov VV, Van Gemen B, Goudsmit J;
XX
XX WPI; 2002-156696/21.
XX
XX Collection of binding groups for determining or typing samples,
XX especially clinical samples, has groups capable to identify essentially
XX all members of the family of nucleic acids of relatively high
XX significance.
XX
XX Disclosure; Page 14; 166pp; English.
XX
XX The present invention describes a collection of binding groups for a
XX family of nucleic acids comprising members of relative high and relative
XX low significance, where the binding groups are selected to be capable to
XX identify, alone or in combination, essentially all members of the family
XX of nucleic acids of relatively high significance. The collection of
XX binding groups is useful for typing of nucleic acid in a clinical sample,
XX by contacting the nucleic acid with the collection and determining
XX whether one or more binding groups bound to the nucleic acid of the
XX sample. This method is useful for determining whether the sample
XX comprises at least a part of a member of relatively high significance of
XX a family of nucleic acids. The collection of binding groups is useful for
XX diagnosing the severity of a disease caused by a pathogen containing a
XX member of a family of nucleic acids. ABL88779 to ABL89321 represent
XX oligonucleotide sequences used in the exemplification of the present
XX invention
XX
XX Sequence 18 BP; 7 A; 1 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 9.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1717 GTACGAGATGGAGA 1731
DB 1 GTACAGAGATGGAGA 15
|||||
1 GTACGAGATGGAGTCTC 15

RESULT 109
AC83346
ID ACC83346 standard; DNA; 18 BP.
XX
XX ACC83346;
XX
XX 29-SEP-2003 (first entry)
XX
DT T7 forward PCR primer SEQ ID #8.
XX
DE G protein-coupled receptor; GPCR; receptor; GAVE10; antirheumatic;
XX
```

```

KW antiarthritic; antiasthmatic; antiinflammatory; antiallergic;
KW rheumatoid arthritis; asthma; Crohn's disease; inflammation; allergy;
KW edema; gene therapy; PCR; primer; ss.
XX
OS Bacteriophage t7.
XX
PN WO2003029413-A2.
XX
PD 10-APR-2003.
XX
PF 30-SEP-2002; 2002WO-US031045.
XX
PR 01-OCT-2001; 2001US-0325591P.
XX
XX (AVET ) AVENTIS PHARM INC.
XX
XX Fisingdrelo H, Ardati A, Cai J;
XX
XX WPI; 2003-381619/36.
XX
XX New GAVE10 nucleic acid and polypeptide, useful for diagnosing, screening
XX and treating disorders with aberrant signaling activity of the GAVE10
XX polypeptide, such as rheumatoid arthritis, asthma, Crohn's disease,
XX allergy and edema.
XX
XX Example 2; Page 82; 102pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a GAVE10
XX polypeptide. GAVE10 is part of the family of G protein-coupled receptors.
XX The methods and compositions of the present invention are useful for
XX diagnosing, screening, preventing and treating disorders associated with
XX the signalling activity of the GAVE10 polypeptide. These include
XX rheumatoid arthritis, asthma, Crohn's disease, inflammation, allergy and
XX edema. They can also be used in chromosomal mapping, tissue typing,
XX forensic biology, prognostic assays, monitoring clinical trials,
XX pharmacogenomics, and also in gene therapy. The current sequence
XX represents a T7 forward primer used in an example from the invention in
XX the cloning of hGAVE10 cDNA
XX
XX Sequence 18 BP; 2 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
XX
Query Match 5.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 GGCTCCCAACTCTC 1748
DB 1 GGCTCCCAACTCTC 15
|||||
1 GGCTCCCAACTCTC 15

RESULT 110
ACF05396
ID ACF05396 standard; DNA; 18 BP.
XX
XX ACF05396;
XX
XX 06-NOV-2003 (first entry)
XX
DT Bacteriophage T7 forward primer.
XX
DE Human; GAVE7; G-protein coupled receptor; receptor; signal transduction;
XX antiinflammatory; gene therapy; PCR; primer; ss.
XX
XX Bacteriophage t7.
XX
XX WO2003054156-A2.
XX
XX 03-JUL-2003.
XX
XX 18-DEC-2002; 2002WO-US040354.
XX
XX 20-DEC-2001; 2001US-0341271P.
XX
```

PA (AVET) AVENTIS PHARM INC.
 PA (CALJ) CAI J.
 XX Eishingdrelo H, Ardatti A;
 XX WPI; 2003-559136/52.
 DR Nucleic acid molecule encoding a GAVE7 polypeptide, useful for
 XX diagnosing, preventing or treating disorders characterized by
 PT insufficient or excessive production of GAVE7 protein, e.g. inflammation
 PT associated with asthma.
 XX Example 1; Page 82; 52pp; English.
 PS
 XX The present sequence is that of a bacteriophage T7 forward primer, which
 CC was used to sequence PCR products comprising cDNA (see ACC84400) encoding
 CC GAVE7 (see ABR62587), a novel human G-protein coupled receptor, was
 CC isolated. The invention provides GAVE7 nucleic acids, expression vectors,
 CC host cells, polypeptides and methods for their production, and antibodies
 CC that bind specifically to GAVE7. Also claimed are methods for identifying
 CC an agonist, inverse agonist or antagonist of GAVE7, and a therapeutic
 CC method for modulating GAVE7 signalling activity or signal transduction
 CC using an agonist, antagonist or an inverse agonist of GAVE7
 XX
 XX Sequence 18 BP; 2 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 9.6%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. NO. 1.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1734 GGTCCCAACTCTCC 1748
 DB 1 GGTCCCAACTCTC 15
 RESULT 111
 AAA82923/C
 ID AAA82923 standard; DNA; 19 BP.
 XX
 AC AAA82923;
 XX
 XX 04-DEC-2000 (first entry)
 DT
 DE cdk4 ribozyme binding site #104.
 XX
 XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 XX Mammalia.
 OS
 XX WO2000032765-A2.
 PN
 PD 08-JUN-2000.
 XX
 XX 06-DEC-1999; 99WO-US028772.
 PF
 XX 04-DEC-1998; 98US-0110954P.
 PR
 XX (IMMU-) IMMUSOL INC.
 PA
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;
 PI WPI; 2000-412314/35.
 XX
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 PT
 XX Disclosure; Page 53; 109pp; English.
 PS
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in

CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX
 XX Sequence 19 BP; 5 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 9.6%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. NO. 2.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1735 GCTCCCAACTCTCC 1749
 DB 16 GCTCCCGACTCTCC 2
 RESULT 112
 AAA51763
 ID AAA51763 standard; DNA; 19 BP.
 XX
 AC AAA51763;
 XX
 XX 31-OCT-2000 (first entry)
 DT
 DE Primer to amplify CYP3A5 gene in real time PCR.
 XX
 XX CYP3A5; Cytochrome P450; transcription regulatory region; polymorphism;
 KW Activator protein-3 motif; AP-3; basic transcription element;
 KW drug metabolism; phenotype; primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO2000039332-A1.
 PN
 PD 06-JUL-2000.
 XX
 XX 22-DEC-1999; 99WO-GB004380.
 PF
 XX 23-DEC-1998; 98GB-00028619.
 PR
 XX (JANC) JANSSEN PHARM NV.
 PA
 XX Paulussen ADC, Armstrong M;
 PI WPI; 2000-452418/39.
 XX
 XX Identifying subjects with a high drug metabolizing phenotype associated
 PT with cytochrome CYP3A5 expression for establishing whether a drug will be
 PT metabolized by the subject.
 XX
 XX Disclosure; Page 21; 68pp; English.
 PS
 XX Primers AAA51762-63 were used to amplify cytochrome P450 CYP3A5 gene in a
 CC real time PCR assay to ensure specificity. Cytochrome P450 subfamily
 CC CYP3A5 transcription regulatory regions can be screened for the
 CC presence/absence of a polymorphic variant, preferably at positions -475
 CC or -147 of the DNA of the 5' flanking region adjacent to the CYP3A5
 CC coding sequence. The variants are present in an activator protein-3 (AP-
 CC 3) motif and/or a basic transcription element (BRE). The polymorphisms
 CC cause increased CYP3A5 gene expression and this has been linked to drug
 CC metabolic activity. Screening for the presence of variants can be used to
 CC identify subjects with a high or low drug metabolizing phenotype
 CC associated with cytochrome CYP3A5 expression. Primers are used which in
 CC addition to hybridizing to the site of interest, are capable of
 CC introducing a restriction site which is absent in either the wild type
 CC sequence or polymorphic variants. Restriction enzyme cleavage analysis
 CC can then be used to indicate the presence or absence of the variant. The
 CC methods are used to establish, before treatment with a drug, whether the
 CC drug will be effectively metabolized by the patient, to identify
 CC compounds and transcription factors that can bind to a DNA sequence
 CC encoding CYP3A5, diagnosing susceptibility to a disease which is caused
 CC by toxins or procarcinogens metabolized by CYP3A5 and for identifying
 CC mutagenic effects of a compound

XX Sequence 19 BP; 6 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
 SQ Query Match 9.6%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 2.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACA 1669
 |||||
 Db 5 AGCACCAGGCTGACA 19

RESULT 113
 AAHS8085/c
 ID AAHS8085 standard; DNA; 19 BP.
 AC AAHS8085;
 DT 10-SEP-2001 (first entry)
 XX Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:509.

DE Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulneryary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytotstatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisklicking; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200130362-A2.
 PN 03-MAY-2001.
 PD 26-OCT-2000; 2000WO-US029500.
 XX 26-OCT-1999; 99US-0161532P.
 PR (IMMU-) IMMUSOL INC.
 PA Robbins JM, Tritz R;
 PI WPI; 2001-300427/31.
 DR Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX Example 1; Page 109; 408pp; English.

XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisklicking,
 CC ophthalmological, vulneryary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn

CC scar. AAHS7577 to AAHS2099 represent sequences used in the
 CC exemplification of the present invention
 XX Sequence 19 BP; 5 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
 SQ Query Match 9.6%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 2.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 GTCCTCAACTCTCTCC 1749
 |||||
 Db 16 GTCCTCGACTCTCTCC 2

RESULT 114
 ABL43426/c
 ID ABL43426 standard; DNA; 19 BP.
 AC ABL43426;
 XX 11-APR-2002 (first entry)
 DT Human chromosome lp36-35 PCR primer SEQ ID NO:470.
 XX Human; chromosome lp36-35; chromosome 21q22.1; genetic analysis; genome;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS JP2001321190-A.
 PN 20-NOV-2001.
 PD 12-MAR-2001; 2001JP-00068285.
 XX 10-MAR-2000; 2000JP-00066716.
 PR (RIKA) RIKAGAKU KENKYUSHO.
 PA (GENO-) GENOTEX YG.
 XX WPI; 2002-144136/19.
 DR Arraying genome clones.
 XX Claim 4; Page 14; 528pp; Japanese.

XX The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each wells of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome lp36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 CC specifically claimed for use in the present invention
 XX Sequence 19 BP; 1 A; 6 C; 3 G; 9 T; 0 U; 0 Other;
 SQ Query Match 9.6%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 2.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCAAGCA 1658
 Db 18 AGCAGAGGCAAGCA 4

RESULT 115
 ABL43434/C
 ID ABL43434 standard; DNA; 19 BP.
 XX AC ABL43434;
 XX AC ABL43434;
 XX XX
 DT 11-APR-2002 (first entry)
 DE Human chromosome 1p36-35 PCR primer SEQ ID NO:478.
 XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS
 XX JP2001321190-A.
 XX 20-NOV-2001.
 XX 12-MAR-2001; 2001JP-00068285.
 XX 10-MAR-2000; 2000JP-00066716.
 XX (RIKA) RIKAGAKU KENKYUSHO.
 XX (GENO-) GENOTEX YG.
 XX WPI; 2002-144136/19.
 XX Arraying genome clones.
 PT Claim 4; Page 14; 528pp; Japanese.
 PS The present invention describes a method of arraying genome clones. The
 XX method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each wells of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 XX specifically claimed for use in the present invention
 XX Sequence 19 BP; 1 A; 6 C; 3 G; 9 T; 0 U; 0 Other;
 QY Query Match 9.6%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 2.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1644 AGCAGAGGCAAGCA 1658
 18 AGCAGAGGCAAGCA 4

RESULT 116
 AAF60107/C
 ID AAF60107 standard; DNA; 20 BP.
 XX AAF60107;
 XX 27-APR-2001 (first entry)
 DE Human ATM gene exon 1a reverse primer.
 XX Human; ATM; ataxia telangiectasia; mutation detection;
 KW single-stranded conformation polymorphism; SSCP; electrophoresis;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS
 XX WO200107660-A1.
 XX 01-FEB-2001.
 XX 21-JUL-2000; 2000WO-US020011.
 XX 23-JUL-1999; 99US-00360416.
 XX (REGC) UNIV CALIFORNIA.
 XX Gatti RA;
 XX WPI; 2001-168574/17.
 DR Detecting a mutation or polymorphism in human ataxia telangiectasia gene
 PT or polyexonic eukaryotic gene, involves using mega-single stranded
 PT conformation polymorphism analysis.
 XX Claim 7; Page 51; 118pp; English.
 PS The present sequence is one of a number of primers used in a method for
 XX detecting a mutation or a polymorphism in the human ATM gene, which is
 CC associated with the disease ataxia telangiectasia, or a polyexonic
 CC eukaryotic gene of at least 4 kb. The method uses an improved version of
 CC single-stranded conformation polymorphism (SSCP) electrophoresis that
 CC allows electrophoresis of two or three amplified segments in a single
 CC lane. The method is useful for screening large, complex polyexonic
 CC eukaryotic genes such as the ATM gene for mutations and polymorphisms.
 CC The new mutations and polymorphisms in the ATM gene are useful for
 CC performing more accurate screening of human DNA samples for mutations,
 CC for distinguishing mutations from polymorphisms, and for improving the
 CC efficiency of automated screening methods. The mega-SSCP method provides
 CC a screening method of genes for multiple polymorphisms and mutations at
 CC once. The method is particularly suitable for large, polyexonic,
 CC eukaryotic genes, having mutations and polymorphisms at many points and
 CC not merely at one or a few hot spots. Note: the SEQ ID assigned to this
 CC sequence in the disclosure and claims of the the specification is one
 XX number lower than the number given in the sequence listing
 XX Sequence 20 BP; 7 A; 1 C; 11 G; 1 T; 0 U; 0 Other;
 QY Query Match 9.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 2.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1742 ACTCTCCCTATCCT 1756
 15 ACTCTCCCTCTCCT 1

RESULT 117
 AAF86771
 ID AAF86771 standard; DNA; 20 BP.
 XX AAF86771;
 XX 25-JUL-2001 (first entry)
 DE Human cytohesin-2 antisense oligonucleotide, SEQ ID NO:84.

XX Human cytohesin-2; PSCD2; ARNO for ARF nucleotide binding site opener;
 KW mSec7; ARF exchange factor; cytosolic adapter protein;
 KW guanine nucleotide exchange factor; ADP ribosylation factor; ARF1; ARF3;
 KW ARF6; actin cytoskeleton regulation; expression inhibition;
 KW atherosclerosis; allograft rejection; hyperproliferative disorder;
 KW cancer; tumour; phosphorothioate; antisense oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate linkages"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
 FT cytosines are 5-methylcytosine"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
 FT cytosines are 5-methylcytosine"
 XX
 XX WO200130361-A1.
 XX
 XX 03-MAY-2001.
 XX
 XX 20-OCT-2000; 2000WO-US029088.
 XX
 XX 27-OCT-1999; 99US-00428583.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Cowsert LM;
 XX
 XX WPI; 2001-335680/35.
 XX
 XX New antisense compounds modulating expression of human cytohesin-2 useful
 PT for diagnosis, prophylaxis and treatment of diseases associated with
 PT expression of cytohesin-2, e.g. cancer, atherosclerosis, allograft
 PT rejection.
 XX
 XX Claim 3; Page 80; 104pp; English.
 XX
 XX The invention relates to antisense oligonucleotides targetted to the
 CC human cytohesin-2 gene, which inhibit its expression. A series of
 CC oligonucleotides (AAR66697-AAR66776) were designed to target different
 CC regions of the human cytohesin-2 RNA, and were analysed for their effect
 CC on cytohesin-2 mRNA levels by quantitative real-time PCR. Cytohesin-2 is
 CC a member of a small family of cytosolic adapter proteins which function
 CC as guanine nucleotide exchange factors for ADP ribosylation factors
 CC (ARFs), small monomeric G-proteins which regulate critical vesicular
 CC traffic pathways. Cytohesin-2 (also known as PSCD2, ARNO for ARF
 CC nucleotide binding site opener, mSec7, and ARF exchange factor) is
 CC localised to the plasma membrane and promotes guanine nucleotide exchange
 CC on ARF1, ARF3 and ARF6, the latter of which regulates the assembly of the
 CC actin cytoskeleton. Through its interaction with ARF6, and in conjunction
 CC with protein kinase C, cytohesin-2 functions as a critical link between
 CC cell surface receptors and the actin cytoskeleton. The oligonucleotides
 CC of the invention are useful for diagnosis, prevention and treatment of
 CC conditions associated with cytohesin-2 expression, such as
 CC atherosclerosis, allograft rejection and hyperproliferative disorders,
 CC especially cancer
 XX
 XX Sequence 20 BP; 0 A; 8 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 9.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 2.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1685 TCTCTCCAGCGTGG 1699
 |||||
 Db 5 TCTCTCTCGGTGG 19
 |||||
 RESULT 118
 AAD52270
 ID AAD52270 standard; DNA; 20 BP.
 XX
 AC AAD52270;
 XX
 XX 02-MAY-2003 (first entry)
 DT
 XX Human IFNGR2 antisense oligonucleotide, ISIS #142748.
 DE
 XX Antisense; interferon gamma receptor 2; autoimmune disorder; cancer;
 KW autoimmune thyroiditis; autoimmune insulinitis; multiple sclerosis;
 KW diabetes; autoimmune arthritis; Crohn's disease; apoptosis; IFNGR2;
 KW gene therapy; prophylaxis; human; phosphorothioate; ss.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotides"
 XX
 XX WO200288163-A1.
 XX
 XX 07-NOV-2002.
 XX
 XX 16-APR-2002; 2002WO-US012007.
 XX
 XX 26-APR-2001; 2001US-00843377.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Watt AT;
 XX
 XX WPI; 2003-156688/15.
 XX
 XX New antisense oligonucleotides for modulating Interferon gamma receptor
 PT 2, particularly useful for treating autoimmune disorders (e.g. multiple
 PT sclerosis or Crohn's disease), cancers or diseases caused by aberrant
 PT apoptosis.
 XX
 XX Claim 3; Page 85; 127pp; English.
 XX
 XX The invention relates to antisense compounds, composition and methods for
 CC modulating the expression of human interferon gamma receptor 2 (IFNGR2).
 CC The compositions comprise antisense compounds targetted to nucleic acids
 CC encoding IFNGR2. Antisense compounds of the invention are useful for
 CC treating diseases or conditions associated with IFNGR2, e.g. autoimmune
 CC disorder (e.g. autoimmune thyroiditis, diabetes, multiple sclerosis,
 CC autoimmune arthritis, autoimmune insulinitis or Crohn's disease), cancer,
 CC or a disease/disorder caused by aberrant apoptosis. They are also useful
 CC for diagnostics, therapeutics, prophylaxis or as research reagents or
 CC kits. The invention is useful in gene therapy. The present sequence is an
 CC antisense oligonucleotide targetted to human IFNGR2 DNA
 XX
 XX Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 9.6%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 2.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCACTC 1745
 DB 3 ACTGGCTCCCACTC 17

RESULT 119
 AAT60161/c
 ID AAT60161 standard; DNA; 18 BP.
 AC AAT60161;
 XX
 DT 01-DEC-1997 (first entry)
 XX
 DE Collagen gene promoter region binding oligomer Oligo 158 APS.
 KW Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
 KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;
 KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
 KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..18
 FT /*tag= a
 FT /note= "Phosphorothioate linkages"
 FT
 PN W09710254-A1.
 XX
 PD 20-MAR-1997.
 XX
 XX 12-SEP-1996; 96WO-US014640.
 XX
 PR 15-SEP-1995; 95US-00528836.
 PR 11-SEP-1996; 96US-00712357.
 XX
 PA (GUNT/) GUNTAKA R V.
 XX
 XX Guntaka RV, Weber KT, Kovacs A, Kandala J;
 XX WPI; 1997-202172/18.
 XX
 PT Triplex forming oligomer binds to collagen gene promoter region - used to
 PT impede pathological fibrosis etc.
 XX
 PS Claim 18; Page 36; 52pp; English.
 XX
 CC An oligomer has been produced which is capable of inhibiting expression
 CC of a collagen gene. The present sequence represents a specifically
 CC claimed oligomer Oligo 158 APS, which binds to the polypurine-
 CC polypyrimidine region of the rat alpha1(I) collagen gene promoter region.
 CC The oligomer may be used to impede pathological fibrosis which is
 CC associated with myocardial fibrosis in hypertensive heart diseases,
 CC atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin
 CC fibrosis found in scleroderma, in hypertrophic scars and in skin
 CC following burn injury. The oligomer inhibits expression of a collagen
 CC gene after insertion into a cell by causing an intracellular reaction
 CC which inhibits gene expression. The oligomer is preferably a triplex
 CC forming oligomer (TFO) which is targeted to a 30-mer polypurine
 CC oligonucleotide corresponding to the noncoding strand of the promoter
 CC between -170 and -140. This section was chosen due to its binding
 CC stability at physiological pH
 XX
 SQ Sequence 18 BP; 6 A; 0 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 9.5%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 CTCCCAACCTCTCCCTAT 1753
 DB 18 CTCGCCCTCTCTCCCTTT 1

RESULT 120
 AAT94803/c
 ID AAT94803 standard; DNA; 18 BP.
 XX
 AC AAT94803;
 XX
 DT 19-FEB-1998 (first entry)
 XX
 DE Human leukocyte antigen class I gene URSTO probe 531-548.
 XX
 KW Human leukocyte antigen; HLA; probe; tissue transplantation; MHC gene;
 KW major histocompatibility complex; paternity test; forensic medicine;
 KW haematological malignancy; inherited disorder; adoptive immunotherapy;
 KW identification; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09720197-A2.
 XX
 PD 05-JUN-1997.
 XX
 PF 29-NOV-1996; 96WO-GB002959.
 XX
 PR 29-NOV-1995; 95GB-00024381.
 XX
 PA (NOLA-) NOLAN BONE MARROW TRUST ANTHONY.
 XX
 PI Arguello R, Avakian H, Madrigal A;
 XX WPI; 1997-310717/28.
 XX
 PT Identifying unknown allele(s) of a polyallelic gene using panel of
 PT probes each recognising a sequence motif present in some allele(s) -
 PT useful for donor matching in tissue transplantation.
 XX
 PS Claim 5; Page 19; 64pp; English.
 XX
 CC A novel method has been developed for identifying an unknown allele of a
 CC polyallelic gene. The method involves: (a) contacting the unknown allele
 CC with a panel of probes, each of which recognises a sequence motif that is
 CC present in some alleles of the polyallelic gene but not in others; (b)
 CC observing which probes recognise the unknown allele so as to obtain a
 CC fingerprint of the unknown allele; and (c) comparing the fingerprint with
 CC fingerprints of known alleles. The present sequence represents a
 CC specifically claimed probe for use in the method where the polyallelic
 CC gene is a human leukocyte antigen class I gene. The method can be used
 CC for genes such as mammalian MHC genes, specifically the HLA class I and
 CC II genes, the T cell receptor genes in mammals, TAP, LMP, ras,
 CC nonclassical HLA class I genes, human complement factor genes C4 and C2,
 CC Bf in the HLA complex, and genes located in mitochondrial DNA, bacterial
 CC chromosomes and viral DNA. The method is particularly useful for matching
 CC the alleles of the HLA genes in a prospective donor and a prospective
 CC recipient in tissue or organ transplantations. The method can also be
 CC used in paternity testing, in forensic medicine, as a follow up technique
 CC in treatment of haematological malignancies or inherited disorders, in
 CC adoptive immunotherapy, and in identification of bacteria and viruses.
 CC The method can provide for the identification of alleles of the
 CC polyallelic genes using a limited number of selected recurring motif
 CC probes
 XX
 SQ Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 9.5%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1732 TTGGCTCCCACTCTCTCC 1749


```
PR 29-MAR-1999; 99US-00280409.
XX
XX (ISIS-) ISIS PHARM INC.
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Cowsett LM, Bennett CF, O'malley BW;
XX WPI; 2000-586211/55.
XX
XX Antisense compounds targeted to steroid receptor RNA activator useful for
PT diagnosis, prophylaxis and treatment of diseases associated with the
PT steroid activator, such as infection, inflammation or tumor formation.
XX
XX Claim 3; Col 41; 47pp; English.
XX
XX The present sequence is one of a large number of antisense
CC oligonucleotides which is directed against one of four human steroid
CC receptor RNA activator (SRA) nucleic acid sequences. Two series of
CC antisense oligonucleotides were synthesised. The first series comprised 8
CC -30 oligodeoxynucleotides with a phosphorothioate backbone. The second
CC series comprised chimeric oligonucleotides composed of a central gap
CC region, consisting of ten 2'-deoxynucleotides, which was flanked on both
CC sides by four-nucleotide wings. The wings were composed of 2'-
CC methoxyethyl (2'-MOE) nucleotides. Both series contained the same
CC nucleotide sequences. The antisense compounds are useful for research,
CC diagnosis, treatment and prophylaxis to prevent or delay infection,
CC inflammation or tumour formation. Therapeutically the oligonucleotides
CC are highly safe and are effectively administered to humans
XX
XX Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 9.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1668 CAGCTGGAACCCCTGGTGT 1685
DB 1 CTGCTGGAAGCCTGGTAT 18
RESULT 124
AAD20365/c
ID AAD20365 standard; DNA; 18 BP.
AC AAD20365;
XX
XX 03-JAN-2002 (first entry)
XX
XX Antisense oligo, ISIS# 29889, targeted to human SRC-1 DNA.
XX
XX Human; antisense; steroid receptor coactivator-1; SRC-1; F-SRC-1; NcoA-1;
KW diagnostic; therapeutic; prophylaxis; infection; inflammation;
KW cytostatic; tumour formation; antiinflammatory; antibacterial;
KW phosphorothioate; ss.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..4
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 1
FT /tag= c
FT /mod_base= m5c
FT modified_base 7
FT /tag= d
FT /mod_base= m5c
```

```
FT modified_base 8
FT /tag= e
FT /mod_base= m5c
FT modified_base 10
FT /tag= f
FT /mod_base= m5c
FT modified_base 11
FT /tag= g
FT /mod_base= m5c
FT modified_base 13
FT /tag= h
FT /mod_base= m5c
FT modified_base 15..18
FT /tag= j
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 15
FT /tag= i
FT /mod_base= m5c
XX
XX US6294382-B1.
XX
XX 25-SEP-2001.
XX
XX 27-NOV-2000; 2000US-00723534.
XX
XX 27-NOV-2000; 2000US-00723534.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowsett LM;
XX
XX WPI; 2001-638016/73.
XX
XX New antisense oligonucleotides for inhibiting the expression of human
PT steroid receptor coactivator-1, particularly useful for preventing,
PT delaying or treating infection, inflammation or tumor formation.
XX
XX Claim 3; Col 42; 36pp; English.
XX
XX The present invention relates to an antisense compound of up to 30
CC nucleobases in length, which specifically hybridises with and inhibits
CC the expression of human steroid receptor coactivator-1 (SRC-1) (also
CC known as F-SRC-1 and NcoA-1) gene. The antisense compounds are useful for
CC diagnostics, therapeutics, prophylaxis, or as research reagents or kits.
CC The antisense oligonucleotides are useful for treating an animal,
CC particularly a human, suspected of having or being prone to a disease or
CC condition associated with the expression of SRC-1. In particular, the
CC antisense oligonucleotides are useful for preventing, delaying or
CC treating infection, inflammation or tumour formation. The present
CC sequence is an antisense oligonucleotide, ISIS# 29889, targeted to human
CC SRC-1 DNA
XX
XX Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
```

```
Query Match 9.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1691 CCAGCGTGGTGAAGTTG 1708
DB 18 CCAGTGTGGTGAATTTCG 1
RESULT 125
ABA83557/c
ID ABA83557 standard; DNA; 18 BP.
XX
XX ABA83557;
AC
XX
XX 08-FEB-2002 (first entry)
XX
XX Mouse MP-1 antisense oligonucleotide SEQ ID NO 96.
```

```
XX Human; mouse; rat; antisense gene therapy; MP-1; MAP kinase Partner 1;
KW antinflammatory; cyostatic; antimicrobial; infection; tumour;
KW phosphorothioate; ss.
XX
OS Mus musculus.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone linkage, all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..4
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-MOE wings"
FT modified_base 15..18
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-MOE wings"
XX
XX US6306606-B1.
XX
XX 23-OCT-2001.
XX
XX 22-NOV-2000; 2000US-00721822.
XX
XX 22-NOV-2000; 2000US-00721822.
XX
XX (ISIS-) ISIS PHARM INC.
XX (UYVI-) UNIV VIRGINIA.
XX
XX Weber MJ, Wyatt J, Cowsest LM;
XX
XX WPI; 2002-040199/05.
XX
XX New antisense oligonucleotides for modulating the expression of MP-1 (MAP
XX kinase partner 1), for preventing, delaying or treating infection,
XX inflammation or tumor formation, especially in humans.
XX
XX Example 17; Col 43-44; 47pp; English.
XX
XX The invention relates to an antisense compound (ABA83459-ABA83576) which
XX is up to 30 nucleobases in length and that inhibits the expression of MP-
XX 1 (MAP kinase Partner 1) in cells or tissues comprising contacting the
XX cells or tissues in vitro with the antisense compound so that expression
XX of MP-1 is inhibited. The antisense compounds have potential
XX antinflammatory, cyostatic and antimicrobial activity. The antisense
XX compounds are useful for diagnostics, therapeutics, prophylaxis or as
XX research reagents or kits. The antisense oligonucleotides are useful in
XX gene therapy for treating an animal, particularly a human, suspected of
XX having or being prone to a disease or condition associated with the
XX expression of MP-1. In particular, the antisense oligonucleotides are
XX useful for preventing, delaying or treating infection, inflammation or
XX tumour formation. The present sequence is that of a mouse MP-1 antisense
XX oligonucleotide, comprising a chimeric oligonucleotide gapmer 18.
XX nucleotides in length, composed of a central gap region of ten 2'-
XX deoxynucleotides flanked by four nucleotide 2'-MOE wings
XX
XX Sequence 18 BP; 3 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 9.5%; Score 13.2; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1664 CTCACAGCTGGACCGCTG 1681
XX ||||| |||||
XX 18 CTCACAGCTGGACCGCTG 1
XX
XX RESULT 126
```

```
ABL45037/c
ID ABL45037 standard; DNA; 18 BP.
XX
AC ABL45037;
XX
XX 11-APR-2002 (first entry)
XX
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:2081.
XX
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001321190-A.
XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-00068285.
XX
XX 10-MAR-2000; 2000JP-00066716.
XX
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX
XX Arraying genome clones.
XX
XX Claim 4; Page 45; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each wells of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX are detected from the amplified products; (h) the clones in the multiwell
XX plates are specified from the detected result; and (i) the clones are
XX reconstituted as the positions on the chromosome and arrayed. The
XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX represent PCR primers for human chromosome 21q22.1, which are
XX specifically claimed for use in the present invention
XX
XX Sequence 18 BP; 6 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 9.5%; Score 13.2; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1720 CGGAGATGGAGATTGGCT 1737
XX ||||| ||||| |||||
XX 18 CTGAGATGGAGTTTCGCT 1
XX
XX RESULT 127
XX AAD41916/c
XX ID AAD41916 standard; DNA; 18 BP.
XX
XX AAD41916;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human SRC-1 antisense oligonucleotide, ISIS 29849.
```

```
XX Human; steroid receptor coactivator-1; SRC-1; antisense compound;
KW diagnostic; therapeutic; prophylaxis; antisense therapy; antisense;
KW phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "Phosphorothioate backbone"
FT modified_base 1..4
FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "2'methoxyethyl nucleotides"
FT modified_base 1
FT FT /*tag= d
FT FT /mod_base= m5c
FT modified_base 7
FT FT /*tag= e
FT FT /mod_base= m5c
FT modified_base 8
FT FT /*tag= f
FT FT /mod_base= m5c
FT modified_base 10
FT FT /*tag= g
FT FT /mod_base= m5c
FT modified_base 11
FT FT /*tag= h
FT FT /mod_base= m5c
FT modified_base 13
FT FT /*tag= i
FT FT /mod_base= m5c
FT modified_base 15..18
FT FT /*tag= c
FT FT /mod_base= OTHER
FT modified_base 15
FT FT /note= "2'methoxyethyl nucleotides"
FT FT /*tag= j
FT FT /mod_base= m5c
XX
PN WO200244325-A2.
XX
PN 06-JUN-2002.
XX
XX 26-NOV-2001; 2001WO-US044179.
XX
XX 27-NOV-2000; 2000US-00723379.
XX
XX (ISIS-) ISIS PHARM INC.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX O'malley BW, Bennett CF, Cowsert LM;
XX
XX WPI; 2002-537447/57.
XX
XX Novel antisense compound targeted to nucleic acid molecules encoding
XX human steroid receptor coactivator-1 (SRC-1), useful for inhibiting
XX expression of SRC-1 in human cells or tissues.
XX
XX Example 15; Page 79; 103pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of human steroid receptor coactivator-1
XX (SRC-1). The compositions comprise antisense oligonucleotides targeted
XX to nucleic acids encoding SRC-1. The antisense compound is useful for
XX inhibiting the expression of SRC-1 in human cells or tissues. It is also
XX useful for treating a human having a disease or condition associated with
XX SRC-1, by inhibiting expression of SRC-1. It is also useful for
XX diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX It is also used in antisense therapy. The present sequence is an
CC antisense oligonucleotide targeted to human SRC-1 DNA. This sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 9.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1691 CCAGCGTGTGGAGTTG 1708
Db 18 CCAGTGTGTGGAAATCG 1
RESULT 128
AAQ91454/c
ID AAQ91454 standard; DNA; 19 BP.
XX
XX AAQ91454;
AC
XX 25-MAR-2003 (revised)
DT 30-AUG-1995 (first entry)
XX
XX Dysprosium (III) texaphyrin (DyTx) DNA conjugate.
XX
XX Dysprosium (III) texaphyrin (DyTx) DNA conjugate; liver disease;
KW targeted intracellular mRNA hydrolysis; gene expression inhibition;
KW hormone regulation; hydrolysis reagents; alkyl phosphate esters;
KW detoxification; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "DyTx-NH(CH2)6-PO4-adenine"
XX
XX WO9429316-A2.
XX
XX 22-DEC-1994.
XX
XX 09-JUN-1994; 94WO-US006284.
XX
XX 09-JUN-1993; 93US-00075123.
XX 14-APR-1994; 94US-00227370.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX (PHAR-) PHARMACYCLICS INC.
XX
XX Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;
XX Kral VA, Iverson B, Mody T, Miller RA, Magda D;
XX
XX WPI; 1995-036382/05.
XX
XX Texaphyrin metal complex mediated ester hydrolysis - esp. useful for
XX targeted intracellular hydrolysis of mRNA and for inhibiting gene
XX expression.
XX
XX Disclosure; Fig 21; 125pp; English.
XX
XX AAQ91451-Q91457 are texaphyrin lanthanide metal DNA conjugates, which are
XX esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting
XX gene expression. They may also be used for the treatment of liver disease,
XX as hormone regulation agents and as hydrolysis reagents for the
XX detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to
XX correct FN field.)
XX
XX Sequence 19 BP; 2 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 9.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

OY 1655 AGCACCAGGCTCACAGCT 1672
 Db 18 AACACCCGGCTCACAGAT 1

RESULT 129
 AAV07302/c

ID AAV07302 standard; DNA; 19 BP.
 AC AAV07302;
 DT 14-AUG-1998 (first entry)
 DE Metallotexaphyrin-oligonucleotide conjugate #16.
 XX Metallotexaphyrin; dysprosium; europium; conjugate; RNase H;
 KW antisense therapy; ss.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /mod base
 FT /note= "DyTxNH-(CH2)6-PO4-adenine, where DyTx is
 FT dysprosium (III) texaphyrin"

US5763172-A.
 XX
 XX 09-JUN-1998.
 XX
 XX 07-JUN-1995; 95US-00486962.
 XX
 XX 21-JAN-1992; 92US-00822964.
 XX 09-JUN-1993; 93US-00075123.
 XX 14-APR-1994; 94US-00227370.
 XX 09-JUN-1994; 94WO-US006284.
 XX 26-MAY-1995; 95US-00452261.
 XX 07-JUN-1995; 95US-00485581.
 XX (PHAR-) PHARMACYCLICS INC.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Sessler JL, Wright M, Miller RA, Dow WC, Magda D;
 XX WPI; 1998-347306/30.
 XX
 XX Enhancing therapeutic activity of oligo-nucleotides in cells - using
 XX conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester
 XX bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.
 XX
 XX Example 6; Fig 5; 34pp; English.

The invention relates to a method of enhancing the therapeutic activity
 of oligonucleotides in cells. It comprises contacting a targeted
 intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide
 conjugate. The contact is carried out under physiological conditions for
 a time sufficient to hydrolyse the phosphate ester bond of the targeted
 RNA. The metallotexaphyrin of the conjugate has catalytic activity for
 phosphate ester bond hydrolysis. The oligonucleotide of the conjugate has
 complementary binding affinity to the targeted RNA. The conjugate may be
 used in antisense therapies for treating, e.g. cancer, viral infections,
 autoimmune diseases and restenosis. The conjugate may also be used as
 hydrolysis reagents for the detoxification of di- and trialkyl phosphate
 esters, which are used in solvents, insecticides and chemical nerve
 gases. The metallotexaphyrin complex enhances the therapeutic activity of
 the oligonucleotide, not only by facilitating cellular uptake of the
 oligonucleotide but also by hydrolysing target RNA within the cell,
 independent of RNase H. Attachment to the complex may also cause the
 oligonucleotide to take on some of the pharmacodynamic and biodistribution
 properties of the texaphyrin, such as selective localisation in tumours.
 The present sequence represents a metallo- texaphyrin-oligonucleotide

CC conjugate
 XX
 SQ Sequence 19 BP; 2 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
 Query Match 9.5%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1655 AGCACCAGGCTCACAGCT 1672
 Db 18 AACACCCGGCTCACAGAT 1

RESULT 130
 AAC66840
 ID AAC66840 standard; DNA; 19 BP.
 XX
 AC AAC66840;
 XX
 DT 27-FEB-2001 (first entry)
 XX
 DE Human tankyrase II coding sequence PCR primer UTANKII-4A.
 XX
 KW Human; tankyrase II; telomere length; signal transduction; PCR primer;
 KW ss.
 OS Homo sapiens.
 XX
 XX WO2000061813-A1.
 XX 19-OCT-2000.
 XX
 XX 10-APR-2000; 2000WO-US009558.
 XX
 XX 09-APR-1999; 99US-0128577P.
 XX 13-APR-1999; 99US-0129123P.
 XX (GERO-) GERON CORP.
 XX
 XX Morin GB, Funk WD, Piatyszek MA;
 XX WPI; 2000-679503/66.
 XX
 XX Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding
 XX the polypeptide useful for modulating or maintaining telomere length,
 XX replicative capacity, apoptosis, chromosome packing or gene expression.
 XX
 XX Example 4; Page 19; 52pp; English.

The present invention relates to the isolation of the protein and coding
 sequences of human tankyrase II. This protein is thought to be involved
 in signal transduction in the cell, and to have binding activity for
 other telomere-associated proteins. It is possible that it plays a role
 in the regulation of telomere length, thus affecting the replicative
 ability of the cell. The protein is useful for ribosylating target
 proteins, for determining tankyrase II binding activity in a sample, and
 for modulating telomere length in a cell. The present sequence is a PCR
 primer used to amplify the tankyrase II coding sequence

XX
 SQ Sequence 19 BP; 6 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 9.5%; Score 13.2; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1715 GAGTACGAGATGGAGAT 1732
 Db 1 GAGCAGAGATGGAGGT 18

RESULT 131
 ABX95438/c
 ID ABX95438 standard; DNA; 19 BP.

AC ADE29874;
XX 29-JAN-2004 (first entry)
XX Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:496.
XX short interfering nucleic acid; siNA; downregulation; inhibition;
XX mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytosolic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW immunosuppressive; antibacterial; antiarthritis;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX Synthetic.
OS WO2003072590-A1.
PN
XX
XX 04-SEP-2003.
PD
XX 28-JAN-2003; 2003WO-US002510.
PF
XX 20-FEB-2002; 2002US-0358580P.
PR
XX 11-MAR-2002; 2002US-0363124P.
PR
XX 06-JUN-2002; 2002US-0386782P.
PR
XX 29-AUG-2002; 2002US-0406784P.
PR
XX 05-SEP-2002; 2002US-0408378P.
PR
XX 09-SEP-2002; 2002US-0409293P.
PR
XX 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) siRNA THERAPEUTICS INC.
PA
XX Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;
PI WPI; 2003-689980/65.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PT protein kinase genes.
XX
XX Example 3; SEQ ID NO 496; 164pp; English.
PS
XX The present invention describes a short interfering nucleic acid (siNA)
XX that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours, and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.
XX
XX Sequence 19 BP; 2 A; 5 C; 7 G; 0 T; 5 U; 0 Other;
SQ

Query Match 9.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1673 GGAACCTGTGTCTCTCT 1690
||||| : : : : :
Db 1 GGAAGCGUGGUGUCU 18

RESULT 134
AAQ29803/c
ID AAQ29803 standard; DNA; 20 BP.
XX
XX AAQ29803;
AC
XX 25-MAR-2003 (revised)
DT 19-MAR-1993 (first entry)
XX
XX A allele probe VP68.
DE
XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
KW paternity; forensic; ss.
KW
XX Synthetic.
OS
XX BP512342-A2.
PN
XX 11-NOV-1992.
PD
XX 25-APR-1992; 92EP-00107084.
PF
XX 07-MAY-1991; 91US-00696793.
PR
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA
XX Saiiki RK, Nasarabadi SL;
PI WPI; 1992-374679/46.
DR
XX
XX Determn. of an individuals genotype at the gamma-globin locus - using
PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
PT
XX Disclosure; Page 17; 29pp; English.
PS
XX The sequences given in AAQ2987-816 are probes which were used within the
CC method of the invention for detecting the presence of a variant sequence
CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
CC distinguished from one another by the polymorphic sequence corresponding
CC to the HindIII site of the A allele. The sequences of the three alleles
CC are given in AAQ29842-44. The methods for determining an individuals
CC genotype at the GGG locus with respect to a set of alleles improves the
CC discriminatory power of GGG typing methodology compared to previous
CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 20 BP; 5 A; 10 C; 2 G; 3 T; 0 U; 0 Other;
SQ

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1670 GCTGGAACCTGTGTCT 1687
||||| : : : : :
Db 19 GGTGGAAGCCTGTGTGT 2

RESULT 135
AAQ80655
ID AAQ80655 standard; DNA; 20 BP.
XX
XX AAQ80655;
AC
XX 22-AUG-1995 (first entry)
DT
XX Primer amplifies part of 5' UTR and VP4/VP2 of enterovirus.
DE
XX primer; amplification; PCR; polymerase chain reaction; enterovirus; VP4;
KW VP2; 5' UTR; untranslated region; detection; identification; ss.
KW
XX Synthetic.
OS
XX JF06311900-A.
PN

XX 08-NOV-1994.
 XX PD
 XX CC
 XX PF 28-APR-1993; 93JP-00102254.
 XX PR 28-APR-1993; 93JP-00102254.
 XX PA (M1TP) MITSUBISHI YUKA BCL KK.
 XX PA (INCU//) INOUE S.
 XX DR
 XX DR WPI; 1995-027267/04.
 XX XX
 XX PT Detection and identification of enterovirus - by amplification of part
 XX PT of 5' -UTR and VP4 and VP2 protein sequences.
 XX XX
 XX PS Claim 3; Page 2; 10pp; Japanese.
 XX XX
 XX CC AAQ80654-55 are used to amplify a part of the 5' UTR (untranslated
 XX CC region) and DNA encoding VP4 and VP2 proteins of an enterovirus. The
 XX CC method can detect enterovirus and identify the serum type simply and
 XX CC precisely
 XX XX
 XX SQ Sequence 20 BP; 3 A; 2 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 9.5%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1696 GTGGTGAAGTTGGTTA 1713
 Db 3 GTGGTGAAGTTGGCTGA 20
 RESULT 136
 AAT39874/C
 ID AAT39874 standard; DNA; 20 BP.
 XX AC AAT39874;
 XX DT
 XX DT 05-DEC-1996 (first entry)
 XX DE
 XX DE Primer #4 for enterovirus Vp4 coding sequence.
 XX KW Probe; enterovirus type 71; EV71; Vp4; coxsackie group A virus type 16;
 XX KW CA16; Vp2; 5' untranslated region; polymerase chain reaction; primer;
 XX KW amplify; PCR; ss.
 XX OS Synthetic.
 XX OS JP08173195-A.
 XX PN 09-JUL-1996.
 XX PD
 XX PF 17-OCT-1995; 95JP-00268660.
 XX PR 28-OCT-1994; 94JP-00265124.
 XX XX
 XX PA (M1TP) MITSUBISHI YUKA BCL KK.
 XX XX
 XX DR WPI; 1996-365607/37.
 XX XX
 XX PT Differentiation between enterovirus type 71 and coxsackie gp. A virus
 XX PT type 16 - by amplifying and probing the 5' non-translated region of Vp4
 XX PT and Vp2 proteins.
 XX PS
 XX PS Example 1; Page 22; 28pp; Japanese.
 XX CC
 XX CC AAT39871-T39874 represent amplification primers for Vp4 coding sequences,
 XX CC used within the scope of the invention. The invention is a method for
 XX CC differentiating between enterovirus type 71 (EV71) coxsackie group A
 XX CC virus type 16 (CA16) using Vp4 protein coding sequences. In this method,
 XX CC part of the 5' untranslated region of the Vp4 and Vp2 proteins from these
 XX CC viruses are amplified, and the Vp4 fragment is sequenced. Probes specific

CC for each serum type of EV71 and CA16 (see AAT39837-T39841 for EV71
 CC probes, and AAT39842-T39847 for CA16 probes) are then designed, and the
 CC binding ability of the probes with the amplified DNA is analysed. As the
 CC 5' UTR is a sequence specific to each serum type of enterovirus, this
 CC method can differentiate EV71 from CA16 with high precision
 XX
 XX SQ Sequence 20 BP; 6 A; 9 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 9.5%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1696 GTGGTGAAGTTGGTTA 1713
 Db 18 GTGGTGAAGTTGGCTGA 1

RESULT 137
 AAV29418/C
 ID AAV29418 standard; DNA; 20 BP.
 XX AC AAV29418;
 XX DT 31-JUL-1998 (first entry)
 XX DE Calcium ion channel alpha subunit exon 21 specific reverse primer.
 XX DE Calcium ion channel alpha subunit; human; episodic ataxia type 2;
 XX KW familial hemiplegic migraine; FHM; EA-2; treatment; diagnosis;
 XX KW PCR primer; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN EP834561-A1.
 XX PD 08-APR-1998.
 XX PF 27-SEP-1996; 96EP-00202707.
 XX PR 27-SEP-1996; 96EP-00202707.
 XX PA (UYLE-) RIJXSUNIV LEIDEN.
 XX XX
 XX DR WPI; 1998-195461/18.
 XX PT
 XX PT New human nucleic acid associated with migraine and episodic ataxia type
 XX PT 2 - useful for diagnosis and development of, e.g. familial hemiplegic
 XX PT migraine and episodic ataxia type 2.
 XX PS Disclosure; Page 9; 157pp; English.

XX This primer is used for the PCR amplification of an exon of the human
 XX calcium ion channel alpha 1 subunit. The channel is related to familial
 XX hemiplegic migraine (FHM) and/or episodic ataxia type 2 (EA-2) and is
 XX derived from, related to or associated with a gene present in humans on
 XX chromosome 19p13.1-13.2. The encoding nucleic acid can be used to
 XX localise or identify genes related to episodic neurological disorders,
 XX specifically migraine, FHM or EA-2, but also epilepsy. It can also be
 XX used to distinguish between alleles of the corresponding gene. Cells and
 XX animals containing recombinant expression vectors comprising the nucleic
 XX acid can be useful in study, development and treatment of migraine, FHM,
 XX EA-2 and epilepsy. Proteins or peptides encoded by the nucleic acid and
 XX natural or synthetic antibodies against the proteins can be used to
 XX diagnose FHM, EA-2, migraine and other neurological conditions associated
 XX CC with cation channel dysfunction

XX SQ Sequence 20 BP; 2 A; 8 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 9.5%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1689 CTCACGGCTGGTGAAGT 1706
 Db 20 CACCAGGCTGGCGGAAGT 3

RESULT 138
 AAX96823
 ID AAX96823 standard; DNA; 20 BP.
 AC AAX96823;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.
 XX
 OS Synthetic.
 OS Chlamydia pneumoniae.
 XX
 PN WO9927105-A2.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-IB001890.
 XX
 PR 21-NOV-1997; 97FR-00014673.
 PR 04-NOV-1998; 98US-0107078P.
 XX
 PA (GEST) GENSET.
 XX
 PI Griffais R;
 XX
 DR WPI; 1999-357842/30.
 XX
 PT Genome sequence of Chlamydia pneumoniae.
 XX
 PS Page 1856; Disclosure; 1912pp; English.
 XX
 CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotides sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 9.5%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1744 TCCTCCCTATCTCTAAAGG 1761
 Db 3 TGTCTCTTACCTAAAGG 20

RESULT 139
 AAA13141/C
 ID AAA13141 standard; DNA; 20 BP.
 XX
 AC AAA13141;
 XX
 DT 17-JUL-2000 (first entry)
 XX
 DE PI3K antisense inhibitor oligonucleotide ISIS# 32155.

XX
 KW Phosphatidyl inositol 3 kinase; PI3K; antisense oligonucleotide; p110;
 KW catalytic subunit; treatment; rheumatoid arthritis; asthma; research;
 KW diagnostic; infection; inflammation; tumour formation; inhibitor; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..20
 FT /tag= a
 FT /note= "Phosphorothioate internucleoside linkage"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Optionally 2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "Optionally 2'-methoxyethyl (2'-MOE) nucleotides"
 XX
 PN US6046049-A.
 XX
 XX 04-APR-2000.
 XX
 PF 19-JUL-1999; 99US-00357070.
 XX
 PR 19-JUL-1999; 99US-00357070.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Cowser LM;
 XX
 DR WPI; 2000-282691/24.
 XX
 XX New antisense compounds targeting nucleic acids encoding human PI3 kinase
 PT p110 delta useful for treating a disease or condition associated with PI3
 PT kinase p110 delta expression, e.g. rheumatoid arthritis, asthma.
 XX
 PS Claim 3; Col 41; 35pp; English.
 XX
 CC This sequence represents a phosphatidyl inositol 3 kinase (PI3K)
 CC targeting antisense oligonucleotide. Phosphatidyl inositol 3 kinases act
 CC as downstream effectors of hormone and growth factor receptors, and have
 CC been implicated in growth factor mediated cell transformation,
 CC mitogenesis, protein trafficking, cell survival and proliferation, and
 CC many other cellular activities. PI3K is a heterodimer, consisting of a
 CC 110KD catalytic subunit (p110), and an 85KD regulatory subunit (p85). The
 CC invention relates to antisense oligonucleotides which target the p110
 CC delta mRNA of PI3K. The antisense oligonucleotides specifically hybridise
 CC with various regions of the PI3K mRNA sequence, and inhibit the
 CC expression of PI3K. The antisense oligonucleotides may be used to treat
 CC an animal, particularly human, suspected of having or being prone to a
 CC disease or condition associated with the expression of PI3K, e.g.
 CC rheumatoid arthritis or asthma. The treatment works through the
 CC modulation (preferably inhibition) of the expression of PI3K. The
 CC antisense oligonucleotides may also be used for research and diagnostics,
 CC in pharmaceutical compositions and formulations, in the preparation of
 CC kits for detecting the level of PI3K in a sample, and as prophylaxis,
 CC e.g. to prevent or delay infection, inflammation or tumour formation.
 CC Antisense oligonucleotides, which are able to inhibit gene expression
 CC specifically, are used to elucidate the function of particular genes, and
 CC to distinguish between functions of various members of a biological
 CC pathway
 XX
 SQ Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 9.5%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1656 GCACACGGCTCACGCTG 1673
 Db 18 GCACCTGGCTCTCGCTG 1

RESULT 140
 AAS15246/c
 ID AAS15246 standard; DNA; 20 BP.
 XX
 AC AAS15246;
 XX
 DT 16-JAN-2002 (first entry)
 DE
 DE Mouse GAPDH PCR primer, MoGAPDH251F.
 XX
 XX Mouse; GAPDH; glyceraldehyde phosphate dehydrogenase; MoGAPDH251F; ss;
 KW PCR primer; neurotropic; neuroprotective; antiinflammatory;
 KW interleukin-beta; IL-1b; tumour necrosis factoralpha; TNFalpha;
 KW macrophage inflammatory protein-1alpha; MIP-1alpha; fractalkane;
 KW glial fibrillar associated protein; GFAP; MHC; CX3CR1; CD86;
 KW major histocompatibility complex; Alzheimer's disease; cerebral ischaemia;
 KW neurodegenerative disease.
 XX
 OS Mus sp.
 XX
 PN WO200175165-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US010247.
 XX
 PR 30-MAR-2000; 2000US-0193847P.
 XX
 PA (ELAN-) ELAN PHARM INC.
 XX
 PI Mcconlogue LC, Games KD, Yednock TA, Hua T, Messersmith E;
 PI Bard F;
 XX
 DR WPI; 2001-639367/73.
 XX
 PT Selecting compounds useful for treating or preventing Alzheimer's
 PT disease, from their ability to reduce levels of specific disease markers
 PT in animal models.
 XX
 PS Example 1; Page 17; 36pp; English.
 XX
 CC The invention relates selecting compounds that reduce symptoms of
 CC Alzheimer's disease using a non-human mammal that has been subjected to
 CC cerebral ischaemia or lesion of a nerve so as to produce, in the affected
 CC region, increased levels of specific markers of Alzheimer's disease-
 CC associated inflammation. Test compounds are selected if they reduce
 CC levels of these markers significantly, in the affected region, relative
 CC to controls. The markers are interleukin-beta (IL-1b), tumour necrosis
 CC factoralpha (TNFalpha), macrophage inflammatory protein-1alpha (MIP-
 CC 1alpha), glial fibrillar associated protein (GFAP), MHC (major
 CC histocompatibility complex) Italpha or IL 1, CD86, fractalkane or CX3CR1
 CC (a receptor for fractalkane). The method is used to identify compounds
 CC useful in treatment or prevention of Alzheimer's disease or other
 CC neurodegenerative diseases that have an inflammatory component. The
 CC method provides fast, accurate and quantitative drug screens. The present
 CC sequence is a PCR primer used in a quantitative PCR experiment to
 CC determine the level of a transcript for GAPDH as a control for the
 CC determining the levels of the markers of the invention
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 9.5%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1723 AGATGGAGATTGGCTCC 1740
 Db 19 AGATGGTGGTGGCTCC 2
 ||||| ||| |||||
 RESULT 141

AAC86126
 ID AAC86126 standard; cDNA; 20 BP.
 XX
 AC AAC86126;
 XX
 DT 29-AUG-2001 (first entry)
 DE
 DE Primer UNF14 to isolate APEX cDNA.
 XX
 XX Antigen presenting cell expression protein; APEX-1; APEX-2; APEX-3;
 KW extracellular domain; immunoglobulin-like domain; Ig-like structure;
 KW N-glycosylation site; transmembrane domain; cytoplasmic domain; PCR;
 KW SH2-binding motif; asthma; arteriosclerosis; AIDS; cirrhosis; primer;
 KW Crohn's disease; atopic dermatitis; autoimmune anaemia; bursitis;
 KW cholecystitis; diabetes mellitus; emphysema; atrophic gastritis;
 KW inflammatory bowel disease; multiple sclerosis; myasthenia gravis;
 KW myocardial inflammation; pericardial inflammation; osteoarthritis;
 KW osteoporosis; psoriasis; Reiter's syndrome; rheumatoid arthritis;
 KW inflammation; cancer; autoimmune disease; graft rejection; amplify;
 KW graft versus host disease; systemic lupus erythematosus;
 KW polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN WO200146260-A2.
 XX
 PD 28-JUN-2001.
 XX
 PF 22-DEC-2000; 2000WO-US034963.
 XX
 PR 23-DEC-1999; 99US-0172025P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Starling GC, Finger J;
 XX
 DR WPI; 2001-418044/44.
 XX
 PT Novel Antigen presenting cell expression protein useful for treating
 PT asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's
 PT disease and atopic dermatitis.
 XX
 PS Claim 50; Page 83; 112pp; English.
 XX
 CC The sequences given in AAC86117-42 are primers which were used to isolate
 CC the cDNA sequences which encode antigen presenting cell expression (APEX)
 CC -1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2 comprise an
 CC extracellular domain having one immunoglobulin (Ig)-like structure and N-
 CC glycosylation site, a transmembrane domain, and a cytoplasmic domain
 CC having at least one SH2-binding motif. APEX proteins and antibodies are
 CC useful in the study, diagnosis, prevention and treatment of disease
 CC associated with the presence of an APEX protein e.g., asthma,
 CC arteriosclerosis, AIDS, cirrhosis, Crohn's disease, atopic dermatitis,
 CC autoimmune anaemia, bursitis, cholecystitis, diabetes mellitus,
 CC emphysema, atrophic gastritis, inflammatory bowel disease, multiple
 CC sclerosis, myasthenia gravis, myocardial or pericardial inflammation,
 CC osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome, rheumatoid
 CC arthritis, inflammation, cancer, immune disorders, autoimmune diseases,
 CC graft rejections, graft versus host reaction and systemic lupus
 CC erythematosus. APEX proteins are useful as diagnostic and/or prognostic
 CC markers on APCs or APEX expressing cells, the ability to elicit the
 CC generation of antibodies and as targets for various therapeutic
 CC modalities. APEX proteins are also useful for identifying and isolating
 CC ligand that bind APEX
 XX
 SQ Sequence 20 BP; 4 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 9.5%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1662 GGCTCAGCTGGACCC 1679
 ||||| ||| ||| ||| |||

```

Db      2 GGCTCACACCTGTATATCC 19

RESULT 142
AAI69777
ID      AAI69777 standard; DNA; 20 BP.
XX
AC      AAI69777;
XX
DT      13-DEC-2001 (first entry)
XX
DE      16S/23S rRNA spacer region PCR primer #3.
XX
KW      Bacterium detection; 16S/23S rRNA spacer region; PCR primer; ss.
XX
OS      Pseudomonas putida.
XX
PN      JP2001190279-A.
XX
PD      17-JUL-2001.
XX
PF      13-JAN-2000; 2000JP-00004160.
XX
PR      13-JAN-2000; 2000JP-00004160.
XX
PA      (MITO ) MITSUBISHI JUKOGYO KK.
XX
DR      WPI; 2001-605311/69.
XX
FT      Detection method of Pseudomonas bacteria.
XX
PS      Claim 9; Page 8; 11pp; Japanese.
XX
CC      The present invention relates to a method for the detection of the
CC      16S/23S rRNA spacer region of Pseudomonas putida (see AAI69777). The
CC      method can be used to detect Pseudomonas bacteria. The present sequence
CC      is a PCR primer which was used in an example from the present invention
XX
SQ      Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1657 CACCAAGGCTCACAGCTGG 1674
Db      2 CACCAAGTTCACTGCTGG 19

RESULT 143
AAD40844/c
ID      AAD40844 standard; DNA; 20 BP.
XX
AC      AAD40844;
XX
DT      30-OCT-2002 (first entry)
XX
DE      Human hepsin antisense oligonucleotide, ISIS 107118.
XX
KW      Human; hepsin; antisense compound; antisense therapy; antisense;
KW      phosphorothioate backbone; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key Location/Qualifiers
FT      modified_base 1..20
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone"
FT      modified_base 1..5
FT      /tag= b
FT      /mod_base= OTHER
XX

/note= "2'methoxyethyl nucleotides"
2
modified_base
/*tag= d
/mod_base= m5c
8
modified_base
/*tag= e
/mod_base= m5c
9
modified_base
/*tag= f
/mod_base= m5c
10
modified_base
/*tag= g
/mod_base= m5c
11
modified_base
/*tag= h
/mod_base= m5c
13
modified_base
/*tag= i
/mod_base= m5c
16..20
modified_base
/*tag= c
/mod_base= OTHER
/note= "2'methoxyethyl nucleotides"
WO200250247-A2.
XX
PN      27-JUN-2002.
XX
PD      14-DEC-2001; 2001WO-US048341.
XX
PR      20-DEC-2000; 2000US-00742482.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Cowsert LM;
XX
DR      WPI; 2002-519882/55.
XX
PT      Novel antisense compound targeted to nucleic acids encoding human hepsin,
PT      useful for inhibiting the expression of hepsin in human cells or tissues,
PT      and for treating humans having a disease associated with human hepsin.
XX
PS      Claim 3; Page 95; 100pp; English.
XX
CC      The invention relates to antisense compounds, compositions and methods
CC      for modulating the expression of hepsin. The compositions comprise
CC      antisense compounds, particularly antisense oligonucleotides, targeted
CC      to nucleic acids encoding hepsin. The antisense compound is useful for
CC      inhibiting the expression of hepsin in human cells or tissues. It is also
CC      useful for treating an animal having a disease or condition associated
CC      with hepsin, by inhibiting expression of hepsin. It is useful for
CC      diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC      It is also used in antisense therapy. The present sequence is an
CC      antisense oligonucleotide targeted to human hepsin DNA. This sequence is
CC      used in the exemplification of the invention
XX
SQ      Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1664 CTCACAGCTGGAACCTG 1681
Db      19 CTCACTGGGGGACCTG 2

RESULT 144
AAD40662/c
ID      AAD40662 standard; DNA; 20 BP.
XX
AC      AAD40662;
XX

```

DT 30-OCT-2002 (first entry)
XX Human hepsin antisense oligonucleotide, ISIS 107118.
XX Human; antisense; hepsin; inflammation; tumour; gene therapy; cytostatic;
KW phosphorothioate backbone; ss.
OS Homo sapiens.
XX Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotides"
FT modified_base 2
FT /tag= d
FT /mod_base= m5c
FT modified_base 8
FT /tag= e
FT /mod_base= m5c
FT modified_base 9
FT /tag= f
FT /mod_base= m5c
FT modified_base 10
FT /tag= g
FT /mod_base= m5c
FT modified_base 11
FT /tag= h
FT /mod_base= m5c
FT modified_base 13
FT /tag= i
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotides"
XX WO200250248-A2.
XX 27-JUN-2002.
XX 14-DEC-2001; 2001WO-US048431.
XX 20-DEC-2000; 2000US-00742703.
XX (ISIS-) ISIS PHARM INC.
XX (ABBO) ABBOTT LAB.
XX Marcotte PA, Cowsett LM;
XX WPI; 2002-519883/55.
XX New antisense oligonucleotides that modulate (particularly inhibit) human
PT hepsin, useful for treating a disease or condition associated with the
PT expression of hepsin, e.g. inflammation or tumor growth.
XX Example 15; Page 82; 101pp; English.
CC The invention relates to an antisense compound 8-30 nucleobases in length
CC targeted to a nucleic acid molecule encoding human hepsin. The antisense
CC compound specifically hybridises with and inhibits the expression of
CC human hepsin. The antisense compound or the pharmaceutical composition is
CC useful for treating animals and humans having a disease or condition
CC associated with the expression of hepsin, e.g. inflammation or tumour
CC growth. The antisense compounds are useful also for diagnostics,
CC prophylaxis (e.g. to prevent or delay infection, inflammation or tumour
CC formation) or as research reagents and kits. The method is useful for
CC modulating, specifically inhibiting the expression of hepsin which may be

CC used in research, e.g to distinguish between functions of various members
CC of a biological pathway. The invention is used in gene therapy. The
CC present sequence is human hepsin antisense oligonucleotide
XX
SQ Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1664 CTCACAGCTGGAGCCCTG 1681
Db 19 CTCACCTGCGGGACCCCTG 2
RESULT 145
ABL94348
ID ABL94348 standard; DNA; 20 BP.
XX AC ABL94348;
XX 29-JUL-2002 (first entry)
XX Mouse C/EBP beta phosphorothioate antisense oligonucleotide, SEQ ID:114.
KW Mouse; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EPB2;
LAP; TCF5; CRP2; NFIL6; IL6BP; NF-M; AGP/EBP; Apc/EBP;
KW transcription factor; tissue development; cellular function;
KW proliferation; differentiation; hormone responsiveness;
KW oxidative stress response; IL-6 signalling mediator; interleukin-6;
KW carbohydrate metabolism; immunity; Th1 response; female fertility;
KW gluconeogenesis; ovarian; cancer; tumour formation; type II; diabetes;
KW infection; inflammation; expression inhibition; phosphorothioate;
antisense oligonucleotide; ss.
XX Mus musculus.
OS
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT cytosines are 5-methylcytosine"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT cytosines are 5-methylcytosine"
XX US6271030-B1.
XX 07-AUG-2001.
XX 14-JUN-2000; 2000US-00593711.
XX 14-JUN-2000; 2000US-00593711.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Butler MM, Wyatt J;
XX WPI; 2002-214451/27.
XX Novel antisense compound targeted to nucleic acids encoding human or
PT mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for
PT inhibiting expression of human or mouse C/EBP beta in cells/tissues.
XX Claim 1; Col 47-48; 69pp; English.
XX

CC Sequences ABL94252-BL94476 represent antisense oligonucleotides targeted
CC to the human or mouse CCAA/enhancer-binding protein alpha (C/EBP alpha)
CC gene, which inhibit its expression. The antisense oligonucleotides were
CC designed to target different regions of the human and/or mouse C/EBP
CC alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels
CC by quantitative real-time PCR. The C/EBP family of proteins are a family
CC of transcription factors which regulate the expression of a wide range of
CC genes that control normal tissue development, cellular function, cellular
CC proliferation and functional differentiation. C/EBP beta (also known as
CC C/EBP2, LAP, TCF5, CRP2, NFIL6, IL6BP, NF-W, AGP/EBP and ApC/EBP)
CC primarily regulates hormone responsiveness and oxidative stress responses
CC and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is
CC thought to be involved in carbohydrate metabolism, immunity, the Th1
CC response, female fertility and gluconeogenic pathways. C/EBP beta is
CC expressed in the liver, lung, spleen, kidney, brain, and testis, with the
CC highest expression found in the lung. It is also expressed at a higher
CC level in malignant ovarian tissue compared with normal ovarian tissue,
CC and its expression in pancreas is upregulated in response to chronically
CC elevated levels of glucose, indicating that it is involved in the
CC impairment of insulin secretion in type II diabetes. The oligonucleotides
CC of the invention are useful for diagnosis, prevention and treatment of
CC conditions associated with C/EBP beta expression, such as cancer
CC (particularly ovarian cancer), tumour formation, diabetes (particularly
CC type II diabetes), infection, or inflammation
XX
XX
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1634 TCGGGCTTGTAGCAGAG 1651
DB 2 TCGGGCTGTAGTAGAAG 19
|||||
|||||

RESULT 146
ABZ86961
ID ABZ86961 standard; DNA; 20 BP.
XX
XX
AC ABZ86961;
XX
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200285308-A2.
XX
XX
PD 31-OCT-2002.
XX
XX
PF 23-APR-2002; 2002WO-US013135.
XX
XX
PR 24-APR-2001; 2001US-0286137P.
XX
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX
DR WPI; 2003-229219/22.
XX
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.
XX
XX
PS Claim 15; SEQ ID NO 2203; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies or a respiratory disease or condition.
CC Note: the sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1685 TCTCTCCAGCGTGTGG 1702
DB 2 TCTCTCCGCGCTGCG 19
|||||
|||||

RESULT 147
ABZ89394/c
ID ABZ89394 standard; DNA; 20 BP.
XX
XX
AC ABZ89394;
XX
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200285308-A2.
XX
XX
PD 31-OCT-2002.
XX
XX
PF 23-APR-2002; 2002WO-US013135.
XX
XX
PR 24-APR-2001; 2001US-0286137P.
XX
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX
DR WPI; 2003-229219/22.
XX
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.
 PS Disclosure; SEQ ID NO 4636; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 3 A; 12 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 9.5%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1699 GTGGAAGTTGGGTAGGA 1716
 Db 20 GGGGAGTTGGGTACGA 3
 XX
 RESULT 148
 ABZ37372
 ID ABZ37372 standard; DNA; 20 BP.
 XX
 AC ABZ37372;
 XX
 DT 18-FEB-2003 (first entry)
 XX
 DE Kappa light chain capture oligonucleotide Readapter SEQ ID NO:468.
 XX
 KW Library; cleavage; display; diverse family; ss.
 XX
 OS Synthetic.
 XX
 FN WO200283872-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 17-APR-2002; 2002WO-US012405.
 XX
 PR 17-APR-2001; 2001US-00837306.
 PR 24-OCT-2001; 2001US-00000516.
 PR 25-OCT-2001; 2001US-00045674.
 XX
 PA (LADN/) LADNER R C.
 PA (COHE/) COHEN E H.
 PA (NAST/) NASTRI H G.
 PA (ROOK/) ROOKEY K L.
 PA (HOET/) HOET R.
 PA (HOOG/) HOOGENDOORN H R J M.
 XX
 XX LADNER RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;
 PI Hoogenboom HRJM;
 PI WPI; 2003-093015/08.
 DR
 XX
 FT Cleaving single-stranded nucleic acid sequences at a desired location by

PT contacting the nucleic acid with an single strand oligonucleotide
 PT complementary to a nucleic acid region where cleavage is desired.
 XX
 PS Example 2; Page 406; 485pp; English.
 XX
 CC The present invention describes a method for cleaving single-stranded
 CC nucleic acid sequences at a desired location. Also described: (1) methods
 CC for displaying or expressing a member of a diverse family of peptides,
 CC polypeptides or proteins on the surface of a genetic package and
 CC collectively displaying at least a part of the diversity of the family,
 CC where the displayed or expressed peptide, polypeptide or protein is
 CC encoded at least in part by a nucleic acid that has been cleaved at a
 CC desired location; (2) a method for preparing single-stranded nucleic
 CC acids; (3) a method for preparing a library comprising a collection of
 CC genetic packages that display a member of a diverse family of peptides,
 CC polypeptides or proteins and that collectively display at least a portion
 CC of the family; (4) a vector comprising a DNA sequence encoding an
 CC antibody variable region linked to a version of PIII anchor which does
 CC not mediate infection of phage particles, and wild-type gene III; (5) a
 CC method for producing a population or a library of immunoglobulin genes;
 CC and (6) a library of immunoglobulins that comprise members having at
 CC least one variable domain in which at least one of CDR1 and CDR2 contain
 CC synthetic diversity and CDR3 diversity is captured from B cells. The
 CC method is useful for cleaving single-stranded nucleic acid sequences at a
 CC desired location, which can be subsequently used to produce libraries of
 CC genetic packages that display and/or express a diverse family of
 CC peptides, polypeptides or proteins. ABZ36912 to ABZ37510 and ABP55464 to
 CC ABP55499 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
 Query Match 9.5%; Score 13.2; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1721 GGAGATGGAGATTGGCTC 1738
 Db 3 GAAGATGGAGATGGGTC 20
 XX
 RESULT 149
 ADB25675
 ID ADB25675 standard; DNA; 20 BP.
 XX
 AC ADB25675;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human connective tissue growth factor antisense oligo DNA (SeqID 68).
 XX
 KW antisense; human; ss; connective tissue growth factor; CTGF;
 KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
 KW fisp-12; NOV2;
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
 KW scleroderma; atherosclerosis; cytostatic; dermatological;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 PN WO2003053340-A2.
 XX
 XX 03-JUL-2003.

XX PF 09-DEC-2002; 2002WO-US038618.
XX PR 10-DEC-2001; 2001US-00006191.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Gaarde WA, Watt AT;
XX DR WPI; 2003-559091/52.
XX PT New antisense oligonucleotides for modulating connective tissue growth
XX PT factor expression, particularly useful for treating cancers (e.g. breast
XX PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
XX PT atherosclerosis.
XX PS Claim 3; Page 86; 139pp; English.
XX CC This invention relates to novel methods for modulating the expression of
XX CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
XX CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
XX CC as ctgrofact, fibroblast inducible secreted protein, flisp-12, NOV2,
XX CC insulin-like growth factor binding protein-related protein 2, IGFBP-rP2,
XX CC IGFBP-8, Hsc24 and ecogenin. It is known to stimulate DNA synthesis and
XX CC promote chemotaxis of fibroblasts, however, it is also upregulated in
XX CC acute lymphoblastic leukaemia and in tumour or endothelial cells
XX CC associated with the vasculature. Accordingly, antisense oligonucleotides
XX CC that inhibit the expression of CTGF in cells or tissues can be used in
XX CC gene therapy to treat various conditions including hyperproliferative
XX CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
XX CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
XX CC such, the present invention describes these antisense oligos as having
XX CC cytotatic, dermatological and antiarteriosclerotic activities. This
XX CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX CC human CTGF of the invention.
XX SQ Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1651 GGCAAGCACCGGCTCAC 1668
Db 3 GTCACGACGAGGCTCAC 20
RESULT 150
ABC47950
ID ABC47950 standard; DNA; 13 BP.
XX AC ABC47950;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 47967 for detecting SNP TSC0013727.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 47968; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 5.4%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1707 TGGGTTAGGAGTA 1719
Db 1 TGGGTTAGGAGTA 13
RESULT 151
ABC47951/c
ID ABC47951 standard; DNA; 13 BP.
XX AC ABC47951;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 47968 for detecting SNP TSC0013727.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 47968; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 9.4%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1707 TGGGTTAGGAGTA 1719
 Db 13 TGGGTTAGGAGTA 1

RESULT 152
 ABF16655
 ID ABF16655 standard; DNA; 13 BP.
 AC ABF16655;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 116652 for detecting SNP TSC0029189.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 116652; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 2 A; 8 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 9.4%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1739 CCAACTCCTCCCT 1751
 Db 1 CCAACTCCTCCCT 13

RESULT 153

ABF16654/C
 ID ABF16654 standard; DNA; 13 BP.

XX AC ABF16654;

XX DT 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 116651 for detecting SNP TSC0029189.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 116651; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 0 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 9.4%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1739 CCAACTCCTCCCT 1751
 Db 13 CCAACTCCTCCCT 1

RESULT 154

AAT50323
 ID AAT50323 standard; RNA; 15 BP.

XX

AC	AAT50323;
XX	11-MAR-1997 (first entry)
DT	Rabbit CETP HH ribozyme target sequence #1580.
XX	Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage; neural lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy; reverse cholesterol transport; high density lipoprotein; therapy; CETP; familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia; peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor; angioplasty restenosis; low density lipoprotein; diabetes; HDL; rabbit; LDL; ss.
XX	Oryctolagus cuniculus.
OS	WO9620279-A1.
XX	04-JUL-1996.
PX	11-DEC-1995; 95WO-US016000.
XX	23-DEC-1994; 94US-00363240.
PR	(RIBO-) RIBOZYME PHARM INC. (WARN) WARNER LAMBERT CO.
XX	Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
PI	WPI; 1996-321852/32.
DR	New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA - useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial hypercholesterolaemia.
XX	Claim 4; Page 43; 72pp; English.
PS	AAT50138-T50359 represent target sequences for the rabbit cholesterol ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT50360- T50546). CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer between plasma lipoproteins. The numbering of the targets refers to the position of the cleavage site in full length CETP. The ribozyme then binds to 5 nucleotides either side of this site. The ribozymes are able to cleave mRNA from the gene encoding CETP, thereby blocking synthesis and/or expression of the mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway can be inhibited (or eliminated) thereby preventing the reduction in size density of the high density lipoproteins (HDL), prolonging HDL half life, and therefore increasing HDL levels. The ribozymes can be used to treat conditions associated with abnormal levels of CETP, specifically atherosclerosis, familial hypercholesterolaemia, peripheral vascular disease, dyslipidaemia, hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, vascular complications of diabetes, transplant, atherectomy and angioplastic restenosis. By inhibiting CETP, the levels of HDL and low density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels). The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH ribozymes target specific regions of the CETP gene, they have low non-specific activity
CC	Sequence 15 BP; 3 A; 6 C; 3 G; 0 T; 3 U; 0 Other;
XX	Query Match 9.4%; Score 13; DB 1; Length 15;
XX	Best Local Similarity 76.9%; Pred.No. 1.8e+02;
XX	Matches 10; Conservative 3; Mismatches 0; Indels 0;
OY	1733 TGGCTCCCACTC 1745 ::: :
DB	3 UGGGUCGCNACUC 15 ::: :
RSULT	155

Query Match 9.4%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1738 CCCAACTCTCTCC 1750
 Db 16 CCCAACTCTCTCC 4

RESULT 156
 ADD19353/c
 ID ADD19353 standard; DNA; 17 BP.

XX AC ADD19353;

XX DT 15-JAN-2004 (first entry)

DE Leptin gene-specific PCR primer #14.

XX KW feline; cat; leptin; leptin inhibitor; obesity; PCR; ss; primer.

XX OS Unidentified.

XX FN JP2003038187-A.

XX PD 12-FEB-2003.

XX PF 31-JUL-2001; 2001JP-00230711.

XX PR 31-JUL-2001; 2001JP-00230711.

XX PA (MOMI) MORINAGA & CO LTD.

XX DE WPI; 2003-527653/50.

PT Novel feline leptin polypeptide encoded by a feline ob gene which is related to obesity in cats, useful for diagnosing and treating obesity.

PS Example; SEQ ID NO 20; 18pp; Japanese.

XX The invention comprises the amino acid and coding sequences of feline leptin proteins. The DNA and protein sequences of the invention are useful for screening for a compound which inhibits the activity of leptin. The DNA and protein sequences of the are also useful for diagnosing and treating obesity. The present DNA sequence represents a PCR primer that was used in an example of the invention.

XX SQ Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 9.4%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1676 ACCCTGGTGTCTC 1688
 Db 13 ACCCTGGTGTCTC 1

RESULT 157

AA160321

ID AAL60321 standard; DNA; 19 BP.

XX AC AAL60321;

XX DT 27-AUG-2003 (first entry)

DE Human Oct-4 specific reverse RT-PCR primer #2.

XX KW Human embryonic stem cells; HES; human; reverse transcription PCR; Oct-4;
 XX KW RT-PCR; primer; ss.

XX OS Homo sapiens.

XX PN W02003040355-A1.
 XX PD 15-MAY-2003.
 XX PF 11-NOV-2002; 2002WO-AU001534.
 XX PR 09-NOV-2001; 2001AU-00008781.
 XX PR 15-MAR-2002; 2002AU-00001129.
 XX PA (ESCE-) ES CELL INT PTE LTD.
 XX PI Pera MF, Laslett A, Hawes S, Gion T;
 XX DR WPI; 2003-449455/42.
 XX PT Identifying a viable subpopulation of human embryonic stem (HES) cells by obtaining a source of HES cells and identifying the subpopulation of HES cells that are at least GCTM-2 positive.
 XX PS Example 1; Page 35; 83pp; English.
 XX CC The invention relates to a method for identifying a viable subpopulation of human embryonic stem (HES) cells. The method involves obtaining a source of HES cells and identifying the subpopulation of HES cells that are at least GCTM-2 positive. The present sequence is human Oct-4 specific reverse transcription PCR (RT-PCR) primer, used to illustrate the method of the invention.
 XX SQ Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 9.4%; Score 13; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1656 GCACCAGGCTCAC 1668
 Db 7 GCACCAGGCTCAC 19

RESULT 158
 ACC40945/c
 ID ACC40945 standard; DNA; 20 BP.
 XX AC ACC40945;
 XX DT 23-MAY-2003 (first entry)
 XX DE Human superoxide dismutase 1 antisense inhibitor # ISIS 150499.
 XX KW Human; superoxide dismutase 1; antisense; neuroprotective; cytostatic; antiinflammatory; amyotrophic lateral sclerosis; apoptosis; hyperproliferative disorder; therapy; infection; inflammation; tumour; ss.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT modified_base 1..20 /tag= a
 XX FT /mod_base= OTHER
 XX FT /note= "Phosphorothioate linkages. All cytosines are 5-methylcytosine"
 XX FT modified_base 1..5 /tag= b
 XX FT /mod_base= OTHER
 XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 XX FT modified_base 16..20 /tag= c
 XX FT /mod_base= OTHER
 XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

/note= 'DyTx-NH(CH2)6-PO4-cytosine'

FT XX WO9429316-A2.
 PN XX 22-DEC-1994.
 PD XX
 PF XX 09-JUN-1994; 94WO-US036284.
 PR XX 09-JUN-1993; 93US-00075123.
 PR XX 14-APR-1994; 94US-00227370.
 XX XX (TEXA) UNIV TEXAS SYSTEM.
 PA (PHAR-) PHARMACYCLICS INC.
 XX XX
 XX Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;
 PI Kral VA, Iverson B, Mody T, Miller RA, Magda D;
 XX WPI; 1995-036382/05.
 DR XX
 XX Texaphyrin metal complex mediated ester hydrolysis - esp. useful for
 PT targeted intracellular hydrolysis of mRNA and for inhibiting gene
 PT expression.
 XX
 PS Disclosure; Fig 21; 125pp; English.
 XX
 CC AAQ91451-Q91457 are texaphyrin lanthanide metal DNA conjugates, which are
 CC esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting
 CC gene expression. They may also be used for the treatment of liver disease,
 CC as hormone regulation agents and as hydrolysis reagents for the
 CC detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 17 BP; 1 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
 Query Match 5.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1655 AGCACCAGGCTCAG 1670
 DB 16 AACACCGGCTCAG 1
 RESULT 160
 AAQ75159/c
 ID AAQ75159 standard; RNA, 17 BP.
 XX
 AC AAQ75159;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #687.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Mus sp.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX

PN XX WO2003000707-A2.
 PD XX 03-JAN-2003.
 PF XX 19-JUN-2002; 2002WO-US019664.
 PR XX 21-JUN-2001; 2001US-00888360.
 PR XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett FC, Dobie K;
 PI WPI; 2003-184032/18.
 DR XX
 XX Novel antisense compounds targeted to nucleic acids encoding human
 PT superoxide dismutase 1, for modulating expression of the dismutase and
 PT treating diseases or conditions, e.g. amyotrophic lateral sclerosis.
 FT
 PS Claim 3; Page 77; 107pp; English.
 XX
 CC The invention relates to a compound of 8-50 nucleobases in length,
 CC targeted to a nucleic acid molecule encoding human superoxide dismutase
 CC 1. The compound specifically hybridises with and inhibits the expression
 CC of human superoxide dismutase 1 by hybridising with at least an 8-
 CC nucleobase portion of the nucleic acid molecule encoding the active site
 CC of the enzyme. The activity of compounds of the invention may be
 CC described as neuroprotective, cytostatic and antiinflammatory. The
 CC mechanism of action of compounds of the invention is antisense inhibition
 CC of human superoxide dismutase 1 expression by chimeric phosphorothioate
 CC oligonucleotides having 2'-methoxyethyl (2'-MOE) wings and a deoxy gap.
 CC Compounds of the invention are useful for inhibiting the expression of
 CC human superoxide dismutase 1 in human cells or tissues, and for treating
 CC a disease or condition associated with this enzyme (antisense therapy),
 CC especially amyotrophic lateral sclerosis, a disease or condition arising
 CC from aberrant apoptosis and a hyperproliferative disorder. It may also be
 CC used in diagnostics, therapeutics and as a research reagent, e.g.
 CC prophylactically to prevent or delay infection, inflammation or tumour
 CC formation. Sequences given in records ACC40880-ACC40957 represent human
 CC superoxide dismutase 1 antisense inhibitor oligonucleotides
 XX
 SQ Sequence 20 BP; 1 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 9.4%; Score 13; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1644 AGCAGAAGGCAAG 1656
 DB 18 AGCAGAAGGCAAG 6
 RESULT 159
 AAQ91452/c
 ID AAQ91452 standard; DNA, 17 BP.
 XX
 AC AAQ91452;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-AUG-1995 (first entry)
 XX
 DE Dysprosium (III) texaphyrin (DyTx) DNA conjugate.
 XX
 KW Dysprosium (III) texaphyrin (DyTx) DNA conjugate; liver disease;
 KW targeted intracellular mRNA hydrolysis; gene expression inhibition;
 KW hormone regulation; hydrolysis reagents; alkyl phosphate esters;
 KW detoxification; ss.
 XX
 OS Synthetic.
 XX
 PN Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT

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PI Pavco P, Meswigen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 175; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 0 A; 4 C; 7 G; 0 T; 6 U; 0 Other;
SQ
Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1646 CAGAGGCGCAACCA 1661
DB ||||| ||||| |||
17 CAGAGCCGCGCCCA 2
RESULT 161
AAV07298/c
ID AAV07298 standard; DNA; 17 BP.
XX
XX AAV07298;
AC
XX
XX 14-AUG-1998 (first entry)
DT
XX
DE Metallotexaphyrin-oligonucleotide conjugate #12.
DE
XX Metallotexaphyrin; dysprosium; europium; conjugate; RNase H;
KW antisense therapy; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /mod_base
XX /note= "DyTxNH-(CH2)6-PO4-cytosine, where DyTx is
XX dysprosium (III) texaphyrin"
XX
XX US5763172-A.
XX
XX 09-JUN-1998.
XX
XX 07-JUN-1995; 95US-00486962.
XX
XX 21-JAN-1992; 92US-00822964.
XX 09-JUN-1993; 93US-00075123.
XX 14-APR-1994; 94US-00227370.
XX 09-JUN-1994; 94WO-US006284.
XX 26-MAY-1995; 95US-00452261.
XX 07-JUN-1995; 95US-00485581.
XX (PHAR-) PHARMACYCLICS INC.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Sessler JL, Wright M, Miller RA, Dow WC, Magda D;
XX WPI; 1998-347306/30.
XX

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XX Enhancing therapeutic activity of oligo-nucleotides in cells - using
PT conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester
PT bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.
XX
XX Example 6; Fig 5; 34pp; English.
XX
XX The invention relates to a method of enhancing the therapeutic activity
CC of oligonucleotides in cells. It comprises contacting a targeted
CC intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide
CC conjugate. The contact is carried out under physiological conditions for
CC a time sufficient to hydrolyse the phosphate ester bond of the targeted
CC RNA. The metallotexaphyrin of the conjugate has catalytic activity for
CC phosphate ester bond hydrolysis. The oligonucleotide of the conjugate has
CC complementary binding affinity to the targeted RNA. The conjugate may be
CC used in antisense therapies for treating, e.g. cancer, viral infections,
CC autoimmune diseases and restenosis. The conjugate may also be used as
CC hydrolysis reagents for the detoxification of di- and trialkyl phosphate
CC esters, which are used in solvents, insecticides and chemical nerve
CC gases. The metallotexaphyrin complex enhances the therapeutic activity of
CC the oligonucleotide, not only by facilitating cellular uptake of the
CC oligonucleotide but also by hydrolysing target RNA within the cell,
CC independent of RNase H. Attachment to the complex may also cause the
CC oligonucleotide to take on some of the pharmacodynamic and biodistribution
CC properties of the texaphyrin, such as selective localisation in tumours.
CC The present sequence represents a metallo- texaphyrin-oligonucleotide
XX conjugate
XX
XX Sequence 17 BP; 1 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
SQ
Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1655 AGCACCAGGCTCACAG 1670
DB ||||| ||||| |||||
16 AACCCCGGCTCACAG 1
RESULT 162
AAV91007/c
ID AAV91007 standard; RNA; 17 BP.
XX
XX AAV91007;
AC
XX
XX 18-FEB-1999 (first entry)
DT
XX
DE Human C-raf target site nucleotide position 582.
DE
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
XX Homo sapiens.
XX
XX WO9850530-A2.
XX
XX 12-NOV-1998.
XX
XX 05-MAY-1998; 98WO-US009249.
XX
XX 09-MAY-1997; 97US-0046059P.
XX 09-JUN-1997; 97US-0049002P.
XX 03-JUL-1997; 97US-0051718P.
XX 22-AUG-1997; 97US-0056808P.
XX 02-OCT-1997; 97US-0061321P.
XX 02-OCT-1997; 97US-0061321P.
XX 05-NOV-1997; 97US-0064866P.
XX 19-DEC-1997; 97US-0068212P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX

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XX	Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;	02-OCT-1997; 97US-0061321P.
PI	Parry T, Beigelman L, McSwiggen JA, Karpeisky A, Burgin A;	05-OCT-1997; 97US-0061324P.
PI	Thompson J, Workman CT, Beaudry A, Sweedler D;	05-NOV-1997; 97US-0064866P.
XX	WPI; 1999-009494/01.	19-DEC-1997; 97US-0068212P.
XX	Identifying new catalytic nucleic acid that modulates selected processes	(RIBO-) RIBOZYME PHARM INC.
XX	- especially ribozymes that cleave Raf RNA for treating cancer,	Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PT	restenosis, and also new ribozymes and modified nucleoside triphosphates	Parry T, Beigelman L, McSwiggen JA, Karpeisky A, Burgin A;
PT	used as antiviral agents and synthons.	Thompson J, Workman CT, Beaudry A, Sweedler D;
XX	Claim 177; Page 147; 259pp; English.	WPI; 1999-009494/01.
XX	A method has been developed for the identification of a nucleic acid	Identifying new catalytic nucleic acid that modulates selected processes
CC	capable of modulating a process in a biological system. The method	- especially ribozymes that cleave Raf RNA for treating cancer,
CC	comprises: (a) introducing into the system a random library of nucleic	restenosis, and also new ribozymes and modified nucleoside triphosphates
CC	acid catalysts (NAC) having a substrate binding domain (SBD), comprising	used as antiviral agents and synthons.
CC	a random sequence, and a catalytic domain (CD); and (b) identifying NAC	Claim 177; Page 147; 259pp; English.
CC	in systems where modulation has occurred and/or determining the sequence	A method has been developed for the identification of a nucleic acid
CC	of at least part of the SBDs in such systems. Nucleic acid molecules with	capable of modulating a process in a biological system. The method
CC	endonuclease activity and catalytic activity, from the present invention,	comprises: (a) introducing into the system a random library of nucleic
CC	cleave target nucleic acid, particularly for treating systemic diseases	acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC	caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic	a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC	ascites and infection. They may also be used to detect genetic drift and	in systems where modulation has occurred and/or determining the sequence
CC	mutations in diseased cells and to determine c-rat. Specifically NACs	of at least part of the SBDs in such systems. Nucleic acid molecules with
CC	with RNA-cleaving activity that modulate expression of the Raf gene, are	endonuclease activity and catalytic activity, from the present invention,
CC	used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or	cleave target nucleic acid, particularly for treating systemic diseases
CC	generally any condition associated with the level of c-rat. Introduction	caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC	of sugar/phosphate modifications increases stability against nuclease and	ascites and infection. They may also be used to detect genetic drift and
CC	activity. AA930922 to AA93877 represent NACs that can be used in the	mutations in diseased cells and to determine c-rat. Specifically NACs
CC	method, specifically for modulating the expression of a Raf gene	with RNA-cleaving activity that modulate expression of the Raf gene, are
XX	Sequence 17 BP; 2 A; 5 C; 3 G; 0 T; 7 U; 0 Other;	used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX	Query Match 9.2%; Score 12.8; DB 1; Length 17;	generally any condition associated with the level of c-rat. Introduction
XX	Best Local Similarity 87.5%; Pred. No. 2.4e+02;	of sugar/phosphate modifications increases stability against nuclease and
XX	Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	activity. AA930922 to AA93877 represent NACs that can be used in the
QY	1641 TGTCACAGAGCAAG 1656	method, specifically for modulating the expression of a Raf gene
DB	16 TGTCACAGAGCAAG 1	Sequence 17 BP; 2 A; 5 C; 3 G; 0 T; 7 U; 0 Other;
RESULT 163	AA93413/c	Query Match 9.2%; Score 12.8; DB 1; Length 17;
ID	AA93413 standard; RNA; 17 BP.	Best Local Similarity 87.5%; Pred. No. 2.4e+02;
XX	AA93413;	Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX	18-FEB-1999 (first entry)	QY 1641 TGTCACAGAGCAAG 1656
DE	Human B-raf substrate nucleotide position 833.	DB 16 TGTCACAGAGCAAG 1
XX	Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;	RESULT 163
KW	target; substrate; catalyst; modulation; expression; Raf gene; delivery;	AA93413/c
KW	screening; identification; synthesis; deprotection; purification; cancer;	ID AA93413 standard; RNA; 17 BP.
KW	inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;	XX AA93413;
KW	restenosis; rheumatoid arthritis; ss.	XX 18-FEB-1999 (first entry)
OS	Homo sapiens.	DE Human B-raf substrate nucleotide position 833.
XX	WO9805030-A2.	XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX	12-NOV-1998.	KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
XX	05-MAY-1998; 98WO-US009249.	KW screening; identification; synthesis; deprotection; purification; cancer;
XX	09-MAY-1997; 97US-0046059P.	KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
PR	09-JUN-1997; 97US-0049002P.	KW restenosis; rheumatoid arthritis; ss.
PR	03-JUL-1997; 97US-0051718P.	OS Homo sapiens.
PR	22-AUG-1997; 97US-0056808P.	XX WO9805030-A2.
XX		XX 12-NOV-1998.
XX		XX 05-MAY-1998; 98WO-US009249.
XX		XX 09-MAY-1997; 97US-0046059P.
XX		XX 09-JUN-1997; 97US-0049002P.
XX		XX 03-JUL-1997; 97US-0051718P.
XX		XX 22-AUG-1997; 97US-0056808P.

[illegible]

PF 05-MAY-1998; 98WO-US009249.
 XX
 PR 09-MAY-1997; 97US-0046059P.
 PR 09-JUN-1997; 97US-0049002P.
 PR 03-JUL-1997; 97US-0051718P.
 PR 22-AUG-1997; 97US-0056808P.
 PR 02-OCT-1997; 97US-0061321P.
 PR 02-OCT-1997; 97US-0061324P.
 PR 05-NOV-1997; 97US-0064866P.
 PR 19-DEC-1997; 97US-0068212P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX
 XX WPI; 1999-009494/01.
 XX
 XX Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer,
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 PT used as antiviral agents and synthons.
 XX
 PS Claim 177; Page 167; 259pp; English.
 XX
 CC A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugarphosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene
 XX
 SQ Sequence 17 BP; 1 A; 6 C; 5 G; 0 T; 5 U; 0 Other;
 Query Match 9.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1667 ACAGCTGGAACCCCTGG 1682
 Db 16 ACAGCGGAACCCCTGG 1
 RESULT 165
 AAA79844
 ID AAA79844 standard; DNA; 17 BP.
 AC AAA79844;
 XX
 XX 20-NOV-2000 (first entry)
 DT
 DE Hepatitis B virus related oligonucleotide probe #107.
 XX
 XX Hepatitis B virus; HBV; Hepatitis A virus; HAV; probe; detection;
 KW mutation; high-density gene chip; ss.
 XX
 XX Hepatitis B virus.
 OS
 XX
 XX CN1252452-A.
 PN

XX 10-MAY-2000.
 XX
 XX 24-SEP-1999; 99CN-00114460.
 XX
 XX 24-SEP-1999; 99CN-00114460.
 XX
 XX (UYDO-) UNIV DONGNAN.
 XX
 XX Sun X, Lu Z, Wang Y;
 XX
 XX WPI; 2000-443233/39.
 XX
 XX High-density gene chip making process.
 PT
 XX
 XX Example 1; Fig 15; 19pp; Chinese.
 XX
 XX The present invention describes a method which comprises making a high-
 CC density gene chip, specifically for making high-density micro-array of
 CC oligonucleotide probes. An oligonucleotide probe selecting process to
 CC seek preferentially length variable and coverage variable probes is
 CC provided to ensure identical cross melting temperature of probes to the
 CC maximum limit, and this can make the cross control of gene chip
 CC relatively simple and raise the reliability of the gene chip detecting
 CC results. The process proposes a specific probe selection method for
 CC detecting target sequence directly, detecting mutation in both specific
 CC and non-specific sites and a probe overall arrangement scheme. AAA79738
 CC to AAA80201 represent oligonucleotide probe sequences which are used in
 CC examples from the present invention
 XX
 SQ Sequence 17 BP; 4 A; 1 C; 10 G; 2 T; 0 U; 0 Other;
 Query Match 9.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1713 AGGAGTACGGAGATGG 1728
 Db 1 AGGAGGACGGAGTGG 16
 RESULT 166
 ABS97987/C
 ID ABS97987 standard; DNA; 17 BP.
 XX
 AC ABS97987;
 XX
 XX 23-DEC-2002 (first entry)
 DT
 DE Human urokinase gene (uPA) PCR primer #2.
 XX
 XX Human; ss; primer; cytochrome P450 A1; CYP450A1A1; UGT2B4; MDR1; PCR;
 KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thiolabile; STM;
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KW multidrug resistance associated protein 3; cancer; prostate;
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR5;
 KW altered drug metabolism; cardiovascular function; colorectal tumour;
 KW central nervous system; pulmonary; immunological.
 XX
 OS Homo sapiens.
 XX
 XX WO200257410-A2.
 XX
 XX 25-JUL-2002.
 PD

09-APR-2002 (first entry)
 Human ERG G-cleaver ribozyme target sequence Seq ID No 1307.
 Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 tumour angiogenesis; diabetic retinopathy; macular degeneration;
 neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 angiofibroma of tuberosus scleriosis; port-wine stain; wound healing;
 Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
 amberzyme.
 Homo sapiens.
 OS
 XX
 WO2001188124-A2.
 XX
 22-NOV-2001.
 PD
 XX
 16-MAY-2001; 2001WO-US015866.
 PF
 XX
 16-MAY-2000; 2000US-00572021.
 PR
 XX
 (RIBO-) RIBOZYME PHARM INC.
 (GLAX) GLAXO GROUP LTD.
 PA
 XX
 Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 WPI; 2002-082995/11.
 XX
 Novel polynucleotide which down regulates expression of Ets-related gene,
 useful for treating cancer, diabetic retinopathy, macular degeneration,
 arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 PT
 XX
 Claim 4; Page 84; 149pp; English.
 PS
 XX
 The invention relates to a nucleic acid molecule (I) which down regulates
 expression of an Ets-related gene (ERG). (I) is useful for treating
 conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 tumour angiogenesis, diabetic degeneration, arthritis, psoriasis, verruca
 vulgaris, angiofibroma of tuberosus scleriosis, port-wine stains, Sturge
 syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 treating a patient having a condition associated with the level of ERG,
 by contacting cells of the patient with (I) under conditions suitable for
 the treatment. The method comprises the use of one or more therapies
 under conditions suitable for the treatment. Leukaemia or tumour
 angiogenesis is treated by administering (I) to the patient in
 conjunction with one or more of other therapies such as radiation or
 chemotherapy treatment. (I) is useful for reducing ERG activity in a
 cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 ERG gene, by contacting (I) with RNA, in the presence of a divalent
 cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 diseases related to the expression of ERG, and as diagnostic tool to
 examine genetic drift and mutations within diseased cells or to detect
 the presence of ERG RNA in a cell. (I) is useful for specifically
 targeting genes that share homology with ERG gene or ERG fusion genes.
 CC
 ABK17354-ABK22719 represent nucleic acids, including antisense and
 enzymatic nucleic acid molecules which regulate expression of ERG, and
 related PCR primers of the invention
 CC
 XX
 Sequence 17 BP; 4 A; 3 C; 7 G; 0 T; 3 U; 0 Other;
 SQ
 Query Match 9.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1674 GAACCTCGTGTCTCC 1689
 DB 16 GAACCTCGTGTCTCC 1

28-NOV-2001; 2001WO-US044838.
 28-NOV-2000; 2000US-00724389.
 (DNAS-) DNA SCI LAB INC.
 Guida M, Hall J;
 WPI; 2002-698522/75.
 Isolated nucleic acid molecules having polymorphisms in known human genes
 e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
 for locating, identifying and characterizing the genes responsible for
 disorder-related traits.
 Example 21; Page 138; 714pp; English.
 This invention relates to the sequence of an isolated nucleic acid
 molecule comprising at least one base variation from that of a known
 human cytochrome p450 A1 (CYP450A1), cytochrome p450 A2 (CYP450A2),
 cytochrome p450 2E1 (CYP4502E1), adrenergic receptor beta1 (ADRB1),
 aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
 protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 transferase (HNMT), (kallikrein 2) KLK2, nicotinamide-N-methyl
 transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 transferase (UGT2B15), uronkinase receptor (UFA), multidrug resistance 1
 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
 (MRP3), orphan nuclear receptor (NRI12), or acetylcholine muscarinic
 receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 The polymorphisms in the human genes cited in the invention are useful as
 genetic linkage markers for locating and characterizing the genes that
 are responsible for specific traits within the genome and eventually
 identifying the genes responsible for a variety of disorder-related
 traits as a result of their e.g., overexpression, constitutive
 expression, mutation or underexpression, which may be used in diagnosing
 and/or treating the disorders. The nucleic acid molecules comprising the
 polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,
 AHR, EPHX2, GST12, NRI12, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 MDR1 and/or MDR3 are useful for screening individuals for altered drug
 metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
 AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 used to screen for altered cardiovascular function, in COX2 for altered
 susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 nervous system function, in FLAP and HNMT for altered pulmonary,
 immunological or haematological function, in KLK2 for altered serine
 protease activity in the prostate, in LTF for altered immunological or
 haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 peripheral nervous system function. The present sequence represents a PCR
 primer used to amplify the sequences of the invention
 XX
 SQ
 Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 9.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1670 GCTGGACCTGGTGTCT 1685
 DB 17 GCTGGACCTGGTGTCT 2
 RESULT 167
 ID ABK18660/c
 XX ABK18660 standard; RNA; 17 BP.
 AC ABK18660;
 XX

RESULT 168
 ABK17683/c
 ID ABK17683 standard; RNA; 17 BP.
 XX AC
 XX ABK17683;
 XX 09-APR-2002 (first entry)
 DT
 DE Human ERG hammerhead ribozyme target sequence, Seq ID No 330.
 XX
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge-Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rena syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
 KW amberzyme.
 XX
 OS Homo sapiens.
 XX
 XX WO200188124-A2.
 XX
 XX 22-NOV-2001.
 PD
 PF 16-MAY-2001; 2001WO-US015866.
 XX
 PR 16-MAY-2000; 2000US-00572021.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 XX WPI; 2002-082995/11.
 DR
 XX Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX
 PS Claim 4; Page 64; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rena
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 3 A; 3 C; 7 G; 0 T; 4 U; 0 Other;
 Query Match 9.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1734 GGCTCCCAACTCTCC 1749
 Db 16 GGCTCCCAACTCTCC 1

RESULT 169
 ABL31561/c
 ID ABL31561 standard; DNA; 17 BP.
 XX AC
 XX ABL31561;
 XX 21-MAR-2002 (first entry)
 DT
 DE Human HLA genotyping oligonucleotide SEQ ID NO 1050.
 XX
 KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
 KW immunogenetic; transplantation; genetic disease; ss.
 KW
 OS Homo sapiens.
 XX
 XX WO200192572-A1.
 XX
 XX 06-DEC-2001.
 PD
 PF 01-JUN-2001; 2001WO-JP004662.
 XX
 PR 01-JUN-2000; 2000JP-00164798.
 XX
 PA (NIN) NISSHINBO IND INC.
 PA (SYST-) SYSTEM RES INC.
 XX
 PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
 XX WPI; 2002-122074/16.
 DR
 XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
 PT individuals e.g. by determining immunogenetic differences when
 PT transplanting between them.
 XX
 PS Claim 10; Page 292; 345pp; Japanese.
 XX
 CC The invention relates to a typing kit for judging human leukocyte antigen
 CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
 CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
 CC genes e.g. belonging to HLA class I antigens on human genome and
 CC containing gene polymorphisms as alloantigens have been immobilised as
 CC primers for amplification of cleaved nucleic acids relating to gene
 CC polymorphisms. The method is useful for judging HLA genotypes of
 CC individuals by determining immunogenetic differences before transplanting
 CC between them, providing genetic information to decide compatibility of
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
 CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
 CC diagnosis of genetic diseases and identifying individuals
 XX
 SQ Sequence 17 BP; 4 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 9.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1734 GGCTCCCAACTCTCC 1749
 Db 16 GGCTCCCAACTCTCC 1

RESULT 170
 ACC53446
 ID ACC53446 standard; DNA; 17 BP.
 XX AC
 AC ACC53446;

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XX 27-JUN-2003 (first entry)
 XX Human tumour suppressor sequence #2213.
 DE ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 XX tumour regression; apoptosis; virus resistance; diagnosis;
 KW cellular degeneration.
 KW Homo sapiens.
 OS FR2826373-A1.
 XX 27-DEC-2002.
 PD 20-JUN-2001; 2001FR-00008139.
 XX 20-JUN-2001; 2001FR-00008139.
 PF (MOLE-) MOLECULAR ENGINEERS LAB SA.
 XX Tuijnder M, Telerman A, Amson R;
 XX WPI; 2003-250498/25.
 XX New nucleic acid sequences associated with tumor suppression, regression,
 PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.
 XX Claim 1; Page 551; 798pp; French.
 PS This sequence represents an isolated nucleic acid sequence associated
 XX with tumor suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumor cells or cellular degeneration
 XX Sequence 17 BP; 3 A; 1 C; 7 G; 6 T; 0 U; 0 Other;
 SQ Query Match 9.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1693 AGCGTGGTGAAGTTG 1708
 DB 2 ATCGTGTGGAAGTTG 17
 RESULT 171
 ACDS2214
 ID ACDS2214 standard; RNA; 17 BP.
 XX AC ACDS2214;
 XX 24-SEP-2003 (first entry)
 DT HBV inozyme substrate sequence #293.
 DE Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 XX RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX Hepatitis B virus.
 OS WO200281494-A1.
 XX

PD 17-OCT-2002.
 XX 26-MAR-2002; 2002WO-US009187.
 PF 26-MAR-2001; 2001US-00817879.
 XX 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0295876P.
 PR 24-OCT-2001; 2001US-0333059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEF/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 DR Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX Example 1; Page 155; 387pp; English.
 PS The present invention relates to nucleic acid molecules which modulate
 XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberyne sequences
 CC disclosed in the present invention
 XX Sequence 17 BP; 2 A; 3 C; 5 G; 0 T; 7 U; 0 Other;
 SQ Query Match 9.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 56.2%; Pred. No. 2.4e+02;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1672 TGGAAACCTCGTGTCT 1687
 DB 2 UGGAACCUUGUGUCU 17
 RESULT 172
 ACDS3479
 ID ACDS3479 standard; RNA; 17 BP.
 XX AC ACDS3479;
 XX 24-SEP-2003 (first entry)
 DT HBV G-cleaver substrate sequence #167.
 DE Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 XX RNA stability; RNA expression; RNA synthesis; antisense;
 KW

XX PN WO2003037931-A2.
XX PN 08-MAY-2003.
XX PF 01-NOV-2002; 2002WO-US035129.
XX PR 01-NOV-2001; 2001US-0334773P.
XX PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX PI Shannon M, Phan T;
XX PI WPI; 2003-430501/40.
XX XX New isolated nucleic acid molecule encoding a human angiominin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 62; 172pp; English.
XX CC The present invention describes the human angiominin-like protein 1
CC (AMLP1). human AMLP1 has cytotostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1, which is used in an example from the
CC present invention.
XX XX Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
SQ Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 1716 AGTACGGAGATGGAGA 1731
DB 2 AATACGGTGTGGAGA 17
RESULT 175
ADC37714
ID ADC37714 standard; DNA; 17 BP.
AC ADC37714;
XX DT 18-DEC-2003 (first entry)
XX DE Human AMLP1 scanning 17-mer oligonucleotide SEQ ID NO:63.
XX XX human; angiominin-like protein 1; AMLP1; cytotostatic; gene therapy;
XX KW AMLP1; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003037931-A2.
XX XX 08-MAY-2003.
XX PF 01-NOV-2002; 2002WO-US035129.
XX PR 01-NOV-2001; 2001US-0334773P.
XX PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX PI Shannon M, Phan T;
XX PI WPI; 2003-430501/40.
XX XX New isolated nucleic acid molecule encoding a human angiominin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 62; 172pp; English.
XX CC The present invention describes the human angiominin-like protein 1
CC (AMLP1). human AMLP1 has cytotostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1, which is used in an example from the
CC present invention.
XX XX Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
SQ Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 1716 AGTACGGAGATGGAGA 1731
DB 2 AATACGGTGTGGAGA 17
RESULT 175
ADC37714
ID ADC37714 standard; DNA; 17 BP.
AC ADC37714;
XX DT 18-DEC-2003 (first entry)
XX DE Human AMLP1 scanning 17-mer oligonucleotide SEQ ID NO:63.
XX XX human; angiominin-like protein 1; AMLP1; cytotostatic; gene therapy;
XX KW AMLP1; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003037931-A2.
XX XX 08-MAY-2003.
XX PF 01-NOV-2002; 2002WO-US035129.
XX PR 01-NOV-2001; 2001US-0334773P.
XX PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX PI Shannon M, Phan T;
XX PI WPI; 2003-430501/40.
XX XX New isolated nucleic acid molecule encoding a human angiominin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 63; 172pp; English.
XX CC The present invention describes the human angiominin-like protein 1
CC (AMLP1). human AMLP1 has cytotostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1, which is used in an example from the
CC present invention.
XX XX Sequence 17 BP; 7 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
SQ Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 1716 AGTACGGAGATGGAGA 1731
DB 1 AATACGGTGTGGAGA 16
RESULT 176
ADD20651
ID ADD20651 standard; DNA; 17 BP.
XX AC ADD20651;
XX DT 15-JAN-2004 (first entry)
XX DE Oreochromis niloticus microsatellite primer SEQ ID NO:1286.
XX KW single nucleotide polymorphism; SNP; fish; Salmo salar;
XX KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod;
XX KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
XX KW detection; primer; ss.
XX OS Synthetic.
XX OS Oreochromis niloticus.
XX PN WO2003060160-A2.
XX XX 24-JUL-2003.
XX PF 17-JAN-2003; 2003WO-IB000112.
XX PR 18-JAN-2002; 2002US-0349950P.
XX PR 16-AUG-2002; 2002US-0404200P.
XX PA (GENO-) GENOMAR ASA.
XX PI Lie O, Slettan A, Hoyum M, Lingaas F;
XX XX WPI; 2003-627388/59.
XX PT Novel isolated nucleic acid molecule comprising single nucleotide
PT polymorphism associated with fish, useful for forming PCR primers which
PT are used for detecting single nucleotide polymorphisms in fish nucleic
PT acids.
XX PS Claim 18; SEQ ID NO 1286; 233pp; English.
XX CC The present invention describes an isolated nucleic acid (I) comprising a
CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
CC Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
CC and (ii) a nucleic acid having nucleotide sequence that hybridises to
CC (i), or its complement under highly stringent hybridisation conditions.
CC Also described: (1) an isolated oligonucleotide (II) comprising at least
CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC polymorphic sites and seabass polymorphic sites, or their complement; (2)

CC a primer pair (III) suitable for use in PCR, comprising two (II) capable
 CC of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.
 CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
 CC polymorphic sites and seabass polymorphic sites; and determining (M1) the
 CC origin of fish sample comprising providing a parentage genotype database
 CC comprising a collection of candidate parent genotypes, where each of the
 CC candidate parent genotype represents a distinct origin, and comparing a
 CC sample genotype to the parentage genotype database, where a match between
 CC the sample genotype and one of the candidate parent genotype identifies
 CC to the origin of the sample. (M1) is useful for determining the origin of
 CC a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
 CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
 CC detecting nucleic acid molecule comprising SNP in a sample, which
 CC involves contacting the sample containing nucleic acids with one or more
 CC (III) derived from nucleotide sequence of S. salar SNPs and O. niloticus
 CC SNPs, and identifying nucleic acid that hybridises to (II). (II) is
 CC useful for detecting nucleic acid molecule comprising a polymorphic
 CC sequence in a sample, comprising contacting the sample containing nucleic
 CC acids with one or more (II) which is derived from O. niloticus
 CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
 CC sites or seabass polymorphic sites, and identifying a nucleic acid that
 CC hybridises to (II). (III) is useful for detecting nucleic acid molecule
 CC comprising a microsatellite sequence in sample. The present sequence is
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 17 BP; 0 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1677 CCTGTGTCCTCTCC 1692

DB 1 CCTGTGTCCTCTCC 16

RESULT 177

AAQ91453/c

ID AAQ91453 standard; DNA; 18 BP.

XX
 AC AAQ91453;

XX 25-MAR-2003 (revised)

DT 30-AUG-1995 (first entry)

XX
 XX

DE Dysprosium (III) texaphyrin (DyTx) DNA conjugate.

XX
 KW Dysprosium (III) texaphyrin (DyTx) DNA conjugate; liver disease;
 KW targeted intracellular mRNA hydrolysis; gene expression inhibition;
 KW hormone regulation; hydrolysis reagents; alkyl phosphate esters;
 KW detoxification; ss.

XX
 OS Synthetic.

XX
 OS

XX
 FH Key

FT modified_base 1 Location/Qualifiers

FT /*tag= a

FT /mod_base= OTHER

FT /note= "DyTx-NH(CH2)6-PO4-thymine"

XX
 PN WO9429316-A2.

XX
 PD 22-DEC-1994.

XX
 PF 09-JUN-1994; 94WO-US006284.

XX
 PR 09-JUN-1993; 93US-00075123.

XX
 PR 14-APR-1994; 94US-00227370.

XX
 PA (TEXA) UNIV TEXAS SYSTEM.

XX (PHAR-) PHARMACYCLICS INC.

XX
 PI Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;

PI Kral VA, Iverson B, Mody T, Miller RA, Magda D;

XX
 DR WPI; 1995-036382/05.

XX
 PT Texaphyrin metal complex mediated ester hydrolysis - esp. useful for
 PT targeted intracellular hydrolysis of mRNA and for inhibiting gene
 PT expression.

XX
 PS Disclosure; Fig 21; 125pp; English.

XX
 CC AAQ91451-091457 are texaphyrin lanthanide metal DNA conjugates, which are

CC esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting
 CC gene expression. They may also be used for the treatment of liver disease,
 CC as hormone regulation agents and as hydrolysis reagents for the
 CC detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX
 SQ Sequence 18 BP; 1 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAG 1670

DB 17 AACACCCGCTCACAG 2

RESULT 178

AAV07301/c

ID AAV07301 standard; DNA; 18 BP.

XX
 AC AAV07301;

XX 14-AUG-1998 (first entry)

DT
 XX

DE Metallotexaphyrin-oligonucleotide conjugate #15.

XX
 KW Metallotexaphyrin; dysprosium; europium; conjugate; RNase H;
 KW antisense therapy; ss.

XX
 OS Synthetic.

XX
 FH Key

FT modified_base 1 Location/Qualifiers

FT /*tag= a

FT /mod_base

FT /note= "DyTxNH-(CH2)6-PO4-thymine, where DyTx is
 XX dysprosium (III) texaphyrin"

XX
 PN US5763172-A.

XX
 PD 09-JUN-1998.

XX
 PF 07-JUN-1995; 95US-00486962.

XX
 PR 21-JAN-1992; 92US-00822964.

XX
 PR 09-JUN-1993; 93US-00075123.

XX
 PR 14-APR-1994; 94US-00227370.

XX
 PR 09-JUN-1994; 94WO-US006284.

XX
 PR 26-MAY-1995; 95US-00452261.

XX
 PR 07-JUN-1995; 95US-00485581.

XX
 PA (PHAR-) PHARMACYCLICS INC.

XX (TEXA) UNIV TEXAS SYSTEM.

XX
 PI Sessler JL, Wright M, Miller RA, Dow WC, Magda D;

XX
 DR WPI; 1998-347306/30.

XX
 XX

XX
 PT Enhancing therapeutic activity of oligo-nucleotides in cells - using
 PT conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester
 bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.

XX Example 6; Fig 5; 34pp; English.

XX The invention relates to a method of enhancing the therapeutic activity

XX of oligonucleotides in cells. It comprises contacting a targeted

XX intracellular RNA in a cell with a metallothexaphyrin-oligonucleotide

XX conjugate. The contact is carried out under physiological conditions for

XX a time sufficient to hydrolyse the phosphate ester bond of the targeted

XX RNA. The metallothexaphyrin of the conjugate has catalytic activity for

XX phosphate ester bond hydrolysis. The oligonucleotide of the conjugate has

XX complementary binding affinity to the targeted RNA. The conjugate may be

XX used in antisense therapies for treating, e.g. cancer, viral infections,

XX autoimmune diseases and retinosis. The conjugate may also be used as

XX hydrolysis reagents for the detoxification of di- and trialkyl phosphate

XX esters, which are used in solvents, insecticides and chemical nerve

XX gases. The metallothexaphyrin complex enhances the therapeutic activity of

XX the oligonucleotide, not only by facilitating cellular uptake of the

XX oligonucleotide but also by hydrolysing target RNA within the cell.

XX independent of RNase H. Attachment to the complex may also cause the

XX oligonucleotide to take on some of the pharmacodynamic and biodistribution

XX properties of the texaphyrin, such as selective localisation in tumours.

XX The present sequence represents a metallo- texaphyrin-oligonucleotide

XX conjugate

XX

XX Sequence 18 BP; 1 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

XX

Query Match 9.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670

Db 17 AACACCGGCTCAG 2

RESULT 179

AAA92642

ID AAA92642 standard; DNA; 18 BP.

XX

AC AAA92642;

XX

DT 04-JAN-2001 (first entry)

XX

DE Antisense oligonucleotide ISIS# 30365.

XX

XX Human; SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;

XX SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.

XX

OS Synthetic.

XX

XX US6107092-A.

XX

PD 22-AUG-2000.

XX

XX 29-MAR-1999; 99US-00280409.

XX

XX 29-MAR-1999; 99US-00280409.

XX

XX (ISIS-) ISIS PHARM INC.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX

XX Cowsert LM, Bennett CF, O'malley BW;

XX

XX WPI; 2000-586211/55.

XX

PD 22-AUG-2000.

XX

XX 29-MAR-1999; 99US-00280409.

XX

XX 29-MAR-1999; 99US-00280409.

XX

XX (ISIS-) ISIS PHARM INC.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX

XX Cowsert LM, Bennett CF, O'malley BW;

XX

XX WPI; 2000-586211/55.

XX

XX Antisense compounds targeted to steroid receptor RNA activator useful for

XX diagnosis, prophylaxis and treatment of diseases associated with the

XX steroid activator, such as infection, inflammation or tumor formation.

XX

XX Claim 3; Col 42; 47pp; English.

XX

XX The present sequence is one of a large number of antisense

XX oligonucleotides which is directed against one of four human steroid

XX

receptor RNA activator (SRA) nucleic acid sequences. Two series of

antisense oligonucleotides were synthesised. The first series comprised 8

-30 oligodeoxynucleotides with a phosphorothioate backbone. The second

series comprised chimeric oligonucleotides composed of a central gap

region, consisting of ten 2'-deoxynucleotides, which was flanked on both

sides by four-nucleotide wings. The wings were composed of 2'-

methoxyethyl (2'-MOE) nucleotides. Both series contained the same

nucleotide sequences. The antisense compounds are useful for research,

diagnosis, treatment and prophylaxis to prevent or delay infection,

inflammation or tumour formation. Therapeutically the oligonucleotides

are highly safe and are effectively administered to humans

XX

XX Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

XX

Query Match 9.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAGACCTGGT 1683

Db 2 CTGCTGGAGACCTGGT 17

RESULT 180

AAA92609

ID AAA92609 standard; DNA; 18 BP.

XX

AC AAA92609;

XX

DT 04-JAN-2001 (first entry)

XX

DE Antisense oligonucleotide ISIS# 30428.

XX

XX Human; SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;

XX SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.

XX

OS Synthetic.

XX

XX US6107092-A.

XX

PD 22-AUG-2000.

XX

XX 29-MAR-1999; 99US-00280409.

XX

XX 29-MAR-1999; 99US-00280409.

XX

XX (ISIS-) ISIS PHARM INC.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX

XX Cowsert LM, Bennett CF, O'malley BW;

XX

XX WPI; 2000-586211/55.

XX

PD 22-AUG-2000.

XX

XX 29-MAR-1999; 99US-00280409.

XX

XX 29-MAR-1999; 99US-00280409.

XX

XX (ISIS-) ISIS PHARM INC.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX

XX Cowsert LM, Bennett CF, O'malley BW;

XX

XX WPI; 2000-586211/55.

XX

XX Antisense compounds targeted to steroid receptor RNA activator useful for

XX diagnosis, prophylaxis and treatment of diseases associated with the

XX steroid activator, such as infection, inflammation or tumor formation.

XX

XX Claim 3; Col 42; 47pp; English.

XX

XX The present sequence is one of a large number of antisense

XX oligonucleotides which is directed against one of four human steroid

XX

SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1670 GCTGGAACCTGGTGT 1685
|||||
Db 2 GCTGGAAGCTGGTAT 17

RESULT 181
AAV01272/c
ID AAV01272 standard; DNA; 19 BP.
XX
XX
AC AAV01272;
XX
XX
DT 23-MAR-1998 (first entry)
XX
DE Chymotrypsinogen PCR primer for universal mammalian STS's.
XX
KW PCR primer; polymerase chain reaction; amplification; UM-STS;
KW universal mammalian sequence tagged site; genomic map; clone; ss.
XX
XX Synthetic.
OS
XX
XX WO9731012-A1.
FN
XX
XX 28-AUG-1997.
PD
XX
XX 18-FEB-1997; 97WO-US002403.
PF
XX
XX 22-FEB-1996; 96US-0012061P.
PR
XX
XX (UNMI) UNIV MICHIGAN.
PA (UNMS) UNIV MICHIGAN STATE.
XX
XX
PI Brewer GJ, Venta RJ, Yuzbasiyan-Gurkan V;
XX
XX WPI; 1997-435083/40.
DR
XX
XX New oligonucleotide primers amplifying gene regions conserved among
PT mammals - useful for developing genomic maps, isolating clones and making
PT cross-species comparisons.
XX
XX
PS Claim 1; Page 11; 26pp; English.
XX

XX The present sequence represents a specifically claimed oligonucleotide
CC PCR primer. The oligonucleotide can be used for polymerase chain reaction
CC (PCR) amplification of DNA, specifically regions of specific genes that
CC are conserved among mammalian species, i.e. pairs of oligonucleotides
CC from the present specification represent universal mammalian sequence-
CC tagged site (UM-STS) primers. The primers are used to develop genomic
CC maps, to isolate clones from libraries, to make cross-species comparisons
CC and to develop additional genetic markers. UM-STS allow genomic
CC comparisons to be made between more species
XX
SQ Sequence 19 BP; 5 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1680 TGGTGCTCTCTCCAGC 1695
|||||
Db 17 TGGGCTCTCTCTCTGC 2

RESULT 182
AAV34507/c
ID AAV34507 standard; DNA; 19 BP.
XX
XX
AC AAV34507;

XX
DT 29-SEP-1998 (first entry)
XX
DE BRCAL exon 21 reverse primer 21R.
XX
KW BRCAL exon 21; CDGE; constant denaturing gradient gel electrophoresis;
KW breast cancer; ovarian cancer; BRCAL gene; PCR; primer; amplification;
ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
PN WO9818966-A1.
XX
XX 07-MAY-1998.
PD
XX
XX 31-OCT-1997; 97WO-US019596.
PF
XX
XX 31-OCT-1996; 96US-0029208P.
PR
XX
XX (LESC/) LESCALLETT J.
PA
XX
XX Lescallett J;
PI
XX
XX WPI; 1998-272249/24.
DR
XX
XX Primers for analysis of the BRCAL gene - used for determining pre-
PT disposition or higher susceptibility to breast or ovarian cancer in
PT patient based on mutation.
XX
XX Claim 24; Page 41; 64pp; English.
XX
CC The reverse primer, together with an appropriate forward primer, was used
CC to amplify exon 21 and its surrounding intron sequences of the BRCAL
CC gene. The invention provides corrected sequences for BRCAL exons 8, 15,
CC 18, 20, 21 and 23, and several portions of the intron regions surrounding
CC these exons. The corrections made it possible to construct primers, such
CC as the present one, which are able to amplify the BRCAL exons with
CC greater fidelity than was previously possible. The primers are also
CC useful in amplifying sequences for constant denaturing gradient gel
CC electrophoresis (CDGE) to detect mutations in the BRCAL gene. The
CC invention claims these primers to be useful for determining a pre-
CC disposition or higher susceptibility to breast or ovarian cancer in a
CC patient based on the presence of mutations of the BRCAL gene
XX
SQ Sequence 19 BP; 6 A; 8 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1670 GCTGGAACCTGGTGT 1685
|||||
Db 17 GCTGGAACCTGGGT 2

RESULT 183
AAA07015
ID AAA07015 standard; DNA; 19 BP.
XX
XX
AC AAA07015;
XX
XX 03-JUL-2000 (first entry)
DT
XX
XX Raf-1 PCR primer, SEQ ID NO:12.
DE
XX

XX Raf-1; CAP kinase; phosphorylation; ceramide-activated protein kinase;
KW lipopolysaccharide; LPS; endotoxin;
KW sphingomyelin signal transduction pathway; PCR primer; ss.
XX
XX Mammalia.
XX
XX US6040149-A.
PN

XX PD 21-MAR-2000.
XX PF 10-JAN-1997; 97US-00785247.
XX PR 11-JAN-1996; 96US-0009900P.
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PI Zhang Y, Liu J, Kolesnick RN;
XX DR WPI; 2000-270133/23.
XX PT Novel method of identifying agents capable of inhibiting
PT lipopolysaccharide induced threonine phosphorylation by a ceramide-
PT activated protein kinase.
XX PS Example VI; Col 56; 84pp; English.
XX CC The invention relates to a novel method of determining whether an agent
CC is capable of specifically inhibiting the ability of a ceramide-activated
CC protein (CAP) kinase to phosphorylate the threonine residue in a
CC polypeptide containing a Thr-Pro- or Thr-Leu-Pro motif. In particular,
CC the peptide substrate that is specifically phosphorylated is Raf-1,
CC the epidermal growth factor receptor (EGFR), or suitable fragments thereof.
CC The CAP kinase is membrane bound and has an apparent molecular weight of
CC 100-110 kD. It is an upstream participant in a sphingomyelin signal
CC transduction pathway which uses ceramide as a second messenger. This
CC pathway is initiated by tumour necrosis factor-alpha (TNF-alpha) and
CC interleukin-beta (IL-beta), causing the hydrolysis of sphingomyelin to
CC ceramide. The ceramide in turn stimulates the kinase to phosphorylate
CC protein substrates which can then mediate signal transduction. The CAP
CC kinase is also stimulated by the bacterial endotoxin lipopolysaccharide
CC (LPS), which is thought to mimic the second messenger function of
CC ceramide. The methods are useful for identifying agents that inhibit
CC lipopolysaccharide-induced Thr phosphorylation by CAP kinase. The agents
CC identified using the method are useful for treating disorders associated
CC with aberrant phosphorylation of target molecules by CAP kinase, e.g.,
CC inflammatory disorders (such as rheumatoid arthritis), ulcerative
CC colitis, graft versus host disease, lupus erythematosus, HIV, infection,
CC disorders associated with poor stem cell growth, and septic shock.
CC Sequences AAA07014-A07015 represent PCR primers used in an
CC exemplification of the present invention to introduce DNA encoding the
CC Flag epitope (DYKDDDDK) immediately 5' of the Raf-1 start codon in the
CC Bluescript KS vector
XX SQ Sequence 19 BP; 7 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1648 GAAGGCAAGCACCAGG 1663
DB 1 GAAGGCAAGCTTCAGG 16

RESULT 184
AAA82742
ID AAA82742 standard; DNA; 19 BP.
AC AAA82742;
XX DT 04-DEC-2000 (first entry)
XX DE cdk3 ribozyme binding site #27.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PI

PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX DR WPI; 2000-412314/35.
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX PS Disclosure; Page 51; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82445 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX SQ Sequence 19 BP; 3 A; 10 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1657 CACCAAGCTCAGAGCT 1672
DB 1 CACCAAGCTCAGAGCT 16

RESULT 185
AAH57904
ID AAH57904 standard; DNA; 19 BP.
AC AAH57904;
XX DT 10-SEP-2001 (first entry)
XX DE Cell-cycle dependent kinase cdk3 ribozyme binding site SEQ ID NO:328.
XX KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisking; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200130362-A2.
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029500.
XX PR 26-OCT-1999; 99US-0161532P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Robbins JM, Tritz R;

XX WPI; 2001-300427/31.

XX Treating proliferative skin or eye diseases and scarring, using ribozymes

PT that cleave RNA encoding cytokines involved in inflammation, matrix

PT metalloproteinases, growth factors and cell-cycle dependent kinases.

XX

PS Example 1; Page 95; 408pp; English.

XX

XX The present invention describes a method for treating a proliferative

CC skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in

CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle

CC dependent kinase, growth factor or a reductase, or administering a

CC nucleic acid molecule (II) comprising a promoter operably linked to a

CC nucleic acid segment encoding (I). (I) can have antipsoriatic,

CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,

CC ophthalmological, vulnary, keratolytic and virucide activities, and

CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used

CC in gene therapy. (I) and (II) are useful for treating proliferative skin

CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic

CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of

CC prematurity and retinal detachment, and for treating and preventing

CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn

CC scar. AAH57577 to AAH62099 represent sequences used in the

CC exemplification of the present invention

XX

XX Sequence 19 BP; 3 A; 10 C; 4 G; 2 T; 0 U; 0 Other;

SQ

Query Match 9.2%; Score 12.8; DB 1; Length 19;

Best Local Similarity 87.5%; Pred. No. 2.8e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1657 CACCAGGCTCAGCT 1672

DB 1 CCCCAGGCTCAGAGCT 16

RESULT 186

ABF35838

ID ABF35838 standard; DNA; 13 BP.

XX

AC ABF35838;

XX

DT 21-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 135835 for detecting SNP TSC0033923.

XX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

XX

Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX Claim 1; SEQ ID NO 135835; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 13 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 9.1%; Score 12.6; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 1.8e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATT 1733

DB 1 GGAGATGGAGATY 13

RESULT 187

ABF35839/C

ID ABF35839 standard; DNA; 13 BP.

XX

AC ABF35839;

XX

DT 21-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 135836 for detecting SNP TSC0033923.

XX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

XX

Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX

Claim 1; SEQ ID NO 135836; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC	was obtained in electronic format from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 13 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 1 Other;	
	Query Match 9.1%; Score 12.6; DB 1; Length 13;	
	Best Local Similarity 92.3%; Pred. No. 1.8e+02;	
	Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1721 GGAGTGGAGATT 1733	
Db	13 GGAGTGGAGATT 1	
RESULT 188		
ID	AAQ84806 standard; DNA; 19 BP.	
XX		
AC	AAQ84806;	
XX		
DT	25-MAR-2003 (revised)	
DT	25-SEP-1995 (first entry)	
XX		
DE	Spinocerebellar ataxia type 1 (SCA 1) PCR primer X2-2 (185-203).	
XX		
KW	Spinocerebellar ataxia type 1; SCA 1; presymptomatic diagnosis;	
KW	PCR primer X2-2 (185-203); ss.	
OS	Synthetic.	
XX		
PN	WO9501437-A2.	
XX		
PD	12-JAN-1995.	
XX		
PF	29-JUN-1994; 94WO-US007336.	
XX		
PR	29-JUN-1993; 93US-00084365.	
PR	28-JUN-1994; 94US-00267803.	
XX		
PA	(MINU) UNIV MINNESOTA.	
PI	Orr HT, Chung M, Zoghbi HV;	
XX		
DR	WPI; 1995-061001/08.	
XX		
PT	New autosomal dominant spinocerebellar ataxia type 1 nucleic acid - used	
PT	to develop prods. for detection or presymptomatic diagnosis of a SCA1	
PT	disorder.	
XX		
PS	Example II; Page 72; 11pp; English.	
CC		
CC	AAQ84805 and AAQ84806 are a pair of primers for the PCR amplification of	
CC	AAQ84793, a new autosomal dominant spinocerebellar ataxia type 1 (SCA 1)	
CC	nucleic acid, which encodes the protein product described in AAR71111.	
CC	Both the nucleic acid and the protein can be used to develop products,	
CC	for the presymptomatic detection of a SCA 1 disorder. (Updated on 25-MAR-	
CC	2003 to correct PN field.)	
XX		
SQ	Sequence 19 BP; 5 A; 7 C; 4 G; 3 T; 0 U; 0 Other;	
	Query Match 9.1%; Score 12.6; DB 1; Length 19;	
	Best Local Similarity 78.3%; Pred. No. 3.1e+02;	
	Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	1657 CACCAGGCTCACAGCTGGA 1675	
Db	1 CACCAGCTCCCTGATGA 19	
RESULT 189		
ID	AAQ85482 standard; DNA; 19 BP.	
XX		

AC	AAQ85482;	
XX		
DT	21-SEP-1995 (first entry)	
XX		
DE	Pathogenic filamentous fungi detection primer #2.	
XX		
KW	Polymerase chain reaction; PCR; amplify; primer pathogenic; fungi;	
KW	ribosomal RNA; probe; Candida albicans; Aspergillus fumigatus; ss.	
XX		
OS	Synthetic.	
XX		
PN	JP06339400-A.	
XX		
PD	13-DEC-1994.	
XX		
PF	01-JUN-1993; 93JP-00130778.	
XX		
PR	01-JUN-1993; 93JP-00130778.	
XX		
PA	(YAMA/) YAMAGUCHI H.	
DR	WPI; 1995-063358/09.	
XX		
PT	Detection of a pathogenic filamentous fungus of aspergillus or	
PT	Penicillium genus - by PCR amplification of ribosome RNA gene.	
XX		
PS	Claim 1; Page 5; 5pp; Japanese.	
XX		
CC	The sequences given in AAQ85481-82 are primers which are used in the	
CC	detection of pathogenic filamentous fungi. These primers bind to, and	
CC	amplify fungi from the genus Aspergillus or Penicillium. These primers	
CC	bind to the ribosomal RNA gene. The amplified product is detected using	
CC	the sequence given in AAQ85483 as a probe. The method allows highly	
CC	sensitive detection of pathogenic fungi. These sequences were used in a	
CC	specific example to detect Candida albicans and Aspergillus fumigatus	
CC	JCM1738	
XX		
SQ	Sequence 19 BP; 7 A; 5 C; 6 G; 1 T; 0 U; 0 Other;	
	Query Match 9.1%; Score 12.6; DB 1; Length 19;	
	Best Local Similarity 78.9%; Pred. No. 3.1e+02;	
	Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	1646 CAGAGGCAAGCACCAGGC 1664	
Db	1 CAGAGGAAGGTCAGCC 19	
RESULT 190		
ID	AAT27635	
XX	AAT27635 standard; DNA; 19 BP.	
XX		
AC	AAT27635;	
XX		
DT	15-NOV-1996 (first entry)	
XX		
DE	Primer/probe #4 for detection of C. albicans 18S rRNA.	
XX		
KW	Primer; probe; detection; pathogenic fungi; diagnosis; mycosis;	
KW	candidiasis; aspergillosis; 18S rRNA; species specific; Candida albicans;	
XX	ss.	
OS	Synthetic.	
XX		
PN	JP08089254-A.	
XX		
PD	09-APR-1996.	
XX		
PF	29-SEP-1994; 94JP-00235339.	
XX		
PR	29-SEP-1994; 94JP-00235339.	
XX		
PA	(TOYO-) TOYOBO GENE ANALYSIS KK.	

XX WPI; 1996-233347/24.
 XX 18S rRNA oligo:nucleotide(s) for detection and identification of fungi -
 PT esp. for diagnosis of mycosis including candidiasis and aspergillosis.
 XX Claim 3; Page 2; 11pp; Japanese.
 XX The sequences given in AAT27632-42 are primer/probes which were used in a
 CC method for the detection of pathogenic fungi. They are esp. useful in the
 CC diagnosis of mycosis including candidiasis and aspergillosis. The
 CC sequences in AAT27632-36 are oligonucleotides which bind to fungal 18S
 CC rRNA sequences, whereas the sequences given in AAT27637-42 are species
 CC specific oligonucleotides. The 18S rRNA sequences are based on sequences
 CC isolated from *Candida albicans* (see also AAT27643)
 XX
 SQ Sequence 19 BP; 7 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 9.1%; Score 12.6; DB 1; Length 19;
 Best Local Similarity 78.9%; Pred. No. 3.1e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1646 CAGAGGCGACGACAGGC 1664
 DB 1 CAGAGGAAAGGTCCAGCC 19
 RESULT 191
 AAT77561
 ID AAT77561 standard; DNA; 19 BP.
 XX AAT77561;
 AC
 XX 11-SEP-1997 (first entry)
 DT
 XX Wheat microsatellite WMS122 left primer.
 DE
 XX Microsatellite marker; hypervariable genomic fragment; *Triticum aestivum*;
 KW wheat; Triticeae; sequence tagged site; STS; primer; PCR; amplify;
 KW polymorphism; genetic analysis; hexaploid; tetraploid; mapping; ss.
 XX Synthetic.
 OS
 XX DE19525284-A1.
 PN
 XX 02-JAN-1997.
 PD
 XX 28-JUN-1995; 95DE-01025284.
 PF
 XX 28-JUN-1995; 95DE-01025284.
 PR
 XX (PFLA-) INST PFLANZENGENETIK & KULTURPFLANZENFOR.
 PA
 XX Roeder M, Plaschke J, Ganai M;
 XX WPI; 1997-053731/06.
 DR
 XX Primers for STS microsatellite markers for wheat and related species -
 PT useful for genetic mapping, analysis and labelling etc. of wheat.
 XX Claim 5; Page 7; 8pp; German.
 XX Microsatellite markers based on hypervariable genomic fragments, from
 CC *Triticum aestivum* (wheat) or the tribe Triticeae, consist of a sequence
 CC tagged site (STS), defined by 2 specific primers (of mean size 17-23
 CC bases) that flank a microsatellite sequence at both ends, which can be
 CC amplified to polymorphisms (PCR products of different sizes). The
 CC microsatellites are n-fold tandem repeats (n = 10 or more) of di-, tri-,
 CC or tetra-nucleotide sequences, combination microsatellite sequences or an
 CC imperfect sequence in which individual bases are mutated. The
 CC microsatellite markers can be used for genetic analysis of hexaploid and
 CC tetraploid forms of wheat and for genetic mapping or labelling of
 CC monogenic and polygenic properties, and for their selection; for

CC analysing relationships and identifying varieties; and for evaluating
 CC varietal purity, hybrid identification and plant growth. The markers can
 CC differentiate between almost all European wheat lines and show a higher
 CC degree of DNA polymorphism than known probes for the wheat genome. They
 CC can be detected by PCR, so large numbers of samples can be analysed
 CC easily (e.g. several hundred per day). Microsatellite marker-related
 CC polymorphisms are stably inherited so can also serve as genetic markers.
 CC AAT77003-22 and AAT77535-716 are primer pairs that define the
 CC microsatellite markers. WMS122 has CT and CA type repeats
 XX
 SQ Sequence 19 BP; 6 A; 0 C; 11 G; 2 T; 0 U; 0 Other;
 Query Match 9.1%; Score 12.6; DB 1; Length 19;
 Best Local Similarity 78.9%; Pred. No. 3.1e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1709 GGTAGGAGTACGAGATG 1727
 DB 1 GGTGGGAGAAAGGAGATG 19
 RESULT 192
 AAA85488
 ID AAA85488 standard; DNA; 19 BP.
 XX AAA85488;
 AC
 XX 04-DEC-2000 (first entry)
 DT
 XX Cyclin A1 ribozyme binding site #110.
 DE
 XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 KW Mammalia.
 XX OS
 XX WO2000032765-A2.
 PN
 XX 08-JUN-2000.
 PD
 XX 06-DEC-1999; 99WO-US028772.
 PF
 XX 04-DEC-1998; 98US-0110954P.
 PR
 XX (IMMU-) IMMUSOL INC.
 PA
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX WPI; 2000-412314/35.
 DR
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 PT
 XX Disclosure; Page 93; 109pp; English.
 PS
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX
 SQ Sequence 19 BP; 5 A; 0 C; 11 G; 3 T; 0 U; 0 Other;
 Query Match 9.1%; Score 12.6; DB 1; Length 19;
 Best Local Similarity 78.9%; Pred. No. 3.1e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1698 GGTGGAGCTGGTTAGGA 1716
 DB 1 GGTGGAGTTGGGAAGA 19

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XX PN WO9954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0083614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX PA (GEST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;
XX PI WPI; 2000-013267/01.
XX DR Novel biallelic markers used to construct a high density disequilibrium
XX PT map of the human genome.
XX PS Claim 8; Page 1995; 2745pp; English.
XX CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX CC invention, which contain a polymorphic base at position 24 of their
XX CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX CC primers for the biallelic markers. The biallelic markers of the invention
XX CC have a variety of uses: they can be used for high density mapping of the
XX CC human genome, and in complex association studies and haplotyping studies
XX CC which are useful in determining the genetic basis for disease states.
XX CC Compositions and methods of the invention can also be useful for the
XX CC identification of the targets for the development of pharmaceutical
XX CC agents and diagnostic methods, as well as the characterisation of the
XX CC differential efficacious responses to and side effects from
XX CC pharmaceutical agents acting on a disease as well as other treatment.
XX CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX CC 3367, are not actually given a sequence in the Sequence Listing from the
XX CC present invention
XX SQ Sequence 19 BP; 7 A; 10 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 5.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1694 GCGTGGTGGAGTTGGGTT 1712
DB 19 GACTTGGGATGTTGGGGT 1

RESULT 195
AAH60650
ID AAH60650 standard; DNA; 19 BP.
XX AC AAH60650;
XX AC AAH60650;
XX DT 10-SEP-2001 (first entry)
XX DE Cyclin A1 ribozyme binding site SEQ ID NO:3074.
XX KW Human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
XX KW recognition site; target; ribozyme binding site; eye disease; vulvar;
XX KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
XX KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
XX KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
XX KW antiproliferative; dermatological; antiseborrheic; keratolytic; gene therapy; viral wart;
XX KW antiscarring; ophthalmological; actinic keratosis; squamous cell carcinoma;
XX KW atopic dermatitis; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
XX KW sickle cell retinopathy; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200130362-A2.

RESULT 193
AAA84289
ID AAA84289 standard; DNA; 19 BP.
XX AC AAA84289;
XX DT 04-DEC-2000 (first entry)
XX DE Cyclin D1 ribozyme binding site #56.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch EV, Barber JR, Robbins JM;
XX PI WPI; 2000-412314/35.
XX DR New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PT PCNA and Cyclin B1.
XX PS Disclosure; Page 74; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX CC Representative examples of ribozyme recognition sites are given in
XX CC AAZ82415 to AAZ86787. The ribozyme of the invention is useful for
XX CC inhibiting restenosis by introduction of the ribozyme into cells. The
XX CC ribozyme is resistant to endonuclease activity and hence is efficient in
XX CC restenosis treatment
XX SQ Sequence 19 BP; 5 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1739 CCAACTCTCTCCCTATCCTA 1757
DB 1 CCAACAACTTCTCTGTCCTA 19

RESULT 194
AAZ73922/c
ID AAZ73922 standard; DNA; 19 BP.
XX AC AAZ73922;
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker downstream amplification primer SEQ ID NO:8278.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX KW haplotyping; hybridisation; identification; characterisation;
XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX KW diagnosis; ss.
XX OS Homo sapiens.

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XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029500.
XX PR 26-OCT-1999; 99US-0161532P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Robbins JM, Tritz R;
XX DR WPI; 2001-300427/31.
XX PT Treating proliferative skin or eye diseases and scarring, using ribozymes
XX PT that cleave RNA encoding cytokines involved in inflammation, matrix
XX PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX PS Example 1; Page 295; 408pp; English.
XX CC The present invention describes a method for treating a proliferative
XX CC skin or eye disease and scarring. The method involves administering a
XX CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX CC dependent kinase, growth factor or a reductase, or administering a
XX CC nucleic acid molecule (II) comprising a promoter operably linked to a
XX CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
XX CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
XX CC ophthalmological, vulnary, keratolytic and virucide activities, and
XX CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX CC in gene therapy. (I) and (II) are useful for treating proliferative skin
XX CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX CC also be used for treating proliferative eye diseases such as diabetic
XX CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
XX CC prematurity and retinal detachment, and for treating and preventing
XX CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
XX CC scar. AAH57577 to AAH62099 represent sequences used in the
XX CC exemplification of the present invention
XX SQ Sequence 19 BP; 5 A; 0 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1698 GGTGGAGTTCGGTACGA 1716
Db ||||| ||||| ||||| ||||| |||||
1 GGTGGAGTTCGGGAAGAA 19

RESULT 196
AAH59451
ID AAH59451 standard; DNA; 19 BP.
XX AC AAH59451;
XX DT 10-SEP-2001 (first entry)
XX DE Cyclin D1 ribozyme binding site SEQ ID NO:1875.
XX KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
XX KW recognition site; target; ribozyme binding site; eye disease; vulnary;
XX KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
XX KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
XX KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
XX KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
XX KW antisickling; ophthalmological; keratolytic; gene therapy; vital wart;
XX KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
XX KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
XX KW sickle cell retinopathy; ss.
XX OS Homo sapiens.
XX OS Synthetic.

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XX PN WO20010362-A2.
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029500.
XX PR 26-OCT-1999; 99US-0161532P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Robbins JM, Tritz R;
XX DR WPI; 2001-300427/31.
XX PT Treating proliferative skin or eye diseases and scarring, using ribozymes
XX PT that cleave RNA encoding cytokines involved in inflammation, matrix
XX PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX PS Example 1; Page 208; 408pp; English.
XX CC The present invention describes a method for treating a proliferative
XX CC skin or eye disease and scarring. The method involves administering a
XX CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX CC dependent kinase, growth factor or a reductase, or administering a
XX CC nucleic acid molecule (II) comprising a promoter operably linked to a
XX CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
XX CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
XX CC ophthalmological, vulnary, keratolytic and virucide activities, and
XX CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX CC in gene therapy. (I) and (II) are useful for treating proliferative skin
XX CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX CC also be used for treating proliferative eye diseases such as diabetic
XX CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
XX CC prematurity and retinal detachment, and for treating and preventing
XX CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
XX CC scar. AAH57577 to AAH62099 represent sequences used in the
XX CC exemplification of the present invention
XX SQ Sequence 19 BP; 5 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1739 CCAACTCTCTCCTATCCTA 1757
Db ||||| ||||| ||||| ||||| |||||
1 CCAACTCTCTCTCTCCTA 19

RESULT 197
AAQ34483
ID AAQ34483 standard; DNA; 15 BP.
XX AC AAQ34483;
XX DT 25-MAR-2003 (revised)
XX DT 12-MAY-1993 (first entry)
XX DE Oligo 9, a PCR primer for plant DHK-hydroxylating enzyme clone.
XX KW Dihydrokaempferol; flavonoid; pigmentation; colour; amplification;
XX KW cytochrome P450; ss.
XX OS Synthetic.
XX PN EP522880-A2.
XX PD 13-JAN-1993.
XX PF 10-JUL-1992; 92EP-00306379.

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XX PR 11-JUL-1991; 91AU-00007173.
XX PR 17-FEB-1992; 92AU-00000923.
XX PA (ITFL-) INT FLOWER DEV PTY LTD.
XX XX Holton TA, Cornish EC, Kovacic F, Tanaka Y, Lester DR;
XX DR WPI; 1993-010688/02.
XX XX Nucleic acid sequence encoding a di:hydro:kaempferol-hydroxylating enzyme
PT - e.g. cytochrome P450 introduced into transgenic plants for controlling
PT flavonoid pigmentation in plants and organisms.
XX PS Disclosure; Page 13; 66pp; English.
XX CC The PCR primer may be used in PCR for amplification of petal cytochrome
CC P450 homologues. See also AAQ34475-91. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX SQ Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
SQ Query Match 8.9%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1683 TGTCTCTCTCCAGCG 1696
XX DB 2 TGTCTCTCTCCAGTG 15
RESULT 199
AAQ56245
ID AAQ56245 standard; cDNA; 15 BP.
XX AC AAQ56245;
XX DT 25-MAR-2003 (revised)
XX DT 08-AUG-1994 (first entry)
XX DE PCR primer for amplifying chi-A gene sequence.
XX KW Anthocyanidin-3-glucoside rhamnosyltransferase; glucosyltransferase;
XX inflorescence; flowering plants; transgenic plant; Petunia hybrida;
XX chi-A; ss.
XX OS Synthetic.
XX PN WO9403591-A1.
XX PD 17-FEB-1994.
XX PF 30-JUL-1993; 93WO-AU000387.
XX PR 30-JUL-1992; 92AU-00003846.
XX PA (ITFL-) INT FLOWER DEV PTY LTD.
XX XX Brugliera F, Holton TA;
XX PI WPI; 1994-065680/08.
XX XX Nucleic acid encoding glycosyltransferase enzymes - used for producing
PT transgenic plants with altered inflorescence properties including
PT modified petal colours.
XX PS Example 17; Page 21; 76pp; English.
XX CC Two primers (AAQ56245, AAQ56246) were used to amplify the chi-A gene.
CC This primer corresponds to nucleotides 6-20 of the published chi-A cDNA
CC sequence. chi-A is a previously characterised flavonoid biosynthesis
CC gene. (Updated on 25-MAR-2003 to correct PN field.)
XX XX
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SQ Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
SQ Query Match 8.9%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1683 TGTCTCTCTCCAGCG 1696
DB 2 TGTCTCTCTCCAGTG 15
RESULT 199
AAQ29808/c
ID AAQ29808 standard; DNA; 16 BP.
XX AC AAQ29808;
XX DT 25-MAR-2003 (revised)
XX DT 19-MAR-1993 (first entry)
XX DE B allele probe VP59.
XX KW G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
XX paternity; forensic; ss.
XX OS Synthetic.
XX PN EP512342-A2.
XX PD 11-NOV-1992.
XX PF 25-APR-1992; 92EP-00107084.
XX PR 07-MAY-1991; 91US-00696793.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI Saiki RK, Nasarabadi EL;
XX DR WPI; 1992-374679/46.
XX PT Determn. of an individuals genotype at the gamma-globin locus - using
XX sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
XX PS Disclosure; Page 18; 29pp; English.
XX CC The sequences given in AAQ29787-816 are probes which were used within the
XX method of the invention for detecting the presence of a variant sequence
XX in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
XX distinguished from one another by the polymorphic sequence corresponding
XX to the HindIII site of the A allele. The sequences of the three alleles
XX are given in AAQ29842-44. The methods for determining an individuals
XX genotype at the GGG locus with respect to a set of alleles improves the
XX discriminatory power of GGG typing methodology compared to previous
XX methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 16 BP; 4 A; 9 C; 1 G; 2 T; 0 U; 0 Other;
SQ Query Match 3.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1698 GGTGGAGTGGGT 1711
DB 16 GGTGGAGTGGGT 3
RESULT 200
AAAT70569/c
ID AAAT70569 standard; DNA; 16 BP.
XX AC AAAT70569;
XX XX
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DT 04-NOV-1997 (first entry)
 DE Haemoglobin G gamma-globin allele B-specific probe.
 XX
 KW Glycophorin A; sialoglycoprotein; human; erythrocyte; membrane;
 XX M blood group antigen; N blood group antigen; allele A; B; A'; A''; B';
 XX polymorphism; detection; sequence-specific oligonucleotide probe;
 KW genotype; forensic; primer; PCR; polymerase chain reaction; amplify; ss.
 XX
 OS Synthetic.
 XX
 XX US5643724-A.
 XX
 XX 01-JUL-1997.
 XX
 XX 06-JUN-1994; 94US-00255264.
 XX
 XX 06-JUN-1994; 94US-00255264.
 XX
 XX (HOFF) ROCHE MOLECULAR SYSTEMS INC.
 XX
 XX Filides NJ, Reynolds RL;
 XX
 XX WPI; 1997-350231/32.
 XX
 XX Detection of glycophorin A allele(s) - by hybridisation assay using
 XX sequence-specific oligonucleotide probes.
 XX
 XX Example 3; Col 15-16; 16pp; English.
 XX
 XX Glycophorin A is a major sialoglycoprotein of the human erythrocyte
 XX membrane. Glycophorin A carries the M or N blood group antigen, which is
 XX determined by the amino acid at residues 1 and 5. Allele A encodes the
 XX protein carrying the N blood group antigen and allele B encodes the
 XX protein carrying the M blood group antigen. Three additional alleles have
 XX been discovered, designated A', A'', and B'. Detecting an A', A'', or B'
 XX allele of the Glycophorin A locus in a human nucleic acid sample
 XX comprises mixing the sample under stringent hybridisation conditions with
 XX a sequence-specific oligonucleotide probe that distinguishes the A', A'',
 XX or B' allele from A and B alleles, and detecting any hybridisation. The
 XX method and probes are used for determining an individual's Glycophorin A
 XX genotype, especially useful for determining an individual's Glycophorin A
 XX forensic purposes. AAT70558-67 (and also AAT70582-83) are primers from
 XX the AmpliType (R) PM kit used in a Glycophorin A typing system developed
 XX by Hoffmann-La Roche. The primers direct the simultaneous amplification
 XX of specific regions of the following six genetic loci: Glycophorin A, HLA
 XX DQA1, low density lipoprotein receptor, Haemoglobin G gamma-globin, D7S8
 XX and group specific component. Probe strips are also provided in the kit
 XX (AAT70568-81)
 XX
 XX Sequence 16 BP; 4 A; 9 C; 1 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 8.9%; Score 12.4; DB 1; Length 16;
 XX Best Local Similarity 92.9%; Pred. No. 2.7e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1698 GGTGGAGAGTTGGGT 1711
 DB |||||||
 16 GGTGGAGAGCTGGGT 3
 RESULT 201
 AAC67540
 ID AAC67540 standard; DNA; 16 BP.
 XX
 XX AAC67540;
 XX
 XX 14-FEB-2001 (first entry)
 XX
 XX Alzheimer's disease-linked mitochondrial SNP PCR primer #240.
 DE
 XX Human; mitochondrial genome; single nucleotide polymorphism; SNP;
 KW Alzheimer's disease; mtDNA; PCR primer; ss.

XX Homo sapiens.
 XX WO200063441-A2.
 XX
 XX 26-OCT-2000.
 XX
 XX PF 19-APR-2000; 2000WO-US010906.
 XX
 XX 20-APR-1999; 99US-0130447P.
 XX 22-OCT-1999; 99US-0160901P.
 XX
 XX (MITO-) MITOKOR.
 XX
 XX Hernstadt C, Davis RE;
 XX WPI; 2000-672748/65.
 XX
 XX Diagnosing a subject at the risk for or having Alzheimer's disease
 XX comprises determining at least one single nucleotide polymorphism in
 XX mitochondrial DNA associated with the disease in the sample from the
 XX subject.
 XX
 XX Example 9; Page 53; 89pp; English.
 XX
 XX The present invention describes a novel method for determining the risk
 XX of or diagnosing Alzheimer's disease using single nucleotide
 XX polymorphisms (SNPs) present in an individual's mitochondrial DNA
 XX (mtDNA). In addition, the SNPs identified can be used to identify agents
 XX suitable for use in treating Alzheimer's disease. Sequences AAC67301-
 XX C67610 are PCR primers used to demonstrate the method of the invention
 XX
 XX Sequence 16 BP; 2 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
 XX
 XX Query Match 8.9%; Score 12.4; DB 1; Length 16;
 XX Best Local Similarity 92.9%; Pred. No. 2.7e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1709 GGTTAGGAGTACGG 1722
 DB |||||||
 3 GGTTAGGAGTACGG 16
 RESULT 202
 ADD43463
 ID ADD43463 standard; DNA; 16 BP.
 XX
 XX AC ADD43463;
 XX
 XX 15-JAN-2004 (first entry)
 XX
 XX Human mitochondrial DNA (mtDNA) PCR primer SEQ ID NO:637.
 XX
 XX mitochondrial haplogroup; mitochondrial DNA; mtDNA;
 XX single nucleotide polymorphism; SNP; genetic relationship; antidiabetic;
 XX neotrophic; neuroprotective; cytosolic; gene therapy; genealogy;
 XX forensic; Alzheimer's disease; cancer; type 2 diabetes mellitus; human;
 XX PCR primer; ss.
 XX
 XX Synthetic.
 XX
 XX Homo sapiens.
 XX
 XX WO2003046225-A1.
 XX
 XX 05-JUN-2003.
 XX
 XX 25-NOV-2002; 2002WO-US038276.
 XX
 XX 26-NOV-2001; 2001US-0333622P.
 XX 28-MAR-2002; 2002US-0369131P.
 XX 01-APR-2002; 2002US-0369539P.
 XX
 XX (MITO-) MITOKOR.
 XX

```

XX PI Herrnstadt C;
XX PS WPI; 2003-505214/47.
XX PT Determining single nucleotide polymorphisms in mtDNA or homoplasmic mtDNA
XX PT mutations, useful for diagnosing and treating diseases, such as
XX PT Alzheimer's disease, cancer and type 2 diabetes mellitus.
XX PS Example 2; SEQ ID NO 637; 193pp; English.
XX CC The present invention describes a method (M1) for determining the
XX CC mitochondrial haplogroup of a subject, comprising determining in a
XX CC biological sample with mitochondrial DNA (mtDNA) from a subject, the
XX CC presence or absence of at least one mitochondrial single nucleotide
XX CC polymorphism (SNP) that is associated with a mitochondrial haplogroup.
XX CC Also described: (1) determining a genetic relationship between two
XX CC subjects; (2) determining a genetic relationship between an unknown
XX CC source or biological subject from which an unidentified sample is
XX CC obtained, and a known source or biological subject from an identified
XX CC sample is obtained; and (3) determining the presence of or the risk of
XX CC having a disease associated with a mtDNA SNP. Mitochondrial DNA can have
XX CC antidiabetic, neurotropic, neuroprotective and cytosolic activities, and
XX CC can be used in gene therapy. M1 and compositions of the present invention
XX CC are useful for detecting the presence or risk of diseases, treating such
XX CC diseases, determining the haplogroup of an individual, and establishing
XX CC genetic relationships between individuals for genealogical and forensic
XX CC purposes. The diseases include Alzheimer's disease, cancer and type 2
XX CC diabetes mellitus. The present sequence represents a PCR primer used in
XX CC the amplification of human mtDNA in an example from the present
XX CC invention.
XX SQ Sequence 16 BP; 2 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1709 GGTTCAGGACTACGG 1722
DB 3 GGTTCAGGCTACGG 16

RESULT 203
AAQ29806/c
ID AAQ29806 standard; DNA; 17 BP.
XX AC AAQ29806;
XX DT 25-MAR-2003 (revised)
XX DT 19-MAR-1993 (first entry)
XX PT B allele probe VP08.
XX DE G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
XX KW paternity; forensic; ss.
XX OS Synthetic.
XX PN EP512342-A2.
XX PD 11-NOV-1992.
XX PF 25-APR-1992; 92EP-00107084.
XX PR 07-MAY-1991; 91US-00696793.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI Saiki RK, Nasarabadi SL;
XX DR WPI; 1992-374679/46.
XX

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PT Determn. of an individuals genotype at the gamma-globin locus - using
PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
XX PS Disclosure; Page 17; 29pp; English.
XX CC The sequences given in AAQ29787-816 are probes which were used within the
XX CC method of the invention for detecting the presence of a variant sequence
XX CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
XX CC distinguished from one another by the polymorphic sequence corresponding
XX CC to the HindIII site of the A allele. The sequences of the three alleles
XX CC are given in AAQ29842-44. The methods for determining an individuals
XX CC genotype at the GGG locus with respect to a set of alleles improves the
XX CC discriminatory power of GGG typing methodology compared to previous
XX CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 17 BP; 4 A; 10 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GGTGGAAGTTGGGT 1711
DB 17 GGTGGAAGCTGGGT 4

RESULT 204
AAT14821
ID AAT14821 standard; DNA; 17 BP.
XX AC AAT14821;
XX DT 17-SEP-1996 (first entry)
XX DE Histocyte-secreted factor 3' PCR primer.
XX KW Histocyte-secreted factor; HSF; cytokine; antitumour; tumour; therapy;
XX KW polymerase chain reaction; PCR; primer; ss.
XX OS Synthetic.
XX PN WO9613586-A2.
XX PD 09-MAY-1996.
XX PF 26-OCT-1995; 95WO-JPC02200.
XX PR 26-OCT-1994; 94JP-00297780.
XX PA (SATO/) SATOMI N.
XX PI Satomi N;
XX DR WPI; 1996-239499/24.
XX PT DNA encoding histocyte-secreted factor and its variants - useful as an
XX PT anti-tumour agent and for studying tumour regression, having low
XX PT cytotoxicity compared to TNF.
XX PS Example 5; Page 28; 52pp; English.
XX CC A 5' PCR primer (AAT14820) and 3' primer (AAT14821) are based on peptides
XX CC derived from rabbit histocyte-secreted factor (HSF). They were used to
XX CC amplify DNA from human TVH histiocytic cells, yielding the PCR product
XX CC given in AAT14819. They were also used to amplify DNA from U-937 (human
XX CC histiocytic lymphoma) cells, which revealed PCR products that led to the
XX CC identification of a genomic clone (AAT14818) coding for human HSF
XX CC (AAR96800), a novel cytokine
XX SQ Sequence 17 BP; 6 A; 5 C; 5 G; 1 T; 0 U; 0 Other;

Query Match      8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;

```

Matches	13; Conservative	0; Mismatches	1; Indels	0; Gaps	0;
Qy	1655 AGCACCAGGCTCAC 1668				
Db	2 AGAACCAGGCTCAC 15				
RESULT 205					
AAF02929/c					
ID	AAF02929 standard; DNA; 17 BP.				
XX	AC AAF02929;				
XX	XX				
DT	16-FEB-2001 (first entry)				
XX	XX				
DE	Hammerhead ribozyme substrate #1224.				
XX	XX				
KW	Ribozyme; erythropoietin; granulocyte colony stimulating factor;				
KW	interferon alpha; ss.				
XX	OS				
XX	Homo sapiens.				
XX	WO2000061729-A2.				
XX	PN				
XX	19-OCT-2000.				
XX	DR				
XX	WPI; 2000-647423/62.				
XX	XX				
PT	Enzymatic and antisense nucleic acid inhibition of repressor genes,				
PT	useful for producing e.g. granulocyte colony stimulating factor protein,				
PT	interferon alpha and erythropoietin.				
XX	OS				
XX	Homo sapiens.				
XX	WO2000061729-A2.				
XX	PN				
PD	19-OCT-2000.				
XX	XX				
XX	11-APR-2000; 2000WO-US009721.				
XX	XX				
PR	12-APR-1999; 99US-0129390P.				
XX	XX				
PA	(RIBO-) RIBOZYME PHARM INC.				
XX	XX				
PI	Blatt L, Zwick M, Pavco P, Mcswiggen J;				
XX	XX				
DR	WPI; 2000-647423/62.				
XX	XX				
PT	Enzymatic and antisense nucleic acid inhibition of repressor genes,				
PT	useful for producing e.g. granulocyte colony stimulating factor protein,				
PT	interferon alpha and erythropoietin.				
XX	OS				
XX	Homo sapiens.				
XX	WO2000061729-A2.				
XX	PN				
PD	19-OCT-2000.				
XX	XX				
XX	11-APR-2000; 2000WO-US009721.				
XX	XX				
PR	12-APR-1999; 99US-0129390P.				
XX	XX				
PA	(RIBO-) RIBOZYME PHARM INC.				
XX	XX				
PI	Blatt L, Zwick M, Pavco P, Mcswiggen J;				
XX	XX				
DR	WPI; 2000-647423/62.				
XX	XX				
PT	Enzymatic and antisense nucleic acid inhibition of repressor genes,				
PT	useful for producing e.g. granulocyte colony stimulating factor protein,				
PT	interferon alpha and erythropoietin.				
XX	OS				
XX	Homo sapiens.				
XX	WO2000061729-A2.				
XX	PN				
PD	19-OCT-2000.				
XX	XX				
XX	11-APR-2000; 2000WO-US009721.				
XX	XX				
PR	12-APR-1999; 99US-0129390P.				
XX	XX				
PA	(RIBO-) RIBOZYME PHARM INC.				
XX	XX				
PI	Blatt L, Zwick M, Pavco P, Mcswiggen J;				
XX	XX				
DR	WPI; 2000-647423/62.				
XX	XX				
PT	Enzymatic and antisense nucleic acid inhibition of repressor genes,				
PT	useful for producing e.g. granulocyte colony stimulating factor protein,				
PT	interferon alpha and erythropoietin.				
XX	OS				
XX	Homo sapiens.				
XX	WO2000061729-A2.				
XX	PN				
PD	19-OCT-2000.				
XX	XX				
XX	11-APR-2000; 2000WO-US009721.				
XX	XX				
PR	12-APR-1999; 99US-0129390P.				
XX	XX				
PA	(RIBO-) RIBOZYME PHARM INC.				
XX	XX				
PI	Blatt L, Zwick M, Pavco P, Mcswiggen J;				
XX	XX				
DR	WPI; 2000-647423/62.				
XX	XX				
PT	Enzymatic and antisense nucleic acid inhibition of				

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PR 27-MAR-2000; 2000US-0192176P.
PR 27-MAR-2000; 2000US-0192179P.
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
XX
XX
XX (UYDE ) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC;
XX
XX WPI; 2001-639230/73.
XX
XX Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.
XX
XX Claim 7; Page 234; 294pp; English.
XX
XX The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention
XX
XX SQ Sequence 17 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
      Query Match      8.9%; Score 12.4; DB 1; Length 17;
      Best Local Similarity 92.9%; Pred. No. 2.9e+02;
      Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1686 CTCCTCCAGCGTGG 1699
Db 14 CTCCTCCAGCTTGG 1

RESULT 208
ABAB0625
ID ABAB0625 standard; DNA; 17 BP.
XX
XX AC ABAB0625;
XX
XX DT 24-JAN-2002 (first entry)
XX
XX DE APOE mutation correcting oligonucleotide SEQ ID NO: 3471.
XX
XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytostatic; antisickling; anti-naemic; haemostatic;
KW antileptic; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200173002-A2.
XX
XX PD 04-OCT-2001.
XX
XX PF 27-MAR-2001; 2001WO-US009761.

XX 27-MAR-2000; 2000US-0192176P.
XX 27-MAR-2000; 2000US-0192179P.
XX 01-JUN-2000; 2000US-0208538P.
XX 30-OCT-2000; 2000US-0244989P.
XX
XX (UYDE ) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC;
XX
XX WPI; 2001-639230/73.
XX
XX Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.
XX
XX Claim 7; Page 234; 294pp; English.
XX
XX The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention
XX
XX SQ Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
      Query Match      8.9%; Score 12.4; DB 1; Length 17;
      Best Local Similarity 92.9%; Pred. No. 2.9e+02;
      Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1686 CTCCTCCAGCGTGG 1699
Db 4 CTCCTCCAGCTTGG 17

RESULT 209
ACD51040/c
ID ACD51040 standard; RNA; 17 BP.
XX
XX AC ACD51040;
XX
XX DT 23-SEP-2003 (first entry)
XX
XX DE HBV hammerhead ribozyme substrate sequence #353.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
KW ambrzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
XX OS Hepatitis B virus.
XX
XX PN WO200281494-A1.
XX
XX PD 17-OCT-2002.
XX
XX PF 26-MAR-2002; 2002WO-US009187.

```


PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 FA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Example 1; Page 143; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
 CC disclosed in the present invention
 XX
 SQ Sequence 17 BP; 3 A; 0 C; 12 G; 0 T; 2 U; 0 Other;
 Query Match 8.9%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 2.9e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1736 CTCCCAACTCTCTC 1749
 Db 14 CCGCCAACTCTCTC 1
 RESULT 210
 ACC68047/C
 ID ACC68047 standard; DNA; 17 BP.
 XX
 AC ACC68047;
 XX
 DT 01-JUL-2003 (first entry)
 DE
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5294.
 XX
 KW Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.

XX WO2003025176-A2.
 XX 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Teierman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 649; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 8.9%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 2.9e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1725 ATGGAGATTGGCTC 1738
 Db 14 ATGGAGATTGGATC 1
 RESULT 211
 ADB40159
 ID ADB40159 standard; DNA; 17 BP.
 XX
 AC ADB40159;
 XX
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #482.
 XX
 KW cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004219.
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Teierman A, Amson R, Tuijnder M;

QY 1718 TACGAGATGAGGA 1731
 Db 1 TACGGTGATGAGGA 14

RESULT 214
 AAQ29798/C
 ID AAQ29798 standard; DNA; 18 BP.
 XX AC AAQ29798;
 XX DE A allele probe VP63.
 XX KW G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
 XX KW paternity; forensic; ss.
 XX OS Synthetic.
 XX PN EP512342-A2.
 XX PD 11-NOV-1992.
 XX PF 25-APR-1992; 92EP-00107084.
 XX PR 07-MAY-1991; 91US-00696793.
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX PI Saiki RK, Nasarabadi SL;
 XX DR WPI; 1992-374679/46.
 XX PT Determn. of an individuals genotype at the gamma-globin locus - using
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
 XX PS Disclosure; Page 15; 29pp; English.
 XX CC The sequences given in AAQ29787-816 are probes which were used within the
 CC method of the invention for detecting the presence of a variant sequence
 CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
 CC distinguished from one another by the polymorphic sequence corresponding
 CC to the HindIII site of the A allele. The sequences of the three alleles
 CC are given in AAQ29842-44. The methods for determining an individuals
 CC genotype at the GGG locus with respect to a set of alleles improves the
 CC discriminatory power of GGG typing methodology compared to previous
 CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 18 BP; 6 A; 10 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 8.9%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 3.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GTTGGGAAGTTGGGT 1711
 Db 17 GGTGGGAAGTTGGT 4

RESULT 215
 AAT60160/C
 ID AAT60160 standard; DNA; 18 BP.
 XX AC AAT60160;
 XX DT 01-DEC-1997 (first entry)
 XX DE Collagen gene promoter region binding oligomer Oligo 164 Aps.
 XX KW Triplex; inhibition; collagen gene; promoter; pathological fibrosis;

KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;
 KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
 KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
 XX OS Synthetic.

XX PH Key Location/Qualifiers
 FT misc_feature 1..18
 FT /*tag= a
 FT /note= "Phosphorothioate linkages"

XX PN WO9710254-A1.
 XX PD 20-MAR-1997.
 XX PF 12-SEP-1996; 96WO-US014640.
 XX PR 15-SEP-1995; 95US-00528836.
 XX PR 11-SEP-1996; 96US-00712357.
 XX PA (GUNT/) GUNTAKA R V.
 XX PI Guntaka RV, Weber KT, Kovacs A, Kandala J;
 XX DR WPI; 1997-202172/18.
 XX PF Triplex forming oligomer binds to collagen gene promoter region - used to
 PF impede pathological fibrosis etc.
 XX PS Claim 18; Page 36; 52pp; English.
 XX CC An oligomer has been produced which is capable of inhibiting expression
 CC of a collagen gene. The present sequence represents a specifically
 CC claimed oligomer Oligo 164 APS, which binds to the polypurine-
 CC polypyrimidine region of the rat alpha(I) collagen gene promoter region.
 CC The oligomer may be used to impede pathological fibrosis which is
 CC associated with myocardial fibrosis in hypertensive heart diseases,
 CC atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin
 CC fibrosis found in scleroderma, in hypertrophic scars and in skin
 CC following burn injury. The oligomer inhibits expression of a collagen
 CC gene after insertion into a cell by causing an intracellular reaction
 CC forming oligomer (TFO) which is targeted to a 30-mer polypurine
 CC oligonucleotide corresponding to the noncoding strand of the promoter
 CC between -170 and -140. This section was chosen due to its binding
 CC stability at physiological pH
 XX SQ Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 8.9%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 3.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
 Db 17 CTCCTCCCTTTCCT 4

RESULT 216
 AAT60165/C
 ID AAT60165 standard; DNA; 18 BP.
 XX AC AAT60165;
 XX DT 01-DEC-1997 (first entry)
 XX DE Collagen gene promoter region binding oligomer Oligo 164 AP.
 XX KW Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
 KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;
 KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
 KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.

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OS Synthetic.
XX WO9710254-A1.
XX 20-MAR-1997.
XX
XX 12-SEP-1996; 96WO-US014640.
XX
XX 15-SEP-1995; 95US-00528836.
XX 11-SEP-1996; 96US-00712357.
XX
XX (GUNT/) GUNTAKA R V.
XX
XX Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX WPI; 1997-202172/18.
XX
XX Triplex forming oligomer binds to collagen gene promoter region - used to
XX impede pathological fibrosis etc.
XX
XX Example 4; Page 35; 52pp; English.
XX
XX An oligomer has been produced which is capable of inhibiting expression
XX of a collagen gene. The present sequence represents an oligomer Oligo 164
XX AP, which binds to the polypurine-polypyrimidine region of the rat
XX alpha(I) collagen gene promoter region. The oligomer may be used to
XX impede pathological fibrosis which is associated with myocardial fibrosis
XX in hypertensive heart diseases, atherosclerosis, restenosis, liver
XX cirrhosis, lung fibrosis, and skin fibrosis found in scleroderma, in
XX hypertrophic scars and in skin following burn injury. The oligomer
XX inhibits expression of a collagen gene after insertion into a cell by
XX causing an intracellular reaction which inhibits gene expression. The
XX oligomer is preferably a triplex forming oligomer (TFO) which is targeted
XX to a 30-mer polypurine oligonucleotide corresponding to the noncoding
XX strand of the promoter between -170 and -140. This section was chosen due
XX to its binding stability at physiological pH
XX
XX Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 8.9%; Score 12.4; DB 1; Length 18;
XX Best Local Similarity 92.9%; Pred. No. 3.2e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1743 CTCCTCCCTATCCT 1756
XX |||||
XX 17 CTCCTCCCTTTCCT 4
XX
XX RESULT 217
XX AAT60158/c
XX ID AAT60158 standard; DNA; 18 BP.
XX
XX AC AAT60158;
XX
XX DT 01-DEC-1997 (first entry)
XX
XX DE Collagen gene promoter region binding oligomer Oligo 147 P.
XX
XX KW Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
XX myocardial fibrosis; hypertensive heart disease; atherosclerosis;
XX restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
XX hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
XX
XX OS Synthetic.
XX
XX PN WO9710254-A1.
XX
XX PD 20-MAR-1997.
XX
XX PF 12-SEP-1996; 96WO-US014640.
XX
XX PR 15-SEP-1995; 95US-00528836.
XX 11-SEP-1996; 96US-00712357.
XX

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XX (GUNT/) GUNTAKA R V.
XX
XX Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX WPI; 1997-202172/18.
XX
XX Triplex forming oligomer binds to collagen gene promoter region - used to
XX impede pathological fibrosis etc.
XX
XX Claim 18; Page 34; 52pp; English.
XX
XX An oligomer has been produced which is capable of inhibiting expression
XX of a collagen gene. The present sequence represents a specifically
XX claimed oligomer Oligo 147 P, which binds to the polypurine-
XX polypyrimidine region of the rat alpha(I) collagen gene promoter region.
XX The oligomer may be used to impede pathological fibrosis which is
XX associated with myocardial fibrosis in hypertensive heart diseases,
XX atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin
XX fibrosis found in scleroderma, in hypertrophic scars and in skin
XX following burn injury. The oligomer inhibits expression of a collagen
XX gene after insertion into a cell by causing an intracellular reaction
XX which inhibits gene expression. The oligomer is preferably a triplex
XX forming oligomer (TFO) which is targeted to a 30-mer polypurine
XX oligonucleotide corresponding to the noncoding strand of the promoter
XX between -170 and -140. This section was chosen due to its binding
XX stability at physiological pH
XX
XX SQ Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 8.9%; Score 12.4; DB 1; Length 18;
XX Best Local Similarity 92.9%; Pred. No. 3.2e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1743 CTCCTCCCTATCCT 1756
XX |||||
XX 17 CTCCTCCCTTTCCT 4
XX
XX RESULT 218
XX AAX70290/c
XX ID AAX70290 standard; RNA; 18 BP.
XX
XX AC AAX70290;
XX
XX DT 28-JUL-1999 (first entry)
XX
XX DE Human flt1 VEGF receptor hairpin ribozyme substrate #58.
XX
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9715662-A2.
XX
XX PD 01-MAY-1997.
XX
XX PF 25-OCT-1996; 96WO-US017480.
XX
XX PR 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-000584040.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX

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PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX
XX Claim 4; Page 94; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
XX Sequence 18 BP; 3 A; 6 C; 5 G; 0 T; 4 U; 0 Other;
SQ
Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. NO. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1663 GCTCACAGCTGGAA 1676
Db 16 GCCCACAGCTGGAA 3

RESULT 219
AAZ29823
ID AAZ29823 standard; DNA; 18 BP.
AC AAZ29823;
XX
XX 27-MAR-2000 (first entry)
DT
DE Forward PCR primer AT.1201F to generate modified human antithrombin III.
XX
XX Modified human antithrombin III; ATIII; elastase-resistant;
KW Igg activated neutrophil resistant; anti-thrombin activity; heparin;
KW anti-factor Xa activity; blood clotting disorder; sepsis; trauma; stroke;
KW thrombin activation-related pathological symptom; restenosis; thrombosis;
KW acute respiratory distress syndrome; thromboembolism; reocclusion;
KW forward primer AT.1201F; PCR mutagenesis; ss.
XX
XX Synthetic.
OS
XX WO9958098-A2.
PN
XX 18-NOV-1999.
XX
XX 12-MAY-1999; 99WO-US010549.
PF
XX 12-MAY-1998; 98US-0085197P.
PR
XX 05-MAY-1999; 99US-00305588.
PR
XX (BOCK/) BOCK S C.
PA (PICA/) PICARD V.
PA (ZENU/) ZENDEHROUH P.
XX
XX Bock SC, Picard V, Zendehtrouh P;
PI
XX WPI; 2000-116274/10.
DR
XX New modified human antithrombin III compounds, used for treating e.g.
XX sepsis, trauma, acute respiratory distress syndrome, restenosis,
PT thrombosis, thromboembolism or stroke.
PT
XX Example 1; Page 38; 75pp; English.
PS
XX The present sequence is a forward primer AT.1201F which was used in PCR
CC mutagenesis for generation of a modified ATIII using a template B1 which
CC is pUC19containing human ATIII.N135A cDNA insert. The modified ATIII has

CC enhanced heparin affinity, improved resistance to elastase and IgG-
CC activated neutrophils and retains anti-thrombin and anti-factor Xa
CC activities. It can be used to treat thrombin activation-related
CC pathological symptoms due to sepsis, trauma, acute respiratory distress
CC syndrome, restenosis, thrombosis, thromboembolism and stroke. Modified
CC ATIII can also be used to reduce the risk of reocclusion and restenosis
CC in percutaneous transluminal coronary angioplasty, thrombosis associated
CC with surgery, ischaemia/reperfusion injury, and coagulation abnormalities
CC in cancer or surgical patients
XX
SQ Sequence 18 BP; 4 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. NO. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1640 TTGTAGCAGGAGGC 1653
Db 3 TTGTGACAGAGGC 16

RESULT 220
AAZ98706/c
ID AAZ98706 standard; DNA; 18 BP.
XX
XX AC AAZ98706;
AC
XX
XX 20-JUN-2000 (first entry)
DT
DE Collagen promoter inhibitory oligonucleotide Oligo 147 P.
XX
XX Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
KW atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
KW peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
XX
XX Rattus sp.
OS
XX WO200008213-A1.
PN
XX 17-FEB-2000.
PD
XX 06-AUG-1999; 99WO-US017824.
PF
XX 07-AUG-1998; 98US-00130888.
PR
XX (GUNT/) GUNTAKA R V.
PA
XX Guntaka RV, Weber KT, Kovacs A, Kandala J;
PI
XX WPI; 2000-205739/18.
DR
XX Inhibitors of collagen gene useful for treating fibrosis associated with
XX atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis,
XX comprises oligomers capable of inhibiting collagen gene.
XX
XX Claim 19; Fig 8; 77pp; English.
XX
XX This sequence represents an oligomer which is capable of inhibiting the
XX expression of the collagen gene. The oligomer is capable of binding to
XX the promoter region of the collagen gene. Collagen is a family of fibrous
XX proteins, and is the major element of skin, bone, tendon, cartilage,
XX blood vessels and teeth. The oligomers are useful for inhibiting
XX expression of the collagen gene, comprising inserting the oligomers into
XX a cell and causing an intracellular reaction to inhibit the gene
XX expression. The collagen inhibitory oligomers of the invention are useful
XX for treating pathological fibrosis associated with myocardial fibrosis in
XX hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
XX lung fibrosis, peritoneal fibrosis and skin fibrosis found in
XX scleroderma, hypertrophic scars and burn injury
XX
SQ Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;
Query Match 8.9%; Score 12.4; DB 1; Length 18;

Best Local Similarity 92.9%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
 Db 17 CTCCTCCCTTCTCT 4

RESULT 221
 AAZ98715/c
 ID AAZ98715 standard; DNA; 18 BP.
 XX
 AC AAZ98715;
 XX
 DT 20-JUN-2000 (first entry)
 XX
 DE Collagen promoter inhibitory oligonucleotide Oligo Col 164 APS.
 XX
 KW Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
 KW atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
 KW peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
 XX
 OS Rattus sp.
 XX
 PN WO2000082113-A1.
 XX
 PD 17-FEB-2000.
 XX
 PF 06-AUG-1999; 99WO-US017824.
 XX
 PR 07-AUG-1998; 98US-00130888.
 XX
 PA (GUNT/) GUNTAKA R V.
 XX
 PI Guntaka RV, Weber KT, Kovacs A, Kandala J;
 XX
 DR WPI; 2000-205739/18.
 XX
 XX Inhibitors of collagen gene useful for treating fibrosis associated with
 PT atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis,
 PT comprises oligomers capable of inhibiting collagen gene.
 XX
 PS Example 4; Fig 8; 77pp; English.
 XX
 CC This sequence represents an oligomer which is capable of inhibiting the
 CC expression of the collagen gene. The oligomer is capable of binding to
 CC the promoter region of the collagen gene. Collagen is a family of fibrous
 CC proteins, and is the major element of skin, bone, tendon, cartilage,
 CC blood vessels and teeth. The oligomers are useful for inhibiting
 CC expression of the collagen gene, comprising inserting the oligomers into
 CC a cell and causing an intracellular reaction to inhibit the gene
 CC expression. The collagen inhibitory oligomers of the invention are useful
 CC for treating pathological fibrosis associated with myocardial fibrosis in
 CC hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
 CC lung fibrosis, peritoneal fibrosis and skin fibrosis found in
 CC scleroderma, hypertrophic scars and burn injury
 XX
 SQ Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;
 Query Match 8.9%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 3.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
 Db 17 CTCCTCCCTTCTCT 4

RESULT 222
 AAZ98708/c
 ID AAZ98708 standard; DNA; 18 BP.
 XX
 AC AAZ98708;

XX 20-JUN-2000 (first entry)
 DT Collagen promoter inhibitory oligonucleotide Oligo Col 164 APS.
 XX
 DE Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
 KW atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
 KW peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
 XX
 OS Rattus sp.
 XX
 PN WO2000082113-A1.
 XX
 PD 17-FEB-2000.
 XX
 PF 06-AUG-1999; 99WO-US017824.
 XX
 PR 07-AUG-1998; 98US-00130888.
 XX
 PA (GUNT/) GUNTAKA R V.
 XX
 PI Guntaka RV, Weber KT, Kovacs A, Kandala J;
 XX
 DR WPI; 2000-205739/18.
 XX
 XX Inhibitors of collagen gene useful for treating fibrosis associated with
 PT atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis,
 PT comprises oligomers capable of inhibiting collagen gene.
 XX
 PS Claim 19; Fig 8; 77pp; English.
 XX
 CC This sequence represents an oligomer which is capable of inhibiting the
 CC expression of the collagen gene. The oligomer is capable of binding to
 CC the promoter region of the collagen gene. Collagen is a family of fibrous
 CC proteins, and is the major element of skin, bone, tendon, cartilage,
 CC blood vessels and teeth. The oligomers are useful for inhibiting
 CC expression of the collagen gene, comprising inserting the oligomers into
 CC a cell and causing an intracellular reaction to inhibit the gene
 CC expression. The collagen inhibitory oligomers of the invention are useful
 CC for treating pathological fibrosis associated with myocardial fibrosis in
 CC hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
 CC lung fibrosis, peritoneal fibrosis and skin fibrosis found in
 CC scleroderma, hypertrophic scars and burn injury
 XX
 SQ Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;
 Query Match 8.9%; Score 12.4; DB 1; Length 18;
 Best Local Similarity 92.9%; Pred. No. 3.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
 Db 17 CTCCTCCCTTCTCT 4

RESULT 223
 AAZ76867
 ID AAZ76867 standard; DNA; 18 BP.
 XX
 AC AAZ76867;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human biallelic marker downstream amplification primer SEQ ID NO:11223.
 XX
 KW Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX
 OS Homo sapiens.
 XX

PN W09954500-A2.
XX 28-OCT-1999.
XX 21-APR-1999; 99WO-IB000822.
XX 21-APR-1998; 98US-0082614P.
XX 23-NOV-1998; 98US-0109732P.
XX (GEST) GENSET.
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX Claim 9; Page 2623; 2745pp; English.
XX AA265654 to AA269578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AA269579 to AA277440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention
XX have a variety of uses: they can be used for high density mapping of the
XX human genome, and in complex association studies and haplotyping studies
XX which are useful in determining the genetic basis for disease states.
XX Compositions and methods of the invention can also be useful for the
XX identification of the targets for the development of pharmaceutical
XX agents and diagnostic methods, as well as the characterisation of the
XX differential efficacious responses to and side effects from
XX pharmaceutical agents acting on a disease as well as other treatment.
XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3157, 3227, 3297 and
XX 3367, are not actually given a sequence in the Sequence Listing from the
XX present invention
XX Sequence 18 BP; 8 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1722 GAGATGGAGATTGG 1735
Db ||||| ||||| ||
5 GAGATGGAGATTAG 18
RESULT 224
AAD21095
ID AAD21095 standard; DNA; 18 BP.
XX AC AAD21095;
XX 15-JAN-2002 (first entry)
XX Patched-1 RT-PCR primer #2 used in the method for modulating hair growth.
XX Signal transduction; Wnt protein; dermal papilla; DP; beta-catenin;
XX GSK3beta kinase; genetic pattern baldness; hormonal disorder;
XX chemotherapy; anagen phase; hair growth promoter; RT-PCR primer; ss.
XX Unidentified.
XX WO200174164-A1.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US010164.
XX 31-MAR-2000; 2000US-0193771P.
XX 12-JAN-2001; 2001US-0261690P.
XX (GEHO) GEN HOSPITAL CORP.
PA

XX Kishimoto J, Burgeson R, Morgan BA;
XX WPI; 2001-648492/74.
XX Promoting or inhibiting hair growth in a subject by inducing or
XX mimicking, or inhibiting effect of Wnt-promoted signal transduction,
XX respectively.
XX Disclosure; Page 22; 63pp; English.
XX The present invention relates to promoting hair growth in a subject which
XX involves inducing or mimicking the effect of Wnt-promoted signal
XX transduction in a subject and inhibiting hair growth in a subject
XX involves inhibiting level of Wnt protein or inhibiting an effect of Wnt-
XX promoted signal transduction in a subject. The invention is used for
XX providing and maintaining dermal papilla (DP) cell graft which involves
XX culturing a DP cell from a subject under conditions that induce or mimic
XX the effect of Wnt-promoted signal transduction, thereby providing and
XX maintaining a DP cell graft. Preferably, the DP cell is cultured in the
XX presence of Wnt, its fragment or analogue; lithium chloride, beta-catenin
XX and/or LEF1, an agent which inhibits beta-catenin phosphorylation or
XX GSK3beta kinase, or an agent which promotes beta-catenin accumulation.
XX Hair growth is promoted in subject's scalp, or face e.g., beard and/or
XX mustache, or in conditions where subject suffers from genetic pattern
XX baldness, suffers from a hormonal disorder which decreases hair growth,
XX has received a treatment, e.g., radiation or chemotherapy, or a drug
XX which inhibits hair growth, or has had a surgical procedure, e.g., skin
XX graft, which is in need of hair growth. Hair growth is inhibited on the
XX subject's scalp, subject's face, e.g., beard and/or mustache, facial hair
XX growth, or eyebrow growth, back, legs, chest, armpits. Promoting hair
XX growth is useful for maintaining or promoting hair inductive activity.
XX Inhibiting hair growth is useful for maintaining or promoting anagen
XX phase gene expression in the subject's scalp, face e.g., upper lip and/or
XX chin. The present sequence is patched-1 RT-PCR primer used in the method
XX for modulating hair growth
XX Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1685 TCTCTCTCCAGCGTG 1698
Db ||||| ||||| ||
4 TCTCTCTCCAGCATG 17
RESULT 225
ABT06527
ID ABT06527 standard; DNA; 18 BP.
XX AC ABT06527;
XX 07-NOV-2002 (first entry)
XX HOXA5 gene promoter sequence methylation specific primer #1.
XX Human; methylated gene; methylation; breast cancer; marker; WT-1;
XX cell proliferative disorder; TWIST; HOXA5; NES-1; RARbeta; cyclin D2;
XX retinoic acid receptor beta; oestrogen receptor; Wilms' tumour;
XX 14.3.3 sigma; HIN-1; RASSF1A; tumour suppressor gene; hypermethylation;
XX PCR; primer; ss.
XX Unidentified.
XX WO200259347-A2.
XX 01-AUG-2002.
XX 28-JAN-2002; 2002WO-US002455.
XX 26-JAN-2001; 2001US-00771357.
PR

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XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA Sukumar S, Evron E, Dooley WC, Sacchi N, Davidson N, Fackler MJ;
XX WPI; 2002-599803/64.
XX
XX Diagnosing and/or determining a predisposition to a cellular
PT proliferative disorder of breast tissue, in particular breast cancer, by
PT determining the state of methylation of one or more nucleic acids
PT isolated from the subject.
XX
XX Disclosure; Fig 5C; 115pp; English.
XX
XX The present invention relates to a method of diagnosing a cellular
CC proliferative disorder of breast tissue, which involves determining the
CC state of methylation of one or more nucleic acids isolated from the
CC subject, where the state of methylation of the nucleic acids as compared
CC with a state of methylation from a subject not having the cellular
CC proliferative disorder of breast tissue is indicative of a cellular
CC proliferative disorder of breast tissue in the subject. The nucleic acids
CC may be TWIST, HoxA5, NES-1, retinoic acid receptor beta (RARbeta),
CC oestrogen receptor, cyclin D2, Wilms' tumour gene (WT-1), 14.3.3 sigma,
CC HIN-1 or RASSF1A. The method is useful for diagnosing and/or determining
CC a predisposition to a cellular proliferative disorder, in particular
CC breast cancer including ductal carcinoma in situ, lobular carcinoma,
CC colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic
CC carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and
CC papillary carcinoma in situ. The present sequence is a primer used in the
CC exemplification of the invention
XX
XX Sequence 18 BP; 2 A; 0 C; 9 G; 7 T; 0 U; 0 Other;
SQ
Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1698 GGTGGAAGTTGGGT 1711
DB 4 GTTGAAGTTGGGT 17
RESULT 226
AAQ25868/c
ID AAQ25868 standard; DNA; 19 BP.
XX
XX AAQ25868;
XX
XX 25-MAR-2003 (revised)
XX 04-JAN-1993 (first entry)
XX
XX 5' Alu primer.
XX
XX PCR; sequence conservation; DNA synthesis; amplification; ss.
XX
XX Synthetic.
XX
XX WO9210566-Al.
XX
XX 25-JUN-1992.
XX
XX 21-NOV-1991; 91WO-US008739.
XX
XX 13-DEC-1990; 90US-00627945.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Siciliano MJ, Liu P;
XX
XX WPI; 1992-234623/28.
XX
XX Chromosome-specific DNA probes free of species-specific repeat DNA - used
PT for identification and banding of human chromosomes.
PT
```

```
XX Claim 64; Page 63; 73pp; English.
XX
XX The sequences given in AAQ25868-9 are nucleotide primers which are
CC characterised by binding to a 5' and a 3' Alu terminus, respectively.
CC These Alu primers were based on a current revision of consensus sequence
CC of Alu repeats. This revision is based on nucleotide sequences of 50
CC different, cloned and sequenced human Alu segments. Two regions on the
CC sequence showed a high degree of conservation and these were used as
CC candidate regions for the primer locations. In order to minimize the
CC incorporation of Alu sequence itself in the inter-Alu-PCR, the 5' primer
CC was designed to recognise a specific region and to direct DNA synthesis
CC off the 5' end and away from the middle of the Alu segment to which it is
CC bound. The converse is true for the 3' primer. Amplification using these
CC two primers yields products ranging from a few hundred to several
CC thousand base pairs. The primer design maximizes both the number of Alu
CC segments recruited and the number of inter-Alu unique sequences
CC amplified. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 19 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 2 Other;
SQ
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCAGCTGGAACCC 1679
DB 18 GGCTCAYRCCTGTATCC 1
RESULT 227
AAQ48682/c
ID AAQ48682 standard; cDNA; 19 BP.
XX
XX AAQ48682;
XX
XX 25-MAR-2003 (revised)
XX 25-FEB-1994 (first entry)
XX
XX Human Alu segment consensus sequence PCR primer Alu-1.
XX
XX Abnormality; polymerase chain reaction; amplification; ss.
XX
XX Synthetic.
XX
XX WO9317104-Al.
XX
XX 02-SEP-1993.
XX
XX 19-FEB-1993; 93WO-US001545.
XX
XX 20-FEB-1992; 92US-00839255.
XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Brook JD, Housman DE;
XX
XX WPI; 1993-288410/36.
XX
XX DNA sequence of myotonic dystrophy gene - used to produce probes and
PT identify CHR 19 abnormality and protein kinase responsible.
PT
XX Example; Page 32; 64pp; English.
XX
XX The sequence is that of a PCR primer Alu-1 which specifically recognises
CC human consensus sequences located at the 5' and 3' ends of Alu segments.
CC It was used with 2F5 template to amplify human unique sequences. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 19 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 2 Other;
SQ
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 3.4e+02;
```


Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1662 GGCTCAGCTGGAACCC 1679
 |||||::|||
 Db 18 GGCTCAYRCTGTATCC 1

RESULT 228
 AAQ85676/c
 ID AAQ85676 standard; DNA; 19 BP.
 AC AAQ85676;
 XX
 XX 25-MAR-2003 (revised)
 DT 04-OCT-1995 (first entry)
 XX
 XX
 DE PCR primer alu 1 for inter-Alu region of Wilson's disease gene.
 XX
 XX Wilson's disease; chromosome 13; Alu; PCR primer; ss.
 XX
 XX Synthetic.
 XX
 XX OS
 XX
 XX Key Location/Qualifiers
 FH misc_difference 1..19
 FT /*tag= a
 FT /note= "Std IUPAC codes used"
 XX
 XX WO9506714-Al.
 PN
 PN 09-MAR-1995.
 PD
 PD
 XX
 XX 01-SEP-1994; 94WO-US009851.
 PF
 PF
 XX
 XX 01-SEP-1993; 93US-00118441.
 PR
 PR
 XX
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 PA (GEO) GEN HOSPITAL CORP.
 XX
 XX Gilliam TC, Tanzi RE;
 PI
 PI WPI; 1995-115430/15.
 DR
 DR
 XX
 XX Isolated Wilson's disease nucleic acid mol. - also probes, vectors, etc.,
 PT useful for diagnosis and gene therapy of Wilson's disease.
 PT
 XX Example; Page 30; 175pp; English.
 PS
 PS
 XX
 XX In order to physically map and clone the region of the Wilson's disease
 CC (WD) gene, a 4.3kb insert from the WD flanking marker D13S31 (probe
 CC pCR1324) was used to screen a large insert, CEPH II YAC sublibrary. A
 CC higher resolution YAC map was constructed using inter-Alu PCR product
 CC from 4 large YAC clones to screen the 1431 colony CEPH I YAC sublibrary.
 CC A total of 16 mid-size YACs were identified. The pattern of mid-size YACs
 CC detected by each large YAC clone was used to order the smaller YAC clones
 CC relative to one another. Inter-Alu PCR "fingerprinting" of YAC clones
 CC further assisted the ordering process. The data for this are not given in
 CC the publication. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX
 XX Sequence 19 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 2 Other;
 SQ
 Query Match 8.9%; Score 12.4; DB 1; Length 19;
 Best Local Similarity 72.2%; Pred. No. 3.4e+02;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1662 GGCTCAGCTGGAACCC 1679
 |||||::|||
 Db 18 GGCTCAYRCTGTATCC 1

RESULT 229
 AAQ76249
 ID AAQ76249 standard; DNA; 19 BP.
 AC AAQ76249;
 XX
 XX 25-MAR-2003 (revised)
 DT 10-AUG-1995 (first entry)
 XX
 XX
 DE Generic primer from Alu-1 primer set.
 XX
 XX Primer; PCR; amplification; primer set; probe; Alu sequence; Alu repeat;
 KW Alu consensus sequence; chromosome; breakpoint; rearrangement;
 KW chronic myelogenous leukemia; Philadelphia chromosome; translocation; ss.
 XX
 XX Synthetic.
 XX
 XX OS
 XX
 XX WO9428178-Al.
 PN
 PN 08-DEC-1994.
 PD
 PD
 XX
 XX 01-JUN-1994; 94WO-US006194.
 PF
 PF
 XX
 XX 01-JUN-1993; 93US-00070517.
 PR
 PR
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 PA Siciliano MJ, Liu P;
 PI
 PI WPI; 1995-022844/03.
 DR
 DR
 XX
 XX DNA probe specific for Human chromosome region 9q34 - allows detection of
 PT bcr/abl rearrangement in interphase nuclei.
 PT
 XX Disclosure; Page 22; 81pp; English.
 PS
 PS
 XX
 XX The consensus sequence, from bases 13-31, of the 5' end of a 300 bp Alu
 CC segment. The sequence was used to generate a set of primers, designated
 CC Alu-1 primers set (AAQ76247). The primers of the set have a reverse
 CC complementary sequence to the Alu consensus sequence. Thus priming with
 CC the Alu-1 set directs synthesis towards the 5' end (i.e. away from the
 CC middle) of the Alu segment. Since the primer set is designed to bind
 CC close to the edge of an Alu segment, amplification with these primers
 CC will reduce the amount of Alu segment sequence and increase the amount of
 CC specific chromosomal DNA present required for probe production. The
 CC primer set is useful in the production of chromosomal specific probes e.g
 CC for the detection of chromosomal breakpoints and rearrangements such as a
 CC probe to detect chronic myelogenous leukemia characterised by the
 CC Philadelphia chromosome, arising from a reciprocal translocation t(9;22)
 CC (q34;q11). (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX
 XX Sequence 19 BP; 3 A; 6 C; 3 G; 5 T; 0 U; 2 Other;
 SQ
 Query Match 8.9%; Score 12.4; DB 1; Length 19;
 Best Local Similarity 72.2%; Pred. No. 3.4e+02;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1662 GGCTCAGCTGGAACCC 1679
 |||||::|||
 Db 2 GGCTCAYRCTGTATCC 19

RESULT 230
 AAQ76247/c
 ID AAQ76247 standard; DNA; 19 BP.
 AC AAQ76247;
 XX
 XX 25-MAR-2003 (revised)
 DT 10-AUG-1995 (first entry)
 XX
 XX
 DE Generic primer from Alu-1 primer set.
 XX
 XX Primer; PCR; amplification; primer set; probe; Alu sequence; Alu repeat;
 KW Alu consensus sequence; chromosome; breakpoint; rearrangement;
 KW chronic myelogenous leukemia; Philadelphia chromosome; translocation; ss.
 XX
 XX Synthetic.
 XX
 XX OS
 XX
 XX WO9428178-Al.
 PN
 PN 08-DEC-1994.
 PD
 PD
 XX
 XX 01-JUN-1994; 94WO-US006194.
 PF
 PF
 XX
 XX 01-JUN-1993; 93US-00070517.
 PR
 PR
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 PA Siciliano MJ, Liu P;
 PI
 PI WPI; 1995-022844/03.
 DR
 DR
 XX
 XX DNA probe specific for Human chromosome region 9q34 - allows detection of
 PT bcr/abl rearrangement in interphase nuclei.
 PT
 XX Disclosure; Page 22; 81pp; English.
 PS
 PS
 XX
 XX The consensus sequence, from bases 13-31, of the 5' end of a 300 bp Alu
 CC segment. The sequence was used to generate a set of primers, designated
 CC Alu-1 primers set (AAQ76247). The primers of the set have a reverse
 CC complementary sequence to the Alu consensus sequence. Thus priming with
 CC the Alu-1 set directs synthesis towards the 5' end (i.e. away from the
 CC middle) of the Alu segment. Since the primer set is designed to bind
 CC close to the edge of an Alu segment, amplification with these primers
 CC will reduce the amount of Alu segment sequence and increase the amount of
 CC specific chromosomal DNA present required for probe production. The
 CC primer set is useful in the production of chromosomal specific probes e.g
 CC for the detection of chromosomal breakpoints and rearrangements such as a
 CC probe to detect chronic myelogenous leukemia characterised by the
 CC Philadelphia chromosome, arising from a reciprocal translocation t(9;22)
 CC (q34;q11). (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX
 XX Sequence 19 BP; 3 A; 6 C; 3 G; 5 T; 0 U; 2 Other;
 SQ
 Query Match 8.9%; Score 12.4; DB 1; Length 19;
 Best Local Similarity 72.2%; Pred. No. 3.4e+02;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1662 GGCTCAGCTGGAACCC 1679
 |||||::|||
 Db 2 GGCTCAYRCTGTATCC 19

OS Synthetic.
 XX WO9428178-A1.
 PN
 XX
 XX
 PD
 XX
 XX 08-DEC-1994.
 PF
 XX 01-JUN-1994; 94WO-US006194.
 XX
 PR 01-JUN-1993; 93US-00070517.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Siciliano MJ, Liu P;
 PI
 XX WPI; 1995-022844/03.
 DR
 XX DNA probe specific for Human chromosome region 9q34 - allows detection of
 PT bcr/abl rearrangement in interphase nuclei.
 PT
 XX Disclosure; Page 11; 81pp; English.
 PS
 XX The generic sequence of a primer set designated Alu-1. The primer set was
 CC based on bases 13-31 of the 5' end of a 300 bp Alu segment (AAQ76249).
 CC The primers of the set have a reverse complementary sequence to the Alu
 CC consensus sequence. Thus priming with the Alu-1 set directs synthesis
 CC towards the 5' end (i.e. away from the middle) of the Alu segment. Since
 CC the primer set is designed to bind close to the edge of an Alu segment,
 CC amplification with these primers will reduce the amount of Alu segment
 CC sequence and increase the amount of specific chromosomal DNA present
 CC required for probe production. The primer set is useful in the production
 CC of chromosomal specific probes e.g. for the detection of chromosomal
 CC breakpoints and rearrangements such as a probe to detect chronic
 CC myelogenous leukemia characterised by the Philadelphia chromosome,
 CC arising from a reciprocal translocation t(9;22) (q34;q11). (Updated on 25
 CC -MAR-2003 to correct PN field.)
 XX
 XX Sequence 19 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 2 Other;
 SQ
 Query Match 8.9%; Score 12.4; DB 1; Length 19;
 Best Local Similarity 72.2%; Pred. No. 3.4e+02;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1662 GGCTCAGCTGGAGCC 1679
 Db 18 GGCTCAYRCTGTATCC 1
 RESULT 231
 AAV83937/c
 ID AAV83937 standard; DNA; 19 BP.
 XX
 AC AAV83937;
 XX
 DT 03-MAR-1999 (first entry)
 XX
 DE PCR primer used to produce a YAC probe.
 XX
 XX Yeast artificial chromosome; YAC; probe; eukaryotic chromosome;
 KW neocentromere; replication; extra-chromosomal element; segregation;
 KW cell division; artificial chromosome; gene therapy;
 KW human artificial chromosome; transgenic; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9851790-A1.
 PN
 XX
 PD 19-NOV-1998.
 XX
 PF 13-MAY-1998; 98WO-AU000352.
 XX
 XX 13-MAY-1997; 97AU-00006784.
 PR
 PR 26-AUG-1997; 97AU-00008791.
 XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PI Choo K, Du Sart D, Cancilla MR;
 XX
 DR WPI; 1999-009773/01.
 XX
 XX New isolated nucleic acid comprising neocentromere sequences from
 PT eukaryotic chromosome - used to produce replicable, segregating
 PT artificial chromosomes that can carry large amounts of DNA for gene
 PT therapy.
 XX
 XX Example 1; Page 24; 540pp; English.
 PS
 XX PCR primers AAV83937-38 were used to amplify total yeast genomic DNA to
 CC produce yeast artificial chromosome (YAC) probes. The YAC probes are used
 CC to isolate the nucleic acid sequences of the invention. The specification
 CC describes nucleic acid sequences derived from a eukaryotic chromosome,
 CC including a neocentromere or its functional derivative or hybrid, that
 CC are able, in a compatible cell, of replicating, acting as extra-
 CC chromosomal element and segregating during cell division. The sequences
 CC can be used to construct artificial chromosomes for use in gene therapy
 CC comprising a replicable, segregating nucleic acid that confers a specific
 CC phenotype on cells. Human artificial chromosomes can propagate in human
 CC cells and carry large amounts of DNA (e.g. therapeutic genes), and, being
 CC extra-chromosomal, they are not mutagenic. The artificial chromosomes are
 CC also useful for generation of transgenic plants and animals, in
 CC production of proteins and to make diagnostic reagents, e.g. for
 CC expression of cytokines, receptors and growth factors, or to increase the
 CC copy number of a gene in a cell. The constructs may also be used for
 CC functional and structural analysis of chromosomes
 XX
 XX Sequence 19 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 2 Other;
 SQ
 Query Match 8.9%; Score 12.4; DB 1; Length 19;
 Best Local Similarity 72.2%; Pred. No. 3.4e+02;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1662 GGCTCAGCTGGAGCC 1679
 Db 18 GGCTCAYRCTGTATCC 1
 RESULT 232
 AAZ76552/c
 ID AAZ76552 standard; DNA; 19 BP.
 XX
 AC AAZ76552;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human biallelic marker downstream amplification primer SEQ ID NO:10908.
 XX
 XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9954500-A2.
 PN
 XX 28-OCT-1999.
 PD
 XX 21-APR-1999; 99WO-IB000822.
 PF
 XX 21-APR-1998; 98US-0082614P.
 PR
 PR 23-NOV-1998; 98US-0109732P.
 XX
 XX (GEST) GENSET.
 PA
 XX Cohen D, Blumenfeld M, Chumakov I;
 PI
 XX


```

PI Boon-Falleur T;
XX
DR WPI; 1995-292948/38.
XX
PT Identification of cells presenting HLA-C-clone 10 or WAGE-1 derived
PT peptide - allows diagnosis and treatment of individuals with cellular
PT abnormalities, e.g. melanoma, also HLA-Cw*1601 derived peptide(s).
XX
XX
PS Claim 20; Page 19; 26pp; English.
XX
CC HLA-C-clone 10 is presented on the surface of certain abnormal cells,
CC MAGS-1 is also expressed by these cells. AAT03827-T03830 are PCR primers
CC for the HLA molecule that may be used in a kit to determine the
CC expression of HLA-C-clone 10. Peptides of such molecules that are
CC expressed and presented on the surface of abnormal cells are useful for
CC the identification of abnormal cells and thus they allow diagnosis and
CC treatment of cellular abnormalities, e.g. melanoma and other cancers. The
CC isolated nucleic acid molecules coding for the peptides are also useful
CC as probes for the determination of HLA-clone-C expression. HLA-C-clone 10
CC is also known as HLA-Cw*1601
XX
SQ Sequence 17 BP; 6 A; 6 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1653 CAAGCACCAGGTCACA 1669
DB 1 CAAGCGCCAGGCACAGA 17
|||||
AAV91297
ID AAV91297 standard; RNA; 17 BP.
XX
AC AAV91297;
XX
DT 18-FEB-1999 (first entry)
XX
DE Human C-raf target site nucleotide position 2318.
XX
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN WO9850530-A2.
XX
PD 12-NOV-1998.
XX
PF 05-MAY-1998; 98WO-US009249.
XX
PR 09-MAY-1997; 97US-0046059P.
PR 09-JUN-1997; 97US-0049002P.
PR 03-JUL-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI Parry T, Beigelman L, Moswiggen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
DR WPI; 1999-009494/01.
XX

```

```

PT Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
XX Claim 177; Page 152; 259pp; English.
XX
CC A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-raf. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX
SQ Sequence 17 BP; 4 A; 8 C; 3 G; 0 T; 2 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 3.2e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1749 CCTATCCTAAAGGCCCA 1765
DB 1 CCCAUGCUCACAGGCCCA 17
|||||
AAV93415/C
ID AAV93415 standard; RNA; 17 BP.
XX
AC AAV93415;
XX
DT 18-FEB-1999 (first entry)
XX
DE Human B-raf substrate nucleotide position 835.
XX
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN WO9850530-A2.
XX
PD 12-NOV-1998.
XX
PF 05-MAY-1998; 98WO-US009249.
XX
PR 09-MAY-1997; 97US-0046059P.
PR 09-JUN-1997; 97US-0049002P.
PR 03-JUL-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI Parry T, Beigelman L, Moswiggen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
DR WPI; 1999-009494/01.
XX

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PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;

DR WPI: 1999-009494/01.

XX Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer,
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 PT used as antiviral agents and synthons.

PS Claim 177; Page 167; 259pp; English.

XX A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-rat. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene

SQ Sequence 17 BP; 2 A; 5 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGACCCCTG 1681

DB 17 TGACAGCGGAACCCCTG 1

RESULT 237
 AAA55987

ID AAA55987 standard; DNA; 17 BP.

AC AAA55987;

DT 05-SEP-2000 (first entry)

DE Murine G713 amplification PCR primer SEQ ID NO:26.

XX Human; chromosome 13; G713; chromosome 13q31-q33; schizophrenia;
 KW biallelic marker; polymorphism; central nervous disease; detection;
 KW neuroleptic; G713 gene expression inhibitor; genotyping; PCR primer;
 KW brain disorder; psychiatric disorder; bipolar disorder; ss.

OS Mus musculus.

XX WO200022122-A2.

PN 20-APR-2000.

PD 12-OCT-1999; 99WO-IB001730.

PF 13-OCT-1998; 98US-0103955P.

PR 30-OCT-1998; 98US-0106457P.

XX (GEST) GENSET.

PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen D, Essieux L;

XX DR

XX WPI: 2000-317979/27.

XX Novel polynucleotide of human G713 gene useful for diagnosis and
 PT prophylactic treatment of brain, psychiatric disorders like schizophrenia
 PT and bipolar disorders.

XX Example 1; Page 144; 271pp; English.

XX The present invention describes an isolated, purified or recombinant
 CC polynucleotide (PN) (I) comprising a contiguous span of 8 to 50
 CC nucleotides, where the span includes a G713 or chromosome 13q31-q33
 CC related biallelic marker. (I) has neuroleptic activity and can be used as
 CC a G713 gene expression inhibitor. (I) can be used genotyping to estimate
 CC the frequency of an allele of a G713 or chromosome 13q31-q33 related
 CC biallelic marker in a population, and of a haplotype for a set of
 CC biallelic markers in a population. (I) is also useful in detecting an
 CC association between a haplotype and a trait. The frequency is used for
 CC detecting an association between a genotype and a trait being
 CC schizophrenia. The genotype is used to determine whether an individual is
 CC at risk of developing schizophrenia. (I) can also be used as a medicament
 CC against several disorders preferably brain, psychiatric disorders such as
 CC schizophrenia and bipolar disorder. Early identification of risk of
 CC developing schizophrenia is possible, which would enable early and/or
 CC prophylactic treatment. AAA55964 to AAA55966 represent human G713 genomic
 CC DNA sequences; AAA55967 encodes the human G713 protein AAY90962; AAA55968
 CC encodes the murine G713 protein AAY90963; AAA55992 to AAA56030 represent
 CC human chromosome 13q31-q33 locus biallelic markers A12 to A49; AAA55969
 CC to AAA55991, and AAA56031 and AAA56032 represent PCR primers used in the
 CC exemplification of the present invention

XX Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1685 TCTCTCCAGCGTGGTG 1701

DB 1 TGTCTCTGAGCGTGGGG 17

RESULT 238

AAA24962

ID AAA24962 standard; DNA; 17 BP.

AC AAA24962;

DT 19-JUL-2000 (first entry)

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1460.

XX Oestrogen receptor; c-rat; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.

XX WO9954459-A2.

PN 28-OCT-1999.

PD 19-APR-1999; 99WO-US008547.

PF 20-APR-1998; 98US-0082404P.

PR 23-JUN-1998; 98US-00103636.

XX (RIBO-) RIBOZYME PHARM INC.

XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

PI Matulic-Adamic J;

XX DR WPI; 2000-013248/01.
 XX PT New nucleic acids that interact, and optionally cleave, target sequences,
 XX PT used to treat cancer.
 XX PS Claim 77; Page 64; 148pp; English.
 XX CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 XX invention
 XX SQ Sequence 17 BP; 2 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
 Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1740 CAACTCTCTCCTATCCT 1756
 DB 1 CAGCTCTCTCTCAFCCT 17
 RESULT 239
 AAF01989/C
 ID AAF01989 standard; DNA; 17 BP.
 AC AAF01989;
 XX 16-FEB-2001 (first entry)
 DT Hammerhead ribozyme substrate #284.
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 XX WO2000061729-A2.
 XX 19-OCT-2000.
 XX 11-APR-2000; 2000WO-US009721.
 XX 12-APR-1999; 99US-0129390P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 PI WPI; 2000-647423/62.
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 XX useful for producing e.g. granulocyte colony stimulating factor protein,
 XX interferon alpha and erythropoietin.
 PS Claim 37; Page 62; 164pp; English.
 XX CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1638 GCTTGTAGTAGAGGCCA 1654
 DB 17 GCTTGTAGTAGAGGCCA 1
 RESULT 240
 ABK00576
 ID ABK00576 standard; RNA; 17 BP.
 XX AC ABK00576;
 XX 12-MAR-2002 (first entry)
 DT Human NOGO Hammerhead Ribozyme #576.
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; cytoprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW Human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004273.
 XX 11-FEB-2000; 2000US-0191797P.
 XX 28-FEB-2000; 2000US-0195516P.
 XX 06-MAR-2000; 2000US-0197128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J.
 XX (CHOW/) CHOWRIRA B M.
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 XX constructs, which down regulate expression of a CD20 gene or neurite
 XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 XX central nervous system injury.
 XX Claim 88; Page 75; 200pp; English.

PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001WO-US000670.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
DR
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 9659; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 4 A; 4 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1672 TGGACCTGTTGCTC 1688
Db 17 TGGACCTGTTGCTC 1
RESULT 243
ABN00536
ID ABN00536 standard; DNA; 17 BP.
XX
AC ABN00536;
XX
XX 29-MAY-2002 (first entry)
DT

XX
DE
XX
KW Human; genome-derived myosin-like protein 1; hGDMPLP-1; heart;
KW vaccine; myosin; chromosome 22; gene therapy; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001WO-US000670.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
DR
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 528; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1645 GCAGAGGCGAGCACCA 1661
DT

Db 1 GCAGATGACAGCATCA 17
|||||
RESULT 244
ABN00535
ID ABN00535 standard; DNA; 17 BP.
XX
AC ABN00535;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:527.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 527; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1644 AGCAGAGGCGAAGCACC 1660
Db 1 AGCAGATGACAGCATC 17
|||||
RESULT 245
ABN01272/c
ID ABN01272 standard; DNA; 17 BP.
XX
AC ABN01272;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1264.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 1264; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be

CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 3 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1729 AGATTGGCTCCCAACTC 1745
|||||
Db 17 AGATCGTCCCAACTC 1

RESULT 246
ABK97683
ID ABK97683 standard; DNA; 17 BP.
AC ABK97683;
XX
DT 07-OCT-2002 (first entry)
XX
DE Cytochrome P450 3A (CYP3A) PCR primer #1.
XX
XX Cytochrome P450; CYP3A1; CYP3A2; CYP3A3; CYP3A4; CYP3A5; CYP3A7;
KW drug metabolism; drug design; drug screening; PCR; primer; ss.
XX
OS Synthetic.
XX
XX WO200244213-A1.
XX
XX 06-JUN-2002.
XX
XX 28-NOV-2001; 2001WO-SE002631.
XX
XX 28-NOV-2000; 2000SE-00004366.
PR 11-JUN-2001; 2001SE-00002061.
XX
XX (ZAPH/) ZAPHIROPOULOS P G.
PA (FINT/) FINTA C.
XX
XX Zaphiropoulos PG, Finta C;
XX
XX WPI; 2002-557532/59.
XX

DR Novel cytochrome P450 protein in which CYP3A43 exon 1 is joined to sets
PT of CYP3A4 or CYP3A5 exons, useful as medicament, and in evaluating drug
PT metabolism, in drug design and drug screening.
XX
XX Example 1; Page 22; 131pp; English.
XX
XX The invention describes a cytochrome P450 protein (I) in which CYP3A43
CC exon 1 is joined to sets of CYP3A4 or CYP3A5 exons, as well as sub
CC fragments, variants and multiples of (I) having essentially the same
CC characteristics. (I) is useful as a medicament, and for evaluating drug
CC metabolism, in drug design, and drug screening, and in tests for
CC adjusting the dose of drugs. This sequence represents a primer used to
CC isolate DNA encoding the novel cytochrome P450 of the invention
XX
SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1673 GGAAACCTGGTCTCTCC 1689
|||||
Db 1 GGAAACCTGGTCTCTCC 17

RESULT 247
ABV79506
ID ABV79506 standard; DNA; 17 BP.
XX
AC ABV79506;
XX
DT 03-JAN-2003 (first entry)

XX Human HTPL scanning oligonucleotide SEQ ID 752.
XX
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.

XX
XX EP1229046-A2.
XX
PD 07-AUG-2002.

XX 28-JAN-2002; 2002EP-00001167.
XX
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00364761.
PR 09-OCT-2001; 2001US-0327898P.
XX
XX (AEOM-) AEOMICA INC.

Zhan J;

WPI; 2002-676582/73.

Novel isolated human testis expressed Patched like protein (HTPL), useful
for identifying agonist and antagonist and specific binding partners, and
for treating subjects having defects in HTPL.

Example 2; Page 162; 718pp; English.

The present invention relates to human testis expressed Patched like
protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL
has two isoforms, with a few single base pair differences between the
two. One of the single base pair changes introduces a premature stop
codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
shares an overall structure organisation with the Patched protein. The
shared structural features strongly imply that HTPL plays a role similar
to that of Patched, and is a potential tumour suppressor. HTPL is
important in regulating male germ cell development, and the HTPL gene was
mapped to human chromosome 10p12.1. HTPL and its coding sequence are
useful for diagnosing a disorder caused by mutation in HTPL, and in
therapy and manufacture of a medicament for treatment or prevention of
such disorder associated with decreased expression or activity of human
HTPL. Such disorders include disorders of testis, or adrenal, adult and
foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
skeletal muscle or colon function. HTPL proteins and nucleic acids are
clinically useful diagnostic markers and potential therapeutic agents for
male infertility and cancer. The present oligonucleotide was used in an
example from the invention

XX

SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GCTCAGCTGGAACC 1678
| | | | | | | | | |
Db 1 GACTCACTGCTGACCC 17

RESULT 248
ABV90893
ID ABV90893 standard; DNA; 17 BP.
XX AC ABV90893;
XX DT 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1606.
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX OS Homo sapiens.
XX PN EPI239051-A2.
XX PD 11-SEP-2002.
XX PF 28-JAN-2002; 2002EP-00001165.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 23-MAY-2001; 2001WO-US000670.
XX PR 10-OCT-2001; 2001US-0328205P.
(ABOM-) ABOMICA INC.
Shannon M;
WPI; 2002-684061/74.
Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
-1, useful for treating disorders associated with decreased expression or
activity of human POSHL1.
Example 2; SEQ ID NO 1606; 60pp + Sequence Listing; English.
The invention relates to an isolated SH3 domain (POSH)-like signalling
protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
(S1) having 95% deviations, especially conservative substitutions or a
fragment of the sequences comprising at least 8 contiguous amino acids.
Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
adaptor protein that interacts with Rho family small GTPases as well as
downstream components of the signal transduction pathway. (I) is useful
for identifying a specific binding partner. (I) and nucleic acids (II)
encoding (I) are useful for diagnosing, monitoring disease and treating
caused by altered expression of human POSHL1 including diagnosing and
treating cancer, they useful in the development of vaccines and (II) is
useful in gene therapy. (II) is useful for constructing microarrays which
transgenic non-human animals capable of producing the proteins. The
present sequence is that of a scanning oligonucleotide useful in examples
of the invention. Note: The present sequence did not form part of the

CC Printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1671 CTGGAACCTGCTGCT 1687
| | | | | | | | | |
Db 1 CCGGAGCCCTGCTCTCT 17

RESULT 249
ABV90895
ID ABV90895 standard; DNA; 17 BP.
XX AC ABV90895;
XX DT 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1608.
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX OS Homo sapiens.
XX PN EPI239051-A2.
XX PD 11-SEP-2002.
XX PF 28-JAN-2002; 2002EP-00001165.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 10-OCT-2001; 2001US-0328205P.
(ABOM-) ABOMICA INC.
Shannon M;
WPI; 2002-684061/74.
Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
-1, useful for treating disorders associated with decreased expression or
activity of human POSHL1.
Example 2; SEQ ID NO 1608; 60pp + Sequence Listing; English.
The invention relates to an isolated SH3 domain (POSH)-like signalling
protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
(S1) having 95% deviations, especially conservative substitutions or a
fragment of the sequences comprising at least 8 contiguous amino acids.
Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
adaptor protein that interacts with Rho family small GTPases as well as
downstream components of the signal transduction pathway. (I) is useful
for identifying a specific binding partner. (I) and nucleic acids (II)
encoding (I) are useful for diagnosing, monitoring disease and treating
caused by altered expression of human POSHL1 including diagnosing and
treating cancer, they useful in the development of vaccines and (II) is
useful in gene therapy. (II) is useful for constructing microarrays which
are useful for measuring and for surveying gene expression and creating

CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1673 GGAACCTGGTGTCTCC 1689
 ||| ||||| |||
 Db 1 GGAGCCTGGTCTCTAC 17

RESULT 250
 ABV91050/c
 ID ABV91050 standard; DNA; 17 BP.

XX
 AC ABV91050;
 XX
 DT 23-DEC-2002 (first entry)

XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1763.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EP1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 23-MAY-2001; 2001US-00864761.

XX 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL

XX -1, useful for treating disorders associated with decreased expression or

XX activity of human POSHL1.

XX Example 2; SEQ ID NO 1763; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
 CC (SI) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and

CC treating cancer, they useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1748 CCTATCTCTAAGGCC 1764
 ||| ||||| |||
 Db 17 CCTGTCTCTAAGTCCC 1

RESULT 251

ID ABV90899 standard; DNA; 17 BP.

XX
 AC ABV90899;

XX 23-DEC-2002 (first entry)

XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1612.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EP1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 23-MAY-2001; 2001US-00864761.

XX 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL

XX -1, useful for treating disorders associated with decreased expression or

XX activity of human POSHL1.

XX Example 2; SEQ ID NO 1512; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
 CC (SI) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful

CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX
 SQ Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1677 CCTGTGCTCTCTCCCA 1693
 Db 1 CCTGTGCTCTCTACCA 17
 RESULT 252
 ABV91049/c
 ID ABV91049 standard; DNA; 17 BP.
 XX AC ABV91049;
 XX DT 23-DEC-2002 (first entry)
 XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1762.
 XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.
 XX OS Homo sapiens.
 XX EW EP1239051-A2.
 XX PD 11-SEP-2002.
 XX PF 28-JAN-2002; 2002EP-00001165.
 XX PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 10-OCT-2001; 2001US-0328205P.
 XX PA (AEOM-) AEOMICA INC.
 XX PI Shannon M;
 XX DR WPI; 2002-684061/74.
 XX PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
 PT -1, useful for treating disorders associated with decreased expression or
 PT activity of human POSHL1.
 XX PS Example 2; SEQ ID NO 1762; 60pp + Sequence Listing; English.
 XX CC The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
 CC (S1) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.

CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX
 SQ Sequence 17 BP; 5 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1749 CCTATCCTAAAGGCCCA 1765
 Db 17 CTGTCTCTAAAGTCCCA 1
 RESULT 253
 ABT34389/c
 ID ABT34389 standard; DNA; 17 BP.
 XX AC ABT34389;
 XX DT 12-JUN-2003 (first entry)
 XX DE Tumour suppression related human fukutin oligo SEQ ID No 26.
 XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX OS Homo sapiens.
 XX PN WO2003025175-A2.
 XX PD 27-MAR-2003.
 XX PF 17-SEP-2002; 2002WO-IB004208.
 XX PR 17-SEP-2001; 2001FR-00011978.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX DR WPI; 2003-313353/30.
 XX PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX PS Disclosure; Page 37; 720pp; French.
 XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,

CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1641 TGTAGCAGAGGCGAGC 1657
Db 17 TGTAGCAGATGGCGATC 1
RESULT 254
ABT40165
ID ABT40165 standard; DNA; 17 BP.
AC
XX
AC ABT40165;
XX
XX
DT 13-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID NO 5802.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001FR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 712; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence;
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, or the complement
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for

CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1735 GCTCCCAACTCTCTCTCT 1751
Db 1 GATCCCACTGCTCTCT 17
RESULT 255
ACA07738
ID ACA07738 standard; RNA; 17 BP.
AC
XX
AC ACA07738;
XX
XX
DT 03-JUN-2003 (first entry)
XX
DE NFKB sub-unit modulating zinzyme substrate #137.
XX
XX Enzymatic nucleic acid, nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW G-cleaver; amberyzyme; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
XX Homo sapiens.
XX
XX US2002177568-A1.
XX
XX 28-NOV-2002.
XX
XX 23-MAY-2001; 2001US-00864785.
XX
XX 07-DEC-1992; 92US-00987132.
XX 18-MAY-1994; 94US-00245466.
XX 15-AUG-1994; 94US-00291932.
XX 23-DEC-1996; 96US-0C777916.
XX
XX (STIN/) STINCHOMB D T.
XX (MCSW/) MCSWIGGEN J.
XX (DRAP/) DRAPER K G.
XX
XX Stinchcomb DT, Mcswiggen J, Draper KG;
XX
XX WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
XX a sequence encoding a subunit of nuclear factor kappa B useful for
XX treating cancer, inflammatory disorders and autoimmune diseases.
XX
XX Claim 3; Page 39; 72pp; English.
XX
XX

CC The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule

Sequence 17 BP; 2 A; 5 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 52.9%; Pred. No. 3.2e+02;

Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1676 ACCCGGTGTCTCCCTCC 1692

Db 1 ACCAUGGUGUUCUUC 17

RESULT 256

ACA09103/c

ID ACA09103 standard; RNA; 17 BP.

AC ACA09103;

DT 03-JUN-2003 (first entry)

DE NFKB sub-unit modulating amberzyme substrate #266.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

OS Homo sapiens.

XX US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

XX 18-MAY-1994; 94US-00245466.

XX 15-AUG-1994; 94US-00291932.

XX 23-DEC-1996; 96US-00777916.

PA (STIN/) STINCHOMB D T.

PA (MCSW/) MCSWIGGEN J.

XX (DRAP/) DRAPER K G.

PI Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.

PS Claim 3; Page 56; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule

Sequence 17 BP; 4 A; 1 C; 11 G; 0 T; 1 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1738 CCCCAACTCTCTCCCTATC 1754

Db 17 CCCAGCTCCCCCTTTC 1

RESULT 257

ACA09102/c

ID ACA09102 standard; RNA; 17 BP.

XX ACA09102;

DT 03-JUN-2003 (first entry)

DE NFKB sub-unit modulating amberzyme substrate #265.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 OS EP1281758-A2.
 PN 05-FEB-2003.
 XX 30-JUL-2002; 2002EP-00016874.
 PF 02-AUG-2001; 2001US-00922181.
 XX (AEOM-) AEOMICA INC.
 PA Shannon M, Gu Y, Nguyen C;
 PI WPI; 2003-423107/40.
 DR New zinc finger-containing proteins and nucleic acids, useful in
 XX manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
 XX Example 8; SEQ ID NO 582; 103pp; English.
 PS The present invention relates to novel human zinc finger-containing
 XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
 SQ Query Match 3.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1666 CACAGCTGGACCTGG 1682
 Db 17 CCCAGCTGGATGCTGG 1
 RESULT 259
 ADA99410
 ID ADA99410 standard; DNA; 17 BP.
 XX AC ADA99410;
 XX AC 20-NOV-2003 (first entry)
 DT Human MDZ3 scanning oligonucleotide SEQ ID 399.
 DE Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 XX

XX Homo sapiens.
 OS US2002175568-A1.
 XX 28-NOV-2002.
 PF 23-MAY-2001; 2001US-00864785.
 XX 07-DEC-1992; 92US-00987132.
 PR 18-MAY-1994; 94US-00245466.
 PR 15-AUG-1994; 94US-00291932.
 PR 23-DEC-1996; 96US-00777916.
 XX (STIN/) STINCHOMB D T.
 PA (MCSW/) MCSWIGGEN J.
 PA (DRAP/) DRAPER K G.
 PI Stinchcomb DT, Mcswiggen J, Draper KG;
 PI WPI; 2003-340953/32.
 DR Novel enzymatic nucleic acid molecules which down regulates expression of
 XX a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX Claim 3; Page 56; 72pp; English.
 PS The invention describes an enzymatic nucleic acid molecule (I) which down
 XX regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX Sequence 17 BP; 4 A; 1 C; 11 G; 0 T; 1 U; 0 Other;
 SQ Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1739 CCAACTCTCCCTATCC 1755
 Db 17 CCAGCTCCCCCTTCC 1
 RESULT 258
 ADA99593/C
 ID ADA99593 standard; DNA; 17 BP.
 XX AC ADA99593;
 XX AC 20-NOV-2003 (first entry)
 DT Human MDZ3 scanning oligonucleotide SEQ ID 582.
 DE


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PN  EP1281758-A2.
FD  05-FEB-2003.
XX  30-JUL-2002; 2002EP-00016874.
XX  02-AUG-2001; 2001US-00922181.
XX  (AEOM-) AEOMICA INC.
XX  Shannon M, Gu Y, Nguyen C;
XX  WPI; 2003-423107/40.
XX  New zinc finger-containing proteins and nucleic acids, useful in
PT  manufacturing a medicament for treating or preventing a disorder
PT  associated with decreased or increased expression or activity of MD23,
PT  MD24, MD27 or MDZ12, e.g. cancer.
XX  Example 8; SEQ ID NO 399; 103pp; English.
XX  The present invention relates to novel human zinc finger-containing
CC  proteins and their coding sequences; MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC  encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC  MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC  15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC  or in manufacturing a medicament for treating or preventing a disorder,
CC  associated with decreased or increased expression or activity of MDZ3,
CC  MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC  acids and proteins are also useful for diagnosing or monitoring a disease
CC  caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC  acids can also be used as probes to detect and characterize gross
CC  alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC  useful in constructing microarrays for measuring gene expression. The
CC  proteins are useful as therapeutic agents for gene therapy or as
CC  vaccines. The present sequence was used to illustrate the invention.
XX  Sequence 17 BP; 3 A; 7 C; 1 G; 6 T; 0 U; 0 Other;
SQ  Query Match 8.8%; Score 12.2; DB 1; Length 17;
    Best Local Similarity 82.4%; Pred. No. 3.2e+02;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY  1740 CAATCTCTCCCTATCCT 1756
    || ||||| |||||
Db  1 CAGTTCCTCACTATCCT 17
RESULT 260
ABZ65014
ID  ABZ65014 standard; RNA; 17 BP.
XX  ABZ65014;
AC  ABZ65014;
XX  21-MAR-2003 (first entry)
XX  Human HER2 DNzyme substrate #471.
XX  Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW  enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KW  anti-rheumatic; cancer; AIDS; ss.
XX  Homo sapiens.
OS  Homo sapiens.
XX  WO200297114-A2.
PN  WO200297114-A2.
XX  05-DEC-2002.
PD  05-DEC-2002.
XX  29-MAY-2002; 2002WO-US016840.
XX  29-MAY-2001; 2001US-0294140P.
PR  06-JUN-2001; 2001US-0296249P.
PR  10-SEP-2001; 2001US-0318471P.

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XX  (RIBO-) RIBOZYME PHARM INC.
FA  Mcswiggen J;
XX  WPI; 2003-140484/13.
XX  Novel short interfering RNA and enzymatic nucleic acid useful for
PT  treating cancer, modulates the expression of a nucleic acid encoding
PT  HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX  Claim 4; Page 142; 185pp; English.
XX  The invention relates to a novel short interfering RNA (siRNA) nucleic
CC  acid molecule or an enzymatic nucleic acid molecule, that modulates
CC  expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC  human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC  acid molecule of the invention has cytosstatic, anti-HIV, and anti-
CC  rheumatic activity. The nucleic acid molecules are useful for reducing
CC  HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC  also useful for treating breast, ovarian, colorectal, lung, prostate,
CC  bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC  shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC  ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC  ribozymes of the invention
XX  Sequence 17 BP; 3 A; 9 C; 1 G; 0 T; 4 U; 0 Other;
SQ  Query Match 8.8%; Score 12.2; DB 1; Length 17;
    Best Local Similarity 64.7%; Pred. No. 3.2e+02;
    Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY  1749 CCTATCTCTAAAGGCCCA 1765
    ||: ||||| |||||
Db  1 CCUCUCCUACAUGCCCA 17
RESULT 261
ACD55654/c
ID  ACD55654 standard; RNA; 17 BP.
XX  ACD55654;
AC  ACD55654;
XX  23-SEP-2003 (first entry)
XX  HBV amberyze substrate sequence #164.
XX  Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW  RNA stability; RNA expression; RNA synthesis; antisense;
KW  enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
KW  amberyze; G-cleaver ribozyme; decoy molecule; aptamer;
KW  HBV reverse transcriptase; Enhancer I region; viral replication;
KW  degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW  liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW  virucide; antiinflammatory; substrate; ss.
XX  Hepatitis B virus.
OS  Hepatitis B virus.
XX  WO200281494-A1.
PN  WO200281494-A1.
XX  17-OCT-2002.
PD  17-OCT-2002.
XX  26-MAR-2002; 2002WO-US009187.
XX  26-MAR-2001; 2001US-00817879.
PR  08-JUN-2001; 2001US-00877478.
PR  08-JUN-2001; 2001US-0296876P.
PR  24-OCT-2001; 2001US-0335059P.
PR  05-DEC-2001; 2001US-0337055P.
XX  (RIBO-) RIBOZYME PHARM INC.
FA  (BLAT/) BLATT L.
PA  (MACE/) MACEJAK D.

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Mon Aug 30 09:26:45 2004

PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 PT
 XX
 PS Example 1; Page 206; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberyse sequences
 CC disclosed in the present invention
 XX
 SQ Sequence 17 BP; 4 A; 0 C; 9 G; 0 T; 4 U; 0 Other;
 Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1740 CAACCTCTCCCTATCCT 1756
 DB 17 CAACCTCTCCCTATCAT 1
 RESULT 262
 ACC67113/C
 ID ACC67113 standard; DNA; 17 BP.
 XX
 AC ACC67113;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4360.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 XX
 (MOLE-) MOLECULAR ENGINES LAB.
 Telerman A, Amson R, Tuijnder M;
 WPI; 2003-333167/31.
 New isolated nucleic acid, useful for treating viral diseases associated
 with tumors and cell degeneration, also related polypeptides, antibodies
 and transfected cells.
 Disclosure; Page 540; 738pp; French.
 The present invention relates to murine oligonucleotides (ACC62754-
 ACC6806), which are associated with tumour suppression, tumour
 reversion, apoptosis and virus resistance. The oligonucleotides are
 useful as (1) as probes and primers for detecting, identifying,
 quantifying and/or amplifying nucleic acid, e.g. as one component of a
 gene chip; in vitro as (anti)sense reagents; and (2) for production of
 recombinant polypeptides. The oligonucleotides are useful for preparation
 of pharmaceuticals for prevention and/or treatment of viral diseases that
 are characterised by development of tumours or cell degeneration,
 specifically cancer but also Alzheimer's disease and schizophrenia
 Sequence 17 BP; 1 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 8.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1650 AGGCAAGCACCAGGCTC 1666
 DB 17 AGGCAAGCACCAGGATC 1
 RESULT 263
 ADB45561/C
 ID ADB45561 standard; DNA; 17 BP.
 XX
 AC ADB45561;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #5884.
 XX
 KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004219.
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 Telerman A, Amson R, Tuijnder M;
 WPI; 2003-441574/41.
 New nucleic acid encoding human prostate membrane-specific antigen,
 useful e.g. for treatment of tumors and viral infection, also related
 polypeptide and antibodies.
 Disclosure; Page 719; 771pp; French.
 The invention relates to the isolation of 6327 nucleotide sequences,
 fragments of at least 15 consecutive nucleotides of these nucleotides, a

The invention describes a composition comprising at least one expression vector comprising a polynucleotide of the invention. The composition has anesthetic, antiarteriosclerotic, cardiant and antidiabetic properties. The invention is used to detect and treat conditions associated with

Y 1658 ACCAGGCTCACAGCTGG 1674

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Db
|||||
17 ACCAGGCTCCAGCAGG 1

RESULT 266
AAT61371
ID AAT61371 standard; DNA; 18 BP.
XX
XX AC
XX AAT61371;
XX
XX DT 17-APR-1997 (first entry)
XX
XX DE Amidophosphoribosyl transferase antisense sequence.
XX KW Complementary; human amidophosphoribosyl transferase; h-Arae;
XX KW phosphorothioate linkage; resistant; nuclease; anticancer activity; ss.
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX FT misc_difference 1..18
XX FT /*tag= a
XX FT /mod_base= Phosphorothioate_linkages
XX
XX PN JP07255487-A.
XX
XX PD 09-OCT-1995.
XX
XX PF 28-MAR-1994; 94JP-00056879.
XX
XX PR 28-MAR-1994; 94JP-00056879.
XX
XX PA (SAKA ) OTSUKA SEIYAKU KOGYO KK.
XX
XX DR WPI; 1995-378542/49.
XX
XX PT DNA fragment complementary to human amido:phospho:ribosyl transferase
XX PT gene portion - useful as anticancer agent with few side effects.
XX
XX PS Claim 5; Page 2; 6pp; Japanese.
XX
XX This sequence represents a DNA fragment which is complementary to part of
XX the human amidophosphoribosyl transferase (h-Arae) gene. The phosphate
XX bonds have been chemically modified so that they are resistant to
XX decomposition by nuclease. This DNA fragment and derivatives of it, have
XX excellent anticancer activity, and have low side effects
XX
XX SQ Sequence 18 BP; 3 A; 11 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCCTCCCTATC 1754
|||||
DB 2 CCCAACTCCTCCAGCTC 18

RESULT 267
AAT35472/c
ID AAT35472 standard; DNA; 18 BP.
XX
XX AC AAT35472;
XX
XX DT 25-MAR-2003 (revised)
XX DT 27-MAY-1997 (first entry)
XX
XX DE Immunoglobulin heavy chain E (enhancer) region oligonucleotide.
XX KW Immunoglobulin heavy chain; IgH; immuno-response; antisense; leukaemia;
XX KW neoplasia; tumour; cancer; lymphoma; lymphocyte; J region; E region;
XX KW enhancer; J6 region; ss.
XX

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PT Activation of polypeptides - by interaction with activating peptide,
 XX resulting in refolding of the polypeptides to give active form.
 PS Example 2; Col 19; 29pp; English.
 XX
 CC PCR primers AAV16094-95 are used in a random mutagenesis reaction in the
 CC presence of an error prone polymerase to introduce mutations into the
 CC prosequence of subtilisin E of *Bacillus subtilis* (see AAW45599). The
 CC prosequence is essential for the production of active, correctly folded
 CC subtilisin. When certain amino acid substitutions are made, no mature,
 CC biochemically active subtilisin protein is produced. The mutations
 CC inhibited folding. The mutations have been observed to occur with high
 CC frequency within the hydrophobic region of the propeptide. It appears
 CC that the propeptide contains select functional domains which interact
 CC with specific regions of the mature region of the polypeptide to promote
 CC the refolding process. An in vitro method to restore or increase the
 CC natural biological activity of a target polypeptide (inactive or with
 CC decreased activity due to improper folding), which is normally expressed
 CC containing a prosequence forms the basis of the invention. An exogenous
 CC activating peptide used to promote refolding of the target polypeptide to
 CC give its active form. The activating peptide comprises the prosequence of
 CC the target or other proteins with a similar sequence and function to the
 CC target polypeptide. The method is used to produce biologically, correctly
 CC folded proteins from their inactive, incorrectly folded forms. Suitable
 CC target polypeptides include members of the serine protease or subtilisin
 CC families
 XX
 SQ Sequence 18 BP; 3 A; 1 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1636 GGGCTTGTCAGCAGG 1652
 DB 2 GGGTTGTTTCAGAGG 18
 |||||
 |||||

RESULT 269
 AAV08683
 ID AAV08683 standard; DNA; 18 BP.
 XX
 AC AAV08683;
 XX
 DT 15-FEB-1999 (first entry)
 XX
 DE Primer ATP/20RT for human ACE gene.
 XX
 KW PCR primer; human; ACE; angiotensin converting enzyme; angiotensinogen;
 KW cardiovascular status; AGT; AT1; type 1 angiotensin II receptor; stroke;
 KW polymorphic pattern; blood pressure; electrocardiographic profile;
 KW cardiac condition diagnosis; myocardial infarction; atherosclerosis;
 KW hypertension; cardiovascular disease; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9845477-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 01-APR-1998; 98WO-IB000475.
 XX
 PR 04-APR-1997; 97US-0042930P.
 XX
 PA (EURO-) EURONA MEDICAL AB.
 XX
 PI Norberg LT, Andersson MK, Lindstroem PHR;
 XX
 DR WPI; 1998-568361/48.
 XX
 PT Assessing cardiovascular status in humans by polymorphic analysis - of
 PT genes for angiotensin converting enzyme, angiotensinogen and angiotensin

PT II receptor, used to diagnose predisposition to disease and to predict
 PT effect of therapy.
 XX
 PS Example 1; Page 32; 71pp; English.

XX This sequence represents a PCR primer for the human ACE (angiotensin
 CC converting enzyme) gene, and can be used in the method of the invention.
 CC The method is for assessing cardiovascular status in humans by
 CC determining the sequence of at least one polymorphic site in the ACE
 CC (angiotensin converting enzyme), AGT (angiotensinogen) and/or AT1 (type 1
 CC angiotensin II receptor) genes, and comparing the polymorphic pattern
 CC with that in patients with predetermined markers of status. The method is
 CC used to assess blood pressure or electrocardiographic profile, to
 CC diagnose a cardiac condition such as (silent) myocardial infarction (MI),
 CC hypertension, atherosclerosis or stroke. They can also be used to predict
 CC response to treatments with ACE inhibitors, angiotensin II receptor
 CC antagonists, diuretics, alpha- or beta-adrenergic receptor antagonists,
 CC etc. It is also used to identify susceptibility to cardiovascular
 CC disease. Libraries of nucleic acids containing polymorphic positions in
 CC the 3 genes, and libraries of targets corresponding to the peptides from
 CC the genes are used to screen for cardiovascular agents. The nucleic acids
 CC contained in the library can be used as source of probes

XX
 SQ Sequence 18 BP; 2 A; 12 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 8.8%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCCTCCCTATC 1754
 DB 2 CCAACTCCTCCCTCTC 18
 |||||
 |||||

RESULT 270
 AAX24515/c
 ID AAX24515 standard; DNA; 18 BP.
 XX
 AC AAX24515;
 XX
 DT 20-MAR-2003 (revised)
 DT 21-JUN-1999 (first entry)
 XX
 DE Human SR-BI gene exon 3 primer 3e30srbl.
 XX
 KW SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
 KW restenosis; congestive heart failure; atherosclerosis; cholesterol;
 KW low density lipoprotein; LDL; high density lipoprotein; HDL; diagnosis;
 KW body mass index; obesity; cachexia; gallstone; PCR; primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9902735-A2.
 XX
 PD 21-JAN-1999.
 XX
 PF 10-JUL-1998; 98WO-US014354.
 XX
 PR 10-JUL-1997; 97US-00890979.
 PR 27-FEB-1998; 98US-00031626.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PA (TUFT) UNIV TUFTS.
 XX
 PI Acton SL, Ordovas JM;
 XX
 DR WPI; 1999-120935/10.
 XX
 PT Detecting genetic predisposition for body mass disorders - by identifying
 PT allelic variants of a polymorphic region of the SR-BI gene.
 XX
 PS Example 2; Page 67; 102pp; English.

XX Primer 3e30srbl is used with primer 5e30srbl (see AAX24514) in the PCR
 CC amplification of exon 3 (see AAX24500) of the human SR-BI gene. The
 CC invention is based on the discovery of the genomic structure of the human
 CC SR-BI gene (see AAX24498-509) and on the identification of polymorphic
 CC regions within the gene which are associated with abnormal body mass
 CC index (BMI) and abnormal lipoprotein levels and hence with disorders such
 CC as obesity, cachexia, cardiovascular disorders and gallstone formation.
 CC primers (see AAX24510-35) are provided for amplification of the exons,
 CC introns and promoter region of the SR-BI gene for detection of
 CC polymorphisms and mutations. The invention provides methods for
 CC determining whether a subject has, or is at risk of developing, a disease
 CC associated with a specific allele of a polymorphic region of an SR-BI
 CC gene. Kits comprising the relevant probe or primer are claimed. (Updated
 CC on 20-MAR-2003 to correct PA field.)
 XX Sequence 18 BP; 6 A; 3 C; 9 G; 0 T; 0 U; 0 Other;
 SQ

Query Match 8.8%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1682 GTGTCCTCCAGCGTG 1698
 DB 17 GTCTCTCCCGCCG 1

RESULT 271
 AAX24607/C
 ID AAX24607 standard; DNA; 18 BP.
 XX AC AAX24607;
 XX
 DT 21-JUN-1999 (first entry)
 XX Human SR-BI gene exon 3 primer 3e30srbl.
 DE
 KW SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;
 KW restenosis; congestive heart failure; atherosclerosis; cholesterol;
 KW low density lipoprotein; LDL; high density lipoprotein; HDL; diagnosis;
 KW body mass index; obesity; cachexia; gallstone; PCR; primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9902736-A2.
 XX
 PN 21-JAN-1999.
 XX
 PD 10-JUL-1998; 98WO-US014359.
 XX
 PF 10-JUL-1997; 97US-00890980.
 XX
 PR 27-FEB-1998; 98US-00032894.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Acton SL;
 XX
 DR WPI; 1999-120936/10.
 XX
 PT New nucleic acids comprising intronic sequence of a human scavenger
 PT receptor-BI (SR-BI) gene - useful for prognosis, diagnosis and treatment
 PT of SR-BI associated diseases or conditions.
 XX
 PS Claim 10; Page 66; 103pp; English.
 CC
 CC Primer 3e30srbl is used with primer 5e30srbl (see AAX24606) in the PCR
 CC amplification of exon 3 (see AAX24592) of the human SR-BI gene. The
 CC invention is based on the discovery of the genomic structure of the human
 CC SR-BI gene (see AAX24590-601) and on the identification of polymorphic
 CC regions within the gene which are associated with abnormal body mass
 CC index (BMI) and abnormal lipoprotein levels and hence with disorders such
 CC as obesity, cachexia, cardiovascular disorders and gallstone formation.

CC Claimed primers (see AAX24602-25) are used for the amplification of the
 CC exons, introns and promoter region of the SR-BI gene for detection of
 CC polymorphisms and mutations. The invention provides methods for
 CC determining whether a subject has, or is at risk of developing, a disease
 CC associated with a specific allele of a polymorphic region of an SR-BI
 CC gene. Kits comprising the relevant probe or primer are claimed
 XX Sequence 18 BP; 6 A; 3 C; 9 G; 0 T; 0 U; 0 Other;
 SQ

Query Match 8.8%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1682 GTGTCCTCCAGCGTG 1698
 DB 17 GTCTCTCCCGCCG 1

RESULT 272
 AAX38311
 ID AAX38311 standard; DNA; 18 BP.
 XX AC AAX38311;
 XX
 DT 21-AUG-2000 (first entry)
 XX Human AT1 regulatory region PCR primer, SEQ ID NO:111.
 DE
 KW Angiotensin II receptor type 1 gene; AT1; regulatory region;
 KW polymorphism; polymorphic marker; cardiovascular disease;
 KW myocardial infarction; unstable angina; hypertension; atherosclerosis;
 KW stroke; prognosis; drug screening; treatment outcome; human; PCR primer;
 KW ss.
 XX Homo sapiens.
 XX WO200022166-A2.
 XX
 PN 20-APR-2000.
 XX
 PD 13-OCT-1999; 99WO-IB01678.
 XX
 PF 14-OCT-1998; 98US-0104286P.
 XX
 PR 14-OCT-1998; 98US-0104302P.
 XX
 PA (EURO-) EURONA MEDICAL AB.
 XX
 PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
 XX WPI; 2000-318010/27.
 XX
 DR Assessing cardiovascular status in humans involves comparing test
 DR polymorphic pattern comprising polymorphic positions within genes
 DR encoding specific proteins, with reference polymorphic pattern.
 XX
 PS Example 1; Page 54; 126pp; English.
 CC
 CC The invention relates to a novel method of assessing the cardiovascular
 CC status in an individual and to newly identified polymorphisms in the
 CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
 CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
 CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
 CC receptors 1 and 2. The method comprises determining the sequence at one
 CC or more polymorphic positions within these genes, and comparing the
 CC pattern of polymorphisms from the individual with a reference polymorphic
 CC pattern obtained from a population of individuals exhibiting a
 CC predetermined cardiovascular disease status. The polymorphic markers are
 CC useful for determining the predisposition of an individual to
 CC cardiovascular disorders such as myocardial infarction, unstable angina,
 CC hypertension, atherosclerosis and stroke. They are also useful for
 CC predicting the likely cardiovascular status of a patient given a
 CC treatment regimen comprising administration of cardiovascular drugs
 CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-

SQ	Sequence 18 BP; 5 A; 7 C; 2 G; 4 T; 0 U; 0 Other;	
	Query Match 8.8%; Score 12.2; DB 1; Length 18;	
	Best Local Similarity 82.4%; Pred. No. 3.5e+02;	
	Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	1721 GGAGATGGAGATTGGCT 1737	
Db	18 GTAAATGGAGCTTGGCT 2	
RESULT 275		
ID	AAC58358 standard; DNA: 18 BP.	
XX		
AC	AAC58358;	
XX		
DT	29-JAN-2001 (first entry)	
XX		
DE	Human PRO2145 reverse PCR primer SEQ ID NO:177.	
XX		
KW	Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;	
KW	proliferation; tumorigenesis; identification; cancer; PCR primer;	
KW	hybridisation; probe; cytostatic; neutrotropic; neuroprotective;	
KW	antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic;	
KW	leukaemia; lymphoid malignancy; neuronal disorder; glial disorder;	
KW	astrocytal disorder; hypothalamic disorder; glandular disorder;	
KW	macrophagal disorder; epithelial disorder; stromal disorder;	
KW	blastocoealic disorder; inflammatory disorder; angiogenic;	
XX		
OS	Homo sapiens.	
XX		
PN	WO200053755-A2.	
XX		
PD	14-SEP-2000.	
XX		
PF	06-JAN-2000; 2000WO-US000376.	
XX		
PR	08-MAR-1999; 99WO-US005028.	
PR	02-JUN-1999; 99WO-US012252.	
PR	23-JUN-1999; 99US-0141037P.	
PR	07-JUL-1999; 99US-0143048P.	
PR	26-JUL-1999; 99US-0145698P.	
PR	30-NOV-1999; 99WO-US028313.	
PR	20-DEC-1999; 99WO-US030911.	
XX		
XX	05-JAN-2000; 2000WO-US000219.	
PA	(GETH) GENENTECH INC.	
XX		
PI	Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;	
PI	Watanabe CK, Wood WI;	
XX		
DR	WPI; 2000-572270/53.	
XX		
PT	Thirty PRO polynucleotides encoding PRO polypeptides, useful in the	
PT	treatment, diagnosis and prevention of cancer.	
XX		
PS	Example 23; Page 139; 286pp; English.	
XX		
CC	The present invention describes an isolated antibody that binds to one of	
CC	the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,	
CC	PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,	
CC	PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,	
CC	PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR	
CC	PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The	
CC	PRO polypeptides and nucleotides are useful in the treatment, diagnosis	
CC	and prevention of cancer. The antibodies and other anti-tumour compounds	
CC	may be used to treat various conditions, including those characterised by	
CC	overexpression and/or activation of the amplified PRO genes. Exemplary	
CC	conditions or disorders to be treated with such antibodies and other	
CC	compounds include benign or malignant tumours (e.g., renal, liver,	
CC	kidney, bladder, breast, ovarian, colorectal, prostate,	

CC	pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,
CC	glioblastomas, and various head and neck tumours), leukaemias and
CC	lymphoid malignancies, other disorders such as neuronal, glial,
CC	astrocytal, hypothalamic and other glandular, macrophagal, epithelial,
CC	stromal and blastocoealic disorders, and inflammatory, angiogenic and
CC	immunologic disorders. AAC58242 to AAC58366 represent PCR primers and
CC	hybridisation probes used in the isolation of the human PRO sequences.
CC	AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO
CC	polynucleotide and protein sequences given in the exemplification of the
CC	present invention
XX	
SQ	Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
	Query Match 8.8%; Score 12.2; DB 1; Length 18;
	Best Local Similarity 82.4%; Pred. No. 3.5e+02;
	Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1728 GAGATTGGCTCCCACT 1744
Db	18 GATGCGGCTCCCACT 2
RESULT 276	
ID	AAH75254/c
XX	
AC	AAH75254 standard; DNA: 18 BP.
XX	
AC	AAH75254;
XX	
DT	02-OCT-2001 (first entry)
XX	
DE	Human inducible NOS antisense oligonucleotide SEQ ID NO 98.
XX	
KW	Antisense oligonucleotide; inducible nitric oxide synthase; NOS;
KW	modulate expression; immunomodulator; antidiabetic; cardiovascular;
KW	cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
KW	2'-O-methoxyethyl; phosphorothioate; human; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	modified_base 1..18
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "phosphorothioate backbone, 5' and 3' four
FT	nucleotide 2'-MOE (2'-O-methoxyethyl) wings, all cytidine
FT	residues are 5-methylcytidines and a deoxy gap"
XX	
XX	WO200152902-A1.
XX	
PD	26-JUL-2001.
XX	
PF	15-JAN-2001; 2001WO-US001381.
XX	
PR	24-JAN-2000; 2000US-00490208.
XX	
XX	(ISIS-) ISIS PHARM INC.
PA	
XX	Bennett CF, Dean NM, Cowseert LM;
PI	
XX	WPI; 2001-465340/50.
XX	
DR	New antisense oligonucleotides for modulating the expression of inducible
PT	nitric oxide synthase in cells or tissues, particularly useful for
PT	treating e.g. immunological, cardiovascular or neurological disorders, or
XX	ischemia.
XX	Claim 3; Page 84; 144pp; English.
XX	
PS	The invention relates to antisense compounds, especially
CC	oligonucleotides, which are targeted to a nucleic acid encoding inducible
CC	nitric oxide synthase and which specifically hybridise to and modulate
CC	expression of inducible nitric oxide synthase. The antisense compounds
CC	have immunomodulator, antidiabetic, cardiovascular, cardiant,

CC neuroprotective, disorder and vasotropic activity. The antisense
CC oligonucleotides are useful for inhibiting the expression of inducible
CC nitric oxide synthase in cells or tissues. In particular, the antisense
CC oligonucleotides are useful for treating diseases or disorders associated
CC with inducible nitric oxide synthase, e.g. diabetes, immunological
CC disorder, cardiovascular disorder, neurological disorder or
CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
CC useful for research and diagnostics. The present sequence is that of an
CC antisense 2'-O-methoxyethyl gapper oligonucleotide with a
CC phosphorothioate backbone, a central "gap" region of ten nucleotides
CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings and 5-
CC methylcytidine residues throughout the oligonucleotide. The antisense
CC oligonucleotide is targeted to human inducible nitric oxide synthase
CC mRNA (AAH47973)
XX
SQ Sequence 18 BP; 5 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1723 AGATGGAGATTGGCTCC 1739
Db 18 AGTTTGAGATGGCTCC 2
RESULT 277
AAS14080/c
ID AAS14080 standard; DNA; 18 BP.
XX
AC AAS14080;
XX
DT 18-DEC-2001 (first entry)
XX
DE Forward PCR primer used in prevention of SMN2 exon 7 skipping.
XX
KW Survival motor neuron gene; SMN1; SMN2; spinal muscular atrophy; SMA; ss;
KW chromosome 5q13; exonic splicing enhancer; ESE; pre-mRNA processing;
KW human; mammal; exon skipping; PCR primer.
XX
OS Homo sapiens.
XX
PN WO200166129-A1.
XX
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-EP002567.
XX
PR 10-MAR-2000; 2000EP-00105081.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Stamm S, Wirth B, Hofmann V, Androphy E, Lorson C;
XX
DR WPI; 2001-589914/66.
XX
PT Substances capable of preventing skipping of exon 7 of survival motor
PT neuron gene 2 are useful for treating spinal muscular atrophy.
XX
PS Example 4; Page 25; 49pp; English.
XX
CC The invention relates to a substance capable of preventing the skipping
CC of exon 7 of the survival motor neuron gene 2 (SMN2). This is the spinal
CC muscular atrophy (SMA) determining gene, present on chromosome 5q13, and
CC can be used as a therapeutic agent. SMN2 expresses reduced full-length
CC and abundant levels of transcripts lacking exon 7, encoding a less stable
CC protein than that encoded by SMN1, with a reduced self-oligomerisation
CC capacity. SMN1 and SMN2 differ by a nucleotide exchange in exon 7 that
CC disrupts an exonic splicing enhancer (ESE) and causes exon 7 skipping in
CC SMN2 transcripts. Substances of the invention are useful for treating
CC spinal muscular atrophy (SMA) and for changing the pre-mRNA processing
CC relating to the SMN gene of mammalian cells. Control of exon 7 inclusion
CC can be determined by monitoring the ratio between exon 7 exclusion and

CC skipping in cells exposed to possible therapeutic agents. This sequence
CC represents a PCR primer used in prevention of skipping of exon 7 of the
CC SMN2 gene
XX
SQ Sequence 18 BP; 6 A; 2 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1731 ATTGGCTCCCAACTCCT 1747
Db 18 ATGGCCTCCCATCTCCT 2
RESULT 278
AAH25354/c
ID AAH25354 standard; DNA; 18 BP.
XX
AC AAH25354;
XX
DT 22-AUG-2001 (first entry)
XX
DE Antisense oligonucleotide targeted to human Her-4 coding region.
XX
KW Antisense oligonucleotide; Her-4; receptor kinase; tyrosine kinase;
KW infection; inflammation; tumour; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /tag= b
FT /note= "all cytidine residues are 5-methylcytidines"
FT modified_base 1..18
FT /tag= c
FT /note= "all internucleoside linkages are phosphorothioate
FT linkages"
FT modified_base 1..4
FT /tag= a
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 5..14
FT /tag= d
FT /note= "2'-deoxynucleotides"
FT modified_base 15..18
FT /tag= e
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
PN US6255111-B1.
XX
XX 03-JUL-2001.
XX
PF 31-JUL-2000; 2000US-00632580.
XX
PR 31-JUL-2000; 2000US-00632580.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowser LM;
XX WPI; 2001-388929/41.
XX
CC Compound for inhibiting the expression of Her-4 (a receptor/tyrosine
CC kinase) e.g. in preventing tumor formation, comprises an antisense
CC oligonucleotide that hybridizes to a nucleic acid encoding Her-4.
XX
PS Claim 1; Col 43-44; 44pp; English.
XX
CC The specification describes antisense oligonucleotides which are targeted
CC to a nucleic acid encoding Her-4 (a receptor/tyrosine kinase). The
CC antisense oligonucleotides are used to inhibit the expression of Her-4 in
CC cells or tissues in vitro. They can be used in diagnostics, therapeutics,
CC prophylaxis and as a probe in research reagents. The antisense

CC oligonucleotides can be used to prevent or delay infection, inflammation
 CC or tumour formation. AAH25315-AAH25398 represent antisense
 CC oligonucleotides which are targeted to different regions of the human Her
 CC -4 gene
 XX
 XX Sequence 18 BP; 5 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1723 AGATGAGATGGCTCC 1739
 ||| ||||| ||||| |||||
 DB 18 AGTTTGAGATGGCTCC 2

RESULT 279
 AAS95242
 ID AAS95242 standard; DNA; 18 BP.

AC AAS95242;
 XX
 XX 14-FEB-2002 (first entry)
 DT
 XX

Otoferlin exon PCR primer #31.

DE Human; mouse; otoferlin; OTOF; brain; auditory function; PCR primer;
 KW autosomal nonsyndromic prelingual deafness; DFNB9; ss.
 KW

OS Homo sapiens.

XX WC200170972-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-IB000578.

XX 24-MAR-2000; 2000US-0191738P.

XX (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX Yasunaga S, Grati M, Cohen-Salmon M, El Amraoui A, Petit C;
 PI Weil D;
 PI

XX WPI; 2001-611499/70.

XX Novel human gene Otoferlin, underlying an autosomal recessive
 PT nonsyndromic prelingual deafness, DFNB9, and proteins encoded by the
 PT gene, implicated in deafness.

XX Claim 25; Page 31; 99pp; English.

PS The invention relates to a purified polynucleotide (I) encoding a protein
 CC sequence (II) encoded by a novel human gene, otoferlin (OTOF) or the long
 CC human otoferlin isoform in brain. (I) was identified as underlying an
 CC autosomal nonsyndromic prelingual deafness DFNB9, and is thus useful for
 CC detecting deafness disease in humans and for characterising the functions
 CC of proteins and genes encoding them in auditory function. AAS95022-
 CC AAS95248 represent human and mouse otoferlin coding sequences, PCR
 CC primers and related sequences of the invention

XX Sequence 18 BP; 3 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 CTGGAAACCCCTGGTGCT 1687
 ||||| ||||| ||||| |||||
 DB 2 CTGGGACCCAGGTGACT 18

RESULT 280
 AAF79532/c
 ID AAF79532 standard; DNA; 18 BP.

XX
 AC AAF79532;
 XX

XX 29-MAY-2001 (first entry)

XX Caspase-4 protease cleavage signal nucleotide sequence.

DE Caspase-4; protease; cleavage signal; transgene expression;
 XX transgene localisation; sodium iodide symporter; NIS; ds.
 KW

XX Unidentified.

XX WO200113106-A1.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US022566.

XX 17-AUG-1999; 99US-0149168P.

XX 16-AUG-2000; 2000US-00639667.

XX 16-AUG-2000; 2000US-00640198.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

XX Russell SJ, Morris J, Peng K;

XX WPI; 2001-257548/26.

XX P-PSDB; AAB73916.

XX Monitoring transgene expression and therapeutic peptide production in
 PT mammals by detecting marker polypeptides linked to transgenes or
 PT therapeutic genes released from cells into extracellular body fluid.
 XX

Example 11; Page 48; 79pp; English.

XX The present sequence is a self-cleaving linker. It may be used in a
 CC method for monitoring expression and/or localisation of a transgene, and
 CC production of therapeutic peptide in a mammal. The method involves
 CC quantifying or detecting the amount of marker polypeptide and/or sodium
 CC iodide symporter (NIS) linked to the product of the transgene or
 CC therapeutic gene released from cells into extracellular body fluid, or
 CC determining the location of labelled molecules which are transported into
 CC the cells bearing the marker peptide. The method provides convenient and
 CC effective monitoring of the level and kinetics of expression of
 CC transgenes and the tissue-specific distribution of expressed transgenes
 CC in cells, tissues, animals or humans without the need for disruptive and
 CC expensive sampling methods including surgery. The transgene location can
 CC be monitored without adversely affecting the mammal or the cell. The NIS
 CC is a self protein and as such does not stimulate a host immune reaction.
 CC Furthermore, the NIS functions solely to sequester iodine into a cell,
 CC which does not adversely affect normal cellular function or overall cell
 CC biology

XX Sequence 18 BP; 4 A; 7 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;

Best Local Similarity 82.4%; Pred. No. 3.5e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGAGATT 1733

DB 17 GTACGGAGATGGAGATT 1

RESULT 281

ABZ80661/c

ID ABZ80661 standard; DNA; 18 BP.

XX ABZ80661;

XX

DT 13-JUN-2003 (first entry)
 XX Magnaporthe grisea plsl gene PCR primer 39+ for expression construct.
 DE plsl; rice blast fungus; ss; fungicide; tetraspamine; pathogenicity;
 KW appressorium; PCR; primer; amplification.
 KW Magnaporthe grisea.
 OS WO200077036-A2.
 XX 21-DEC-2000.
 XX 16-JUN-2000; 2000WO-FR001666.
 XX 16-JUN-1999; 99FR-00007867.
 PR 31-MAR-2000; 2000FR-00004102.
 XX (AVET) AVENTIS CROPS SCIENCE SA.
 XX Cots J, Gourgues M, Latorse M, Lebrun M;
 PI WPI; 2001-080679/09.
 DR Novel nucleic acid essential for pathogenicity of fungi, useful for
 PT identifying agricultural fungicides, also related proteins and
 PT transformants.
 XX Example 4; Page 42; 72pp; French.
 XX The invention relates to the isolation of the rice blast fungus
 CC (Magnaporthe grisea) plsl gene (also known as gene 421). The gene encodes
 CC a tetraspamine that is essential for fungal pathogenicity. The plsl
 CC protein is essential for controlling biological functions of the
 CC appressorium such as differentiation of the penetrative hyphal tip in
 CC this pathogenic fungus. The gene, host cells that express it and/or the
 CC polypeptide encoded by it are used to identify genes involved in fungal
 CC pathogenicity and to identify compounds that inhibit fungal
 CC pathogenicity, potentially useful as plant-protection agents. The gene is
 CC also useful for isolating homologous genes from other fungi and as
 CC antisense sequences (antifungal agents). This sequence represents a
 CC primer used to PCR amplify a Magnaporthe grisea plsl gene to generate an
 CC expression construct
 XX
 SQ Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 8.8%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1647 AGAAGGCAAGCACCAGG 1663
 Db ||||| ||||| |||||
 17 AGAAGCCAGCATCAGG 1
 RESULT 282
 ABS98053/c
 ID ABS98053 standard; DNA; 18 BP.
 XX
 AC ABS98053;
 XX
 DT 23-DEC-2002 (first entry)
 XX Human multidrug resistance gene PCR primer #17.
 DE Human; ss;
 KW cytochrome P450 A1; CYP450A1; UGT2B4; MDR1; PCR;
 KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KW glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase;
 KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;

KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KW multidrug resistance associated protein 3; cancer; prostate;
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KW altered drug metabolism; cardiovascular function; colorectal tumour;
 KW central nervous system; pulmonary; immunological.
 XX Homo sapiens.
 OS
 XX WO200257410-A2.
 XX 25-JUL-2002.
 XX 28-NOV-2001; 2001WO-US044838.
 XX 28-NOV-2000; 2000US-00724389.
 XX (DNAS-) DNA SCI LAB INC.
 PA Guida M, Hall J;
 XX WPI; 2002-698522/75.
 DR Isolated nucleic acid molecules having polymorphisms in known human genes
 XX e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.
 XX Example 22; Page 141; 714pp; English.
 PS This invention relates to the sequence of an isolated nucleic acid
 XX molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GSTI2), histamine-N-methyl
 CC transferase (HNMT), kallikrein 2 (KLK2), nicotinamide -N-methyl
 CC sulfotransferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP45002E1,
 CC ARNT, EPHX2, GSTI2, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a PCR
 CC primer used to amplify the sequences of the invention
 XX
 SQ Sequence 18 BP; 4 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 8.8%; Score 12.2; DB 1; Length 18;

CC stenosis, scleroderma, obesity, metabolic disturbances associated with
CC obesity, transplantation, adrenoleukodystrophy, congenital adrenal
CC hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm,
CC adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,
CC bronchial asthma, Crohn's disease, multiple sclerosis, infectious
CC disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,
CC or Parkinson's disease), immune disorders, haematopoietic disorders,
CC dyslipidaemias, and wasting disorders associated with chronic diseases.
CC The proteins can also be used as immunogens to produce antibodies and as
CC vaccines. The sequences may further be used in chromosome mapping,
CC and in forensic identification from minute biological samples (tissue typing),
CC and in forensic identification of a biological sample. The present
CC sequence represents a PCR primer for a human NOVX sequence, which is used
CC in an example from the present invention.

XX
SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1682 GTGTCCTCCAGCGTG 1698
||| ||||| ||||| ||
Db 2 GTGGCTCTGCAGTTG 18

RESULT 286
ADC98350
ID ADC98350 standard; DNA; 18 BP.
AC ADC98350;
XX
DT 01-JAN-2004 (first entry)
XX
DE ACLP06 polymorphism marker PCR primer B primer seq.
XX
KW low bone mineral density; BMD; bone damage; polymorphism; osteoporosis;
KW single nucleotide polymorphism; SNP; PCR primer; ss; human.
XX
OS Synthetic.
OS Homo sapiens.
PN WO2003054218-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040948.
XX
PR 20-DEC-2001; 2001US-0342711P.
PR 04-NOV-2002; 2002US-0423559P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Jones KA, Valdes A, Townley DJ, Mangion J, Galwey N, Bennett S;
PI McKay I, Schafer A;
XX
DR WPI; 2003-559156/52.
XX
PT Determining whether an individual is predisposed to susceptibility to low
PT bone mineral density (BMD) and/or bone damage, involves identifying
PT polymorphisms in associated genes.
XX
ES Example 8; Page 237; 246pp; English.
XX
CC The present invention describes a method of determining whether an
CC individual is predisposed to susceptibility to low bone mineral density
CC (BMD) and/or bone damage comprising identifying whether the individual
CC has at least one polymorphism in a polynucleotide encoding a protein,
CC where the polynucleotide is one of 81 200-500 nucleotide sequences (S1,
CC see ADC98235 to ADC98315). An agent identified in an method from the
CC present invention which can be used for the prevention or treatment of a
CC disease, resulting in susceptibility to low BMD and/or bone damage is
CC useful in the manufacture of a medicament for use in modulating the

Mon Aug 30 09:26:45 2004

CC susceptibility to low BMD and/or bone damage. The disease associated with
CC low BMD and/or bone damage is osteoporosis. The present PCR primer
CC sequence is used in the exemplification of the present invention.

XX Sequence 18 BP; 4 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
XX Query Match 8.8%; Score 12.2; DB 1; Length 18;
XX Best Local Similarity 82.4%; Pred. No. 3.5e+02;
XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1669 AGCTGGAACCCCTGGTGT 1685
DB 1 AGCTGGAACCCGAGTTT 17

RESULT 287
ADE78579/c
ID ADE78579 standard; DNA; 18 BP.

XX ADE78579;
XX
XX
XX 29-JAN-2004 (first entry)

DE Endogenous carotenoid gene expression RT-PCR primer #3.
XX metabolite; carotene; plant; carotene hydroxylase; lycopene beta-cyclase;
XX beta-carotene hydroxylase; zeaxanthin; beta-carotene;
XX oxygenated carotenoid; RT-PCR; primer; carotenoid; ss.

XX Unidentified.
XX
XX EP1323825-A2.
XX
XX 02-JUL-2003.

XX 08-NOV-2002; 2002EP-00425681.
XX
XX 09-NOV-2001; 2001IT-RM000670.

XX (CNEA) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.
XX (BIOJ) BIOGEN SRL.
XX
XX Giuliano G, Rosati C, Dharmapuri S, Pallara P, Camara B;

XX WPI; 2003-714401/68.
XX
XX Increasing the metabolites of carotene content in a plant useful for
XX producing recombinant plants comprises upregulating a gene encoding
XX carotene hydroxylase activity.

XX Example 1; Page 12; 21pp; English.
XX
XX The invention relates to a novel process for increasing the metabolites
XX of carotene content of a plant. The novel process comprises upregulating
XX at least one gene which encodes carotene hydroxylase activity. The
XX compositions of the novel process have lycopene beta-cyclase or a beta-
XX carotene hydroxylase activity. The process is useful for increasing the
XX metabolites of carotene content of a plant, comprising transforming a
XX plant cell from which viable plants may be recovered, using a plant
XX expression cassette, or a DNA construct, and generating viable plants
XX from the cell. The carotene metabolites are useful for increasing
XX zeaxanthin and beta-carotene, including oxygenated carotenoids. This
XX polynucleotide sequence represents an RT-PCR primer used in the process
XX for the expression of the introduced proteins and endogenous carotenoid
XX genes of the invention.

XX Sequence 18 BP; 0 A; 4 C; 6 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 8.8%; Score 12.2; DB 1; Length 18;
XX Best Local Similarity 82.4%; Pred. No. 3.5e+02;
XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1644 AGCAGAAGCAAGCACC 1660

DB 17 AGCACAAGCAAGCAGC 1

RESULT 288
AAI66686
ID AAI66686 standard; DNA; 21 BP.

XX AAI66686;
XX
XX 07-JAN-2002 (first entry)
XX Human CETP DNA related PCR primer.

XX CETP; arteriosclerosis; cholesterol ester transfer protein; HDL;
XX high density lipoprotein; human; PCR primer; ss.

XX Homo sapiens.

XX WO200171032-A1.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-JP002327.

XX 24-MAR-2000; 2000JP-00084264.

XX (BMLB-) BML INC.

XX Nagano M, Ito M, Sagehashi Y, Hattori H, Egashira T, Yamashita S;
XX Matsuzawa Y;
XX WPI; 2001-611516/70.

XX Determining a risk factor for arteriosclerosis comprises detecting
XX mutations in genes for cholesterol ester transfer protein.
XX Disclosure; Page 21; 58pp; Japanese.

XX The invention relates to detecting the risk factor for arteriosclerosis
XX in a subject that involves detecting mutations in the gene for
XX cholesterol ester transfer protein (CETP) related to the degree of risk
XX of arteriosclerosis. The mutant proteins alter the level of HDL in the
XX blood. The high frequency mutations can be detected for prevention and
XX treatment of arteriosclerosis. Sequences AAI66655-91 represent PCR
XX primers related to the human CETP DNA, used during the course of the
XX invention

XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

XX Query Match 3.8%; Score 12.2; DB 1; Length 21;

XX Best Local Similarity 82.4%; Pred. No. 4.2e+02;

XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1657 CACCAGGCTCACAGCTG 1673

DB 2 CACCAGGCTTCCAGCTG 18

RESULT 289
ABH93471/c
ID ABH93471 standard; DNA; 12 BP.

XX ABH93471;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 293464 for detecting SNP TSC0015629.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT Claim 1; SEQ ID NO 293464; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 PS Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1711 TTAGGAGTACGG 1722
 DB |||||
 12 TTAGGAGTACGG 1
 RESULT 290
 ABH80452
 ID ABH80452 standard; DNA; 12 BP.
 XX AC ABH80452;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide primer SEQ ID NO 280445 for detecting SNP TSC0008642.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX Peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT Claim 1; SEQ ID NO 293464; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 PS Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1711 TTAGGAGTACGG 1722
 DB |||||
 12 TTAGGAGTACGG 1
 RESULT 290
 ABH80452
 ID ABH80452 standard; DNA; 12 BP.
 XX AC ABH80452;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide primer SEQ ID NO 280445 for detecting SNP TSC0008642.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX Peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT Claim 1; SEQ ID NO 293464; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 PS Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1703 AAGTTGGGTTAG 1714
 DB |||||
 1 AAGTTGGGTTAG 12
 RESULT 291
 ABI12177/c
 ID ABI12177 standard; DNA; 12 BP.
 XX AC ABI12177;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide primer SEQ ID NO 312150 for detecting SNP TSC0024874.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX Peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT Claim 1; SEQ ID NO 312150; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 PS Sequence 12 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1703 AAGTTGGGTTAG 1714
 DB |||||
 1 AAGTTGGGTTAG 12

XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT Claim 1; SEQ ID NO 280445; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 PS Sequence 12 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1703 AAGTTGGGTTAG 1714
 DB |||||
 1 AAGTTGGGTTAG 12
 RESULT 291
 ABI12177/c
 ID ABI12177 standard; DNA; 12 BP.
 XX AC ABI12177;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide primer SEQ ID NO 312150 for detecting SNP TSC0024874.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX Peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT Claim 1; SEQ ID NO 312150; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 PS Sequence 12 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1703 AAGTTGGGTTAG 1714
 DB |||||
 1 AAGTTGGGTTAG 12
 RESULT 291
 ABI12177/c
 ID ABI12177 standard; DNA; 12 BP.
 XX AC ABI12177;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide primer SEQ ID NO 312150 for detecting SNP TSC0024874.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX Peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT Claim 1; SEQ ID NO 312150; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 PS Sequence 12 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 12;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1703 AAGTTGGGTTAG 1714
 DB |||||
 1 AAGTTGGGTTAG 12

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 8.6%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1747 TCCCTATCCTAA 1758
 Db 12 TCCCTATCCTAA 1
 RESULT 292
 ABC63273/c
 ID ABC63273 standard; DNA; 13 BP.
 XX AC ABC63273;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 63290 for detecting SNP TSC0016721.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX PS Claim 1; SEQ ID NO 63290; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC SQ Sequence 13 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 1 Other;
 Query Match 8.6%; Score 12; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1747 TCCCTATCCTAA 1758
 Db 12 TCCCTATCCTAA 1
 RESULT 292
 ABC63273/c
 ID ABC63273 standard; DNA; 13 BP.
 XX AC ABC63273;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 63290 for detecting SNP TSC0016721.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX PS Claim 1; SEQ ID NO 63290; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC SQ Sequence 13 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 1 Other;
 Query Match 8.6%; Score 12; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1697 TGGTGAAGTTG 1708
 Db 13 TGGTGAAGTTG 2
 RESULT 293
 ABF24345/c
 ID ABF24345 standard; DNA; 13 BP.
 XX AC ABF24345;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 124342 for detecting SNP TSC0031088.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX PS Claim 1; SEQ ID NO 124342; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC SQ Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 8.6%; Score 12; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1723 AGATGGAGATTG 1734
 Db 13 AGATGGAGATTG 2
 RESULT 294
 ABH00388
 ID ABH00388 standard; DNA; 13 BP.
 XX AC ABH00388;
 XX


```
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 200365 for detecting SNP TSC0049306.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PE 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 200365; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1721 GGAGATGGAGAT 1732
Db 1 GGAGATGGAGAT 12
RESULT 295
ABH00389/c
ID ABH00389 standard; DNA; 13 BP.
AC ABH00389;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 200366 for detecting SNP TSC0049306.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PE 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 200366; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1721 GGAGATGGAGAT 1732
Db 1 GGAGATGGAGAT 12
RESULT 295
ABH00389/c
ID ABH00389 standard; DNA; 13 BP.
AC ABH00389;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 200367 for detecting SNP TSC0060506.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PE 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
```

PT methylation status.

XX Claim 1; SEQ ID NO 247602; 29pp + Sequence Listing; German.

PS

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

SQ

Query Match 8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1705 GTTGGGTAGGA 1716
12 GTTGGGTAGGA 1

Db

RESULT 297

ABF95704

ID ABF95704 standard; DNA; 13 BP.

XX

AC ABF95704;

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 195701 for detecting SNP TSC0009428.

XX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

Homo sapiens.

XX

WO200177384-A2.

XX

18-OCT-2001.

XX

06-APR-2001; 2001WO-IB000713.

XX

07-APR-2000; 2000DE-01019173.

XX

(EPIG-) EPIGENOMICS AG.

XX

Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

XX

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX

Claim 1; SEQ ID NO 195701; 29pp + Sequence Listing; German.

XX

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

SQ

Query Match 8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1705 GTTGGGTAGGA 1716
12 GTTGGGTAGGA 1

Db

RESULT 298

ABC84321/C

ID ABC84321 standard; DNA; 13 BP.

XX

AC ABC84321;

XX

DT 21-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 84338 for detecting SNP TSC0021205.

XX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

Homo sapiens.

XX

WO200177384-A2.

XX

18-OCT-2001.

XX

06-APR-2001; 2001WO-IB000713.

XX

07-APR-2000; 2000DE-01019173.

XX

(EPIG-) EPIGENOMICS AG.

XX

Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

XX

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

XX

Claim 1; SEQ ID NO 84338; 29pp + Sequence Listing; German.

XX

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;

SQ

Query Match 8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1722 GAGATGGAGATT 1733
13 GAGATGGAGATT 2

Db

RESULT 299
 ABC05018
 ID ABC05018 standard; DNA; 13 BP.
 AC ABC05018;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 5009 for detecting SNP TSC0001740.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 WPI; 2001-657177/75.
 XX
 Set of oligonucleotides, useful for diagnosis and cell typing, is
 designed to detect single-nucleotide polymorphisms and cytosine
 methylation status.
 Claim 1; SEQ ID NO 5009; 29pp + Sequence Listing; German.
 This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 oligomers are also used for detecting cell type differentiation. ABC00010
 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 represent the oligomers described in the invention. NOTE: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format from WIPO at
 ftp.wipo.int/pub/published_pct_sequences

Query Match 8.6%; Score 12; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGAT 1732
 |||||
 Db 2 GGAGATGGAGAT 13

RESULT 300
 ABC05019/c
 ID ABC05019 standard; DNA; 13 BP.
 XX
 AC ABC05019;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 5010 for detecting SNP TSC0001740.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 WPI; 2001-657177/75.
 XX
 Set of oligonucleotides, useful for diagnosis and cell typing, is
 designed to detect single-nucleotide polymorphisms and cytosine
 methylation status.
 Claim 1; SEQ ID NO 5010; 29pp + Sequence Listing; German.
 This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 oligomers are also used for detecting cell type differentiation. ABC00010
 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 represent the oligomers described in the invention. NOTE: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format from WIPO at
 ftp.wipo.int/pub/published_pct_sequences

Query Match 8.6%; Score 12; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGAT 1732
 |||||
 Db 12 GGAGATGGAGAT 1

RESULT 301
 ABC63272
 ID ABC63272 standard; DNA; 13 BP.
 XX
 AC ABC63272;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 63289 for detecting SNP TSC0016721.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 63289; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 1 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1697 TGGTGGAGATTG 1708
 DB 1 TGGTGGAGATTG 12
 RESULT 302
 ABF24344
 ID ABF24344 standard; DNA; 13 BP.
 XX AC ABF24344;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 124341 for detecting SNP TSC0031088.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PA (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 124341; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 1 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1697 TGGTGGAGATTG 1708
 DB 1 TGGTGGAGATTG 12
 RESULT 302
 ABF24344
 ID ABF24344 standard; DNA; 13 BP.
 XX AC ABF24344;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 124341 for detecting SNP TSC0031088.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PA (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 124341; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 1 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1723 AGATGGAGATTG 1734
 DB 1 AGATGGAGATTG 12
 RESULT 303
 ABC84320
 ID ABC84320 standard; DNA; 13 BP.
 XX AC ABC84320;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 84337 for detecting SNP TSC0021205.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PA (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 84337; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
 XX Query Match 8.6%; Score 12; DB 1; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1723 AGATGGAGATTG 1734
 DB 1 AGATGGAGATTG 12

[illegible]

FT XX /note= "polymorphic site indicated by an ambiguity base"
PN WO200194365-A2.
XX
PD 13-DEC-2001.
XX
PF 11-JUN-2001; 2001WO-US018814.
XX
PR 09-JUN-2000; 2000US-0210568P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Koshy B, Sanchis A, Sausker EA;
XX WPI; 2002-404359/43.
XX
PT New variants of phosphorylase kinase gamma 2 isogenes, useful for
PT improving efficiency and reliability in the development of drugs for
PT treating diseases e.g. liver cirrhosis.
XX
PS Claim 16; Page 13; 76pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) comprising
CC a nucleotide sequence which is a polymorphic variant of a reference
CC sequence for human phosphorylase kinase gamma2 (testis) (PHKG2) gene or
CC its fragment, or a polymorphic variant of a reference sequence for a
CC PHKG2 cDNA or its fragment. Also described is an isolated polypeptide
CC (II) comprising an amino acid sequence which is a polymorphic variant of
CC a reference sequence for PHKG2 protein or its fragment, where the
CC reference sequence comprises a sequence (see ABB09290) of 406 amino
CC acids, and the polymorphic variant comprises one or more variant amino
CC acids selected from glutamic acid at a position corresponding to amino
CC acid position 153 and tryptophan at position corresponding to amino acid
CC position 329. (I) has hepatotropic activity and can be used in gene
CC therapy. (II) is useful in screening for drugs targeting (II), by
CC contacting a PHKG2 polymorphic variant with a candidate agent and
CC assaying for binding activity. The identified candidate agents targeting
CC PHKG2, are useful for treating liver cirrhosis and glycogen storage
CC diseases. The present sequence represents an allele specific
CC oligonucleotide (ASO) primer for the PHKG2 gene, which is used in the
XX exemplification of the present invention
SQ Sequence 15 BP; 1 A; 10 C; 0 G; 3 T; 0 U; 1 Other;

Query Match 8.6%; Score 12; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1736 CTCCTCACTCTCC 1749
Db 2 CTCCTCACTCTCC 15

RESULT 309
AAL44022
ID AAL44022 standard; DNA; 16 BP.
XX
AC AAL44022;
XX
DT 27-SEP-2002 (first entry)
XX
DE Human cytochrome P450A6 (CYP450A6 or CYP2A6) gene sequencing primer 3.
XX
KW Human; PCR; sequencing; primer; ss; single nucleotide polymorphism; SNP;
KW cytochrome; P450A6; CYP450A6; CYP2A6; chromosome 19;
KW steroid metabolism; drug detoxification; xenobiotic detoxification;
KW procarcinogen activation; inflammation; asthma; habitual smoking.
XX
OS Homo sapiens.
XX
PN WO200194633-A1.
XX
PD 13-DEC-2001.

Query Match 8.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1634 TGGGGCTTTGTAG 1645
Db 1 TGGGGCTTTGTAG 12

RESULT 310
AAF02799/c
ID AAF02799 standard; DNA; 17 BP.
XX
AC AAF02799;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1094.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX WPI; 2000-647423/62.
DR
PD

XX
PF 01-JUN-2001; 2001WO-US017781.
XX
PR 02-JUN-2000; 2000US-00586376.
XX
PA (DNAS-) DNA SCI INC.
XX
PI Guida M, Hall J;
XX
DR WPI; 2002-566448/60.
XX
PT New isolated polynucleotide, useful to screen individuals for asthma,
PT inflammation and susceptibility to habitual smoking, comprises base
PT variation from that of known human cytochrome P450A6 sequence.
XX
PS Example 1; Page 26; 48pp; English.
XX
CC The invention comprises the identification of genetic polymorphisms in
CC the human cytochrome P450A6 (CYP450A6 or CYP2A6) gene. The human
CC cytochrome P450A6 gene is located on chromosome 19 and encodes an enzyme
CC that plays a role in the metabolism of steroids, the detoxification of
CC drugs and xenobiotics, and the activation of procarcinogens. The P450A6
CC polymorphisms identified in the invention are useful for evaluating an
CC individual's risk of developing asthma or an individual's propensity for
CC cigarette consumption. The P450A6 DNA sequences of the invention are
CC useful for identifying individuals having a polymorphic genotype and to
CC screen individuals for altered metabolism for cytochrome P450A6
CC substrates. The P450A6 DNA sequences of the invention are also useful
CC for identifying individuals who are at risk from inflammation or
CC habitual smoking and diseases that result from environmental or
CC occupational exposures to dangerous substances. The present DNA sequence
CC represents a human cytochrome P450A6 sequencing primer
SQ Sequence 16 BP; 1 A; 1 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1634 TGGGGCTTTGTAG 1645
Db 1 TGGGGCTTTGTAG 12

RESULT 310
AAF02799/c
ID AAF02799 standard; DNA; 17 BP.
XX
AC AAF02799;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1094.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX WPI; 2000-647423/62.
DR
PD

Enzymatic and antisense nucleic acid inhibition of repressor genes,
useful for producing e.g. granulocyte colony stimulating factor protein,
interferon alpha and erythropoietin.

Claim 37; Page 80; 164pp; English.

The present invention relates to enzymatic and antisense nucleic acid
molecules that act as inhibitors of the expression of repressor genes
encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
Inhibition of the repressors removes prevents inhibition (and
consequently increases expression of) genes involved in the production of
erythropoietin, granulocyte colony stimulating factor protein and
interferon alpha

Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1651 GCGAAGCACCAG 1662
DB 12 GCGAAGCACCAG 1

RESULT 311
ABV90232
ID ABV90232 standard; DNA; 17 BP.
AC ABV90232;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 945.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX
XX EF1239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M;
XX
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 945; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC

acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
(S1) having 95% deviations, especially conservative substitutions or a
fragment of the sequences comprising at least 8 contiguous amino acids.
Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
adaptor protein that interacts with Rho family small GTPases as well as
downstream components of the signal transduction pathway. (I) is useful
for identifying a specific binding partner. (II) and nucleic acids (II)
encoding (II) are useful for diagnosing, monitoring disease and treating
caused by altered expression of human POSHL1 including diagnosing and
treating cancer, they are useful in the development of vaccines and (II) is
useful in gene therapy. (II) is useful for constructing microarrays which
are useful for measuring and for surveying gene expression and creating
transgenic non-human animals capable of producing the proteins. The
present sequence is that of a scanning oligonucleotide useful in examples
of the invention. Note: The present sequence did not form part of the
printed specification, but is based on sequence information supplied to
Derwent by the European Patent Office

Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1645 GCGAAGGCAAG 1656
DB 6 GCGAAGGCAAG 17

RESULT 312
ABV90236
ID ABV90236 standard; DNA; 17 BP.
XX
AC ABV90236;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 949.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX
XX EP1239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M;
XX
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 949; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC

XX The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
 CC (SI) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX
 XX Sequence 17 BP; 6 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 8.6%; Score 12; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1645 GCAGAAGGCAAG 1656
 Db 2 GCAGAAGGCAAG 13
 |||||
 RESULT 313
 ABV90234
 ID ABV90234 standard; DNA; 17 BP.
 XX
 AC ABV90234;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human POSHL1 scanning oligonucleotide SEQ ID NO 947.
 XX
 KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1239051-A2.
 XX
 PD 11-SEP-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001165.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 23-MAY-2001; 2001US-00864761.
 PR 10-OCT-2001; 2001US-0328205P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M;
 XX
 DR WPI; 2002-684061/74.
 XX
 PT Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
 PT -1, useful for treating disorders associated with decreased expression or

PT activity of human POSHL1.
 XX
 PS Example 2; SEQ ID NO 947; 60pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
 CC (SI) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX
 XX Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 8.6%; Score 12; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1645 GCAGAAGGCAAG 1656
 Db 4 GCAGAAGGCAAG 15
 |||||
 RESULT 314
 ABV90235
 ID ABV90235 standard; DNA; 17 BP.
 XX
 AC ABV90235;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human POSHL1 scanning oligonucleotide SEQ ID NO 948.
 XX
 KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1239051-A2.
 XX
 PD 11-SEP-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001165.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 23-MAY-2001; 2001US-00864761.
 PR 10-OCT-2001; 2001US-0328205P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M;
 XX
 DR WPI; 2002-684061/74.

Mon Aug 30 09:26:45 2004

XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 948; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
XX Sequence 17 BP; 6 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
SQ
Query Match 8.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1645 GCAGAGGCGCAAG 1656
DB 3 GCAGAGGCGCAAG 14
RESULT 315
ABV90233
ID ABV90233 standard; DNA; 17 BP.
XX
XX AC ABV90233;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 946.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX
XX EPI239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 23-MAY-2001; 2001US-00864761.
XX
XX 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEONICA INC.
XX

PI Shannon M;
XX
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 946; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
XX Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
SQ
Query Match 8.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1645 GCAGAGGCGCAAG 1656
DB 5 GCAGAGGCGCAAG 16
RESULT 316
ABV90237
ID ABV90237 standard; DNA; 17 BP.
XX
XX AC ABV90237;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 950.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX
XX EPI239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 23-MAY-2001; 2001US-00864761.
XX
XX 10-OCT-2001; 2001US-0328205P.
XX

XX (AEOM-) AEOMICA INC.
 XX Shannon M;
 XX WPI; 2002-684061/74.
 XX
 PS Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
 PT -1, useful for treating disorders associated with decreased expression or
 PT activity of human POSHL.
 XX
 XX Example 2; SEQ ID NO 950; 60pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
 CC (S1) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX
 SQ Sequence 17 BP; 6 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 8.6%; Score 12; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1645 GCAGAGGCGCAG 1656
 Db 1 GCAGAGGCGCAG 12
 RESULT 317
 ACC64298
 ID ACC64298 standard; DNA; 17 BP.
 AC ACC64298;
 XX
 XX 01-JUL-2003 (first entry)
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1545.
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 XX 27-MAR-2003.
 XX
 XX 17-SEP-2002; 2002WO-IB004210.
 XX
 XX 17-SEP-2001; 2001FR-00011979.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 PI Telerman A, Amson R, Tuijnder M;
 XX

DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 211; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 8.6%; Score 12; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1659 CCAGGCTCACAG 1670
 Db 4 CCAGGCTCACAG 15
 RESULT 318
 AAX28111
 ID AAX28111 standard; DNA; 18 BP.
 XX
 AC AAX28111;
 XX
 XX 11-JUN-1999 (first entry)
 DT
 DE PCR primer for M. kansasii KATS2 sequence.
 XX
 KW KATS2 sequence; Mycobacterium kansasii detection; probe; primer;
 KW microorganism detection; ds.
 XX
 OS Synthetic.
 OS Mycobacterium kansasii.
 XX
 PN EP905259-A1.
 XX
 XX 31-MAR-1999.
 XX
 XX 23-SEP-1998; 98EP-00118036.
 PF
 XX 25-SEP-1997; 97US-00937580.
 PR
 XX (BECT) BECTON DICKINSON & CO.
 PA
 XX Harris JM, You Q;
 PI
 XX WPI; 1999-192672/17.
 DR
 XX
 XX New Mycobacterium kansasii specific DNA fragment (KATS2) useful for
 PT designing oligonucleotides which are useful for detecting M. kansasii
 PT nucleic acid in clinical samples.
 XX
 XX Claim 2; Page 11; 36pp; English.
 PS
 XX This sequence is a primer for a Mycobacterium kansasii KATS2 sequence of
 CC the invention. The KATS2 oligonucleotide is useful as a probe and a
 CC primer for detection of M. kansasii microorganisms or nucleic acids in
 CC veterinary and human clinical samples by hybridisation and amplification
 CC respectively. The KATS2 fragment was hybridized to genomic DNA from M.
 CC kansasii and non-M. kansasii species, and was found to hybridise to all
 CC six M. kansasii strains tested, and none of the 17 non-M. kansasii

CC strains. The new oligonucleotides allows rapid, accurate and sensitive
 CC identification of all strains of M. kansasii, compared to prior art
 CC probes which only identify 73 % of M. kansasii strains (e.g. ACCU-PROBE),
 CC or fail to detect one distinct M. kansasii subgroup (e.g. pMK1-9)
 XX
 SQ Sequence 18 BP; 4 A; 0 C; 9 G; 5 T; 0 U; 0 Other;
 Query Match 8.6%; Score 12; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1721 CGAGATGGAGAT 1732
 DB 4 CGAGATGGAGAT 15
 RESULT 319
 AAX82250
 ID AAX82250 standard; DNA; 18 BP.
 XX
 AC AAX82250;
 XX
 DT 18-AUG-1999 (first entry)
 XX
 DE Influenza virus PA gene specific primer.
 XX
 KW Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein;
 KW PA protein; NP protein; M protein; NS protein; temperature sensitivity;
 KW vaccine; flu; influenza; PCR primer; ss.
 XX
 OS Synthetic.
 OS Influenza virus.
 XX
 PN WO9928445-A1.
 XX
 PD 10-JUN-1999.
 XX
 PF 30-NOV-1998; 98WO-KR000384.
 PR 29-NOV-1997; 97KR-00064854.
 XX
 PA (CHEI-) CHEIL JEDANG CORP.
 XX
 PI Seong BL, Lee KH, Youn JW, Kim SJ, Cheoun KH, Kim J, Kim HG;
 XX
 DR WPI; 1999-385377/32.
 XX
 PT Cold-adapted influenza viruses useful for the production of protective
 PT vaccines against flu.
 XX
 PS Example 4; Page 15; 62pp; English.
 XX
 CC The invention relates to cold-adapted influenza viruses prepared by
 CC passage culture of A/X-31, B/Yamagata/16/88 or B/Lee/40 viruses at low
 CC temperatures. A cDNA gene of cold-adapted influenza virus HTCA-A101 can
 CC be selected from a group consisting of PB2 protein gene, PB1 protein
 CC gene, PA protein gene, NP protein gene, M protein gene and NS protein
 CC gene (AAX82192-X82197). The method is useful for the production of cold-
 CC adapted influenza virus that exhibit temperature sensitivity and can be
 CC actively grown in fertilized eggs. The virus is useful for vaccines for
 CC protection against 'flu. Live vaccines containing cold-adapted viruses
 CC have several advantages over killed vaccines. It can prevent reduction of
 CC immunogenicity, which may occur in the killed vaccine where antigenic
 CC proteins would be denatured at its inactivation. It can also avoid
 CC hypersensitivity due to the prolonged administration of heterologous
 CC proteins. It promotes the immunity by inducing IgA and it can be
 CC administered into a spray formulation via nasal cavity and thus its
 CC application is convenient for children. It is able to inhibit the growth
 CC of the wild-type virus and thus its therapeutic effect can be expected.
 CC Sequences AAX82222-X82257 represent PCR primers specific for the various
 CC genes of influenza virus
 XX
 SQ Sequence 18 BP; 2 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1683 TGTCTCTCTCCAG 1694
 DB 2 TGTCTCTCTCCAG 13
 RESULT 320
 AAZ46979/C
 ID AAZ46979 standard; DNA; 18 BP.
 XX
 AC AAZ46979;
 XX
 DT 14-APR-2000 (first entry)
 XX
 DE Bcl-XL mRNA specific antisense oligo I.
 XX
 KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;
 KW lung; bladder; bcl-2; vascular lesion; antisense; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200001393-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 02-JUL-1999; 99WO-US015250.
 PR 02-JUL-1998; 98US-00109614.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Stein CA;
 XX
 DR WPI; 2000-137140/12.
 XX
 PT New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-
 PT xL, useful for reducing bcl-xL production in tumor cells to treat cancer
 PT or in vascular cells to promote the regression of vascular lesions.
 XX
 PS Claim 1; Fig 1; 69pp; English.
 XX
 CC The invention provides antisense oligonucleotides or their derivatives
 CC which reduce or eliminate expression of the anti-apoptotic protein bcl-
 CC xL. The oligonucleotides can be introduced into tumor cells to reduce
 CC bcl-xL production to treat cancer, especially epithelial cancer, e.g.
 CC prostate, lung or bladder cancer. Oligonucleotides comprising one or more
 CC bases with a C-5 propargyl pyrimidine modification may especially be used
 CC to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in
 CC such treatment. The oligonucleotides can be introduced into vascular
 CC cells to reduce bcl-xL production to promote the regression of vascular
 CC lesions. They can also be included with a carrier (and optionally tetra
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983
 CC represent antisense oligos specific for the bcl-XL mRNA
 XX
 SQ Sequence 18 BP; 2 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 8.6%; Score 12; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1720 CGAGATGGAGA 1731
 DB 14 CGAGATGGAGA 3
 RESULT 321
 ABZ10839
 ID ABZ10839 standard; DNA; 18 BP.

```
XX ABZ10839;
XX
XX 16-JAN-2003 (first entry)
XX
XX Haematopoietic cell proliferation disorder related oligonucleotide #979.
XX
XX Human; haematopoietic cell proliferation disorder; cytostatic;
XX gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
XX cytosine methylation state; probe; primer; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200277272-A2.
XX
XX 03-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-EP003401.
XX
XX 26-MAR-2001; 2001US-0278333P.
XX (EPIG-) EPIGENOMICS AG.
XX
XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
XX Olek A, Piepsbrock C, Adorjan P, Grabs G, Lesche R, Leu E,
XX Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
XX Schwobe I, Ziebarth H;
XX
XX WPI; 2003-018942/01.
XX
XX Detecting and differentiating between hematopoietic cell proliferative
XX disorders, comprises contacting a target nucleic acid with a reagent that
XX distinguishes between methylated and non-methylated CpG dinucleotides.
XX
XX Claim 15; Page 65; 117pp; English.
XX
XX The present invention describes a method for detecting and
XX differentiating between haematopoietic cell proliferative disorders
XX associated with at least 1 gene and/or their regulatory regions in a
XX subject. The method comprises contacting a target nucleic acid in a
XX biological sample obtained from the subject with at least 1 reagent,
XX which distinguishes between methylated and non-methylated CpG
XX dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
XX represent specifically claimed nucleotide sequences from the present
XX invention. Oligonucleotides from the present invention can be used: for
XX differentiating between healthy haematopoietic cells and proliferative
XX disorder haematopoietic cells; for differentiating between acute
XX lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
XX determining the cytosine methylation state and/or single nucleotide
XX polymorphisms (SNPs) of haematopoietic cell proliferation disorder
XX related sequences and their complements; and as primers for the
XX amplification of haematopoietic cell proliferation disorder related
XX sequences. The nucleotide sequences from the present invention can also
XX be used for detecting a predisposition to, differentiation between
XX subclasses, diagnosis, prognosis, treatment and/or monitoring of
XX haematopoietic cell proliferative disorders. The present method enables a
XX highly specific classification of haematopoietic cell proliferative
XX disorders allowing for improved and informed treatment of patients
XX
XX Sequence 18 BP; 5 A; 1 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 8.6%; Score 12; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.8e+02;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1712 TAGGAGTACCGA 1723
XX
XX Db 1 TAGGAGTACCGA 12
XX
XX RESULT 322
XX AAQ50548/c
```

```
ID AAQ50548 standard; DNA; 15 BP.
XX
XX AC AAQ50548;
XX
XX DT 24-MAY-1994 (first entry)
XX
XX DE Human chromosome 6 cCI6-111 VNTR consensus sequence.
XX
XX KW Variable Number of Tandem Repeats; human VNTR; satellite sequence;
XX DNA fingerprint; Southern hybridisation; probe; ss.
XX
XX OS Homo sapiens.
XX
XX PN JP05276949-A.
XX
XX PD 26-OCT-1993.
XX
XX PF 27-DEC-1991; 91JP-00359482.
XX
XX PR 27-DEC-1991; 91JP-00359482.
XX
XX PA (GANK-) ZH GAN KENYUKAI.
XX
XX DR WPI; 1993-373584/47.
XX
XX PT Human VNTR sequence - used to discriminate individual, esp. parent and
XX child.
XX
XX PS Disclosure; Fig 12; 11pp; Japanese.
XX
XX CC The degenerate probe sequence AAQ50544 corresponds to VNTRs found in
XX human chromosome 6. See AAQ61882-3 for the repeat region sequence and
XX AAQ50548 for the consensus sequence
XX
XX SQ Sequence 15 BP; 2 A; 2 C; 10 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 8.5%; Score 11.8; DB 1; Length 15;
XX Best Local Similarity 86.7%; Pred. No. 3.3e+02;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1734 GGCTCCCAACTCCTC 1748
XX
XX Db 15 GGCCCCCACCCTCCTC 1
XX
XX RESULT 323
XX AAT89133/c
XX
XX ID AAT89133 standard; RNA; 15 BP.
XX
XX AC AAT89133;
XX
XX DT 04-MAR-1998 (first entry)
XX
XX DE Lutetium texaphyrin RNA conjugate for light induced cleavage of DNA.
XX
XX KW Photosensitive; texaphyrin; DNA cleavage; light induced; photocleavage;
XX lutetium; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_binding 1..15
XX FT /tag= b
XX FT /note= "this region binds to AAT89134"
XX
XX FT misc_feature 1
XX FT /tag= a
XX FT /mod_base
XX FT /note= "cytosine is modified by lutetium(III)texaphyrin
XX compound"
XX
XX FT misc_feature 15
XX FT /tag= c
XX FT /note= "Guanine is modified by a methoxy group"
XX
```

PN WO9609315-A1.
XX
XX
XX 28-MAR-1996.
XX
XX 21-SEP-1995; 95WO-US012312.
XX
XX 21-SEP-1994; 94US-00310501.
PR 06-JUN-1995; 95US-00469177.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
FA (PHAR-) PHARMACYCLICS INC.
XX
XX Magda D, Sessler JL, Iverson BL, Sansom PI, Wright M, Mody TD;
PI Hemmi GW;
XX
XX WPI, 1996-200644/20.
XX
XX Use of photosensitive tetraphyrin cpds. - for light-induced cleavage of
PT polymers of deoxyribonucleic acid in analyses or therapy.
XX
XX Example 8; Fig 3; Sipp; English.
XX
XX The present sequence represents RNA coupled to a photosensitive
CC tetraphyrin molecule, which was used in a new method for photocleavage of
CC DNA. Targeted intracellular light-induced cleavage of a selected DNA
CC comprises introducing into a cell a photosensitive tetraphyrin (PT)
CC coupled to an oligonucleotide which is complementary to the selected DNA
CC and exposing the cell to light to cleave the DNA. Modulating the activity
CC of a selected DNA comprises contacting the DNA with a PT coupled to an
CC oligonucleotide which binds to the DNA and exposing the DNA-PT mixture to
CC light to cleave the DNA. These methods can be used e.g. in cleavage of
CC DNA in footprinting analysis, DNA sequencing, chromosome analyses, gene
CC isolation, recombinant DNA manipulations, mapping of large genomes and
CC chromosomes and for site-directed mutagenesis. They can also be used in
CC anti-viral therapy and for the treatment of cancers, inflammatory
CC responses that are caused by over expression of certain proteins,
CC infectious diseases and genetically-based disorders
XX
XX Sequence 15 BP; 2 A; 4 C; 6 G; 0 T; 3 U; 0 Other;
SQ
Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1659 CCAGGCTCACAGTG 1673
DB 15 CCCGGCTCACAGTG 1

RESULT 324
AAT65005/c
ID AAT65005 standard; DNA; 15 BP.
XX
XX AAT65005;
XX
XX 25-MAR-2003 (revised)
DT 28-MAY-1997 (first entry)
XX
XX Human chromosome 6 region q27 VNTR consensus repeat sequence.
XX
XX Variable number of tandem repeat; VNTR; genetic marker; satellite;
KW polymorphism; cC16-111; probe; DNA fingerprinting; paternity; forensic;
XX diagnosis; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH repeat_unit 1..15
FT /*tag= b
FT /rpt type= TANDEM
FT /note= "repeat units are 16 nucleotides long in the VNTR
FT region; the last nucleotide (not included in this
FT consensus sequence) can be either T or C"

XX JP08224100-A.
PN
XX
XX 03-SEP-1996.
XX
XX 27-DEC-1991; 95JP-00337988.
XX
XX 27-DEC-1991; 91JP-00359482.
PR
XX (GANK-) ZH GAN KENYUKA.
FA
XX WPI, 1996-449912/45.
XX
XX Human variable number of tandem repeat sequence - from chromosome 6 q27
PT region, has restriction fragment length polymorphism with MspI, RsaI,
PT TaqI, BglII, PstI and PvuII and is useful for genetic fingerprinting.
XX
XX Claim 1; Fig 2; 5pp; Japanese.
XX
XX The present sequence is a consensus repeat corresponding to nucleotides 1
CC -15 of the degenerate sequence RWGRRRTGGGRCCY which is repeated in the
CC variable number of tandem repeat (VNTR) sequence located at the q27
CC position in human chromosome 6. The VNTR has a restriction fragment
CC length polymorphism (RFLP) with Msp I, Rsa I, Taq I, Bgl II, Pst I and
CC Pvu II, i.e. it has at least 9 alleles between 4.4 kb and 1.8 kb with
CC respect to Msp I, at least 11 alleles between 5.5 kb and 1.7 kb with
CC respect to Rsa I, at least 12 alleles between 8.5 kb and 2.6 kb with
CC respect to Taq I, at least 12 alleles between 10 kb and 2.1 kb with
CC respect to Bgl II, at least 11 alleles between 5.2 kb and 0.5 kb with
CC respect to Pst I, and at least 10 alleles between 10 kb and 2.3 kb with
CC respect to Pvu II. The VNTR sequence can be used as a probe to identify
CC an individual, e.g. in paternity or forensic analysis. (Updated on 25-MAR
CC -2003 to correct PF field.)
XX
XX Sequence 15 BP; 2 A; 2 C; 10 G; 1 T; 0 U; 0 Other;
SQ
Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1734 GGCTCCCAACTCTCTC 1748
DB 15 GGCCCCCACTCTCTC 1

RESULT 325
AAT98897
ID AAT98897 standard; DNA; 15 BP.
XX
XX AAT98897;
XX
XX 23-MAR-1998 (first entry)
DT
XX
XX Probe 41w19 for HIV RT gene wild type E40M41K43.
DE
XX Reverse transcriptase gene; HIV; RT gene; antiviral drug susceptibility;
KW virus susceptibility; antiviral drug resistant viral strain; retrovirus;
KW Hepadnaviridae; HIV RT genotyping; probe; ss.
XX
XX Synthetic.
OS
OS Human immunodeficiency virus 1.
XX
XX WO9727332-A1.
XX
XX 31-JUL-1997.
PD
XX 17-JAN-1997; 97WO-EP000211.
XX
XX 26-JAN-1996; 96EP-00370005.
PR
XX 25-JUN-1996; 96EP-00370081.
PR
XX (INNO-) INNOGENETICS NV.
FA
XX

PI Stuyver L, Louwagie J, Rossau R;
 XX WPI; 1997-393716/36.
 DR
 XX Determining susceptibility to antiviral drugs of reverse transcriptase
 PT containing viruses - useful for genotyping HIV RT and detecting antiviral
 PT resistant HIV.
 XX
 XX Claim 13; Page 36; 59pp; English.
 PS
 XX This sequence represents a probe for a wild type HIV reverse
 CC transcriptase (RT) gene fragment. This sequence can be used in the method
 CC of the invention for determining the susceptibility to antiviral drugs of
 CC viruses which contain RT genes and are present in a biological sample. It
 CC comprises: (1) releasing, isolating or concentrating the polynucleic
 CC acids present in a sample; (2) amplifying or concentrating the polynucleic
 CC genes present with at least one suitable primer pair; (3) hybridising the
 CC polynucleic acids of step (1) or (2) with at least two RT gene probes.
 CC The probes being applied to known locations on a solid support, and are
 CC capable of simultaneously hybridising to their respective target regions
 CC under appropriate hybridisation and wash condition allowing the detection
 CC of homologous targets, or with the probes hybridising specifically with a
 CC sequence complementary to any of the target sequences; (4) detecting the
 CC hybrids formed in step (3); and (4) inferring the nucleotide sequence at
 CC the codons of interest (codons 38-44, 47-53, 65-72, 73-77, 148-154, 180-
 CC 187, 212-216, and 217-220), and/or the amino acids of the codons of
 CC interest and/or antiviral drug resistance spectrum, and possible the type
 CC of viral isolates involved from the differential hybridisation signals
 CC obtained in step (4). The method is specifically used to detect antiviral
 CC drug resistant strains of viruses containing RT genes, especially HIV
 CC retroviruses and Hepadnaviridae. The method can also be used for
 CC genotyping HIV RT
 XX
 SQ Sequence 15 BP; 7 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 3.3e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1717 GTACGAGATGGAGA 1731
 Db 1 GTACGAGATGGAAA 15
 RESULT 326
 AAV07304/C
 ID AAV07304 standard; DNA; 15 BP.
 AC AAV07304;
 XX
 DT 14-AUG-1998 (first entry)
 XX
 DE Metallotexaphyrin-oligonucleotide conjugate #18.
 XX
 KW Metallotexaphyrin; dysprosium; europium; conjugate; RNase H;
 KW antisense therapy; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /*mod_base
 FT /note= "DyTxNH-(CH2)6-PSO3-cytosine, where DyTx is
 FT dysprosium (III) texaphyrin"
 XX
 XX US5763172-A.
 PN
 PD 09-JUN-1998.
 XX
 PF 07-JUN-1995; 95US-00486962.
 XX
 PR 21-JAN-1992; 92US-00822964.
 PR

PR 09-JUN-1993; 93US-00075123.
 PR 14-APR-1994; 94US-00227370.
 PR 09-JUN-1994; 94WO-US006284.
 PR 26-MAY-1995; 95US-00452261.
 PR 07-JUN-1995; 95US-00485581.
 XX (PHAR-) PHARMACYCLICS INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Sessler JL, Wright M, Miller RA, Dow WC, Magda D;
 XX
 XX WPI; 1998-347306/30.
 DR
 XX Enhancing therapeutic activity of oligo-nucleotides in cells - using
 PT conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester
 PT bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.
 XX
 XX Example 8; Col 29-30; 34pp; English.
 PS
 XX The invention relates to a method of enhancing the therapeutic activity
 CC of oligonucleotides in cells. It comprises contacting a targeted
 CC intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide
 CC conjugate. The contact is carried out under physiological conditions for
 CC a time sufficient to hydrolyse the phosphate ester bond of the targeted
 CC RNA. The metallotexaphyrin of the conjugate has catalytic activity for
 CC phosphate ester bond hydrolysis. The oligonucleotide of the conjugate has
 CC complementary binding affinity to the targeted RNA. The conjugate may be
 CC used in antisense therapies for treating, e.g. cancer, viral infections,
 CC autoimmune diseases and restenosis. The conjugate may also be used as
 CC hydrolysis reagents for the detoxification of di- and trialkyl phosphate
 CC esters, which are used in solvents, insecticides and chemical nerve
 CC gases. The metallotexaphyrin complex enhances the therapeutic activity of
 CC the oligonucleotide, not only by facilitating cellular uptake of the
 CC oligonucleotide but also by hydrolysing target RNA within the cell.
 CC independent of RNase H. Attachment to the complex may also cause the
 CC oligonucleotide to take on some of the pharmacodynamic and biodistribution
 CC properties of the texaphyrin, such as selective localisation in tumours.
 CC The present sequence represents a metallo- texaphyrin-oligonucleotide
 CC conjugate
 XX
 SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 3.3e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1659 CCAGGCTCACAGCTG 1673
 Db 15 CCGGCTCACAGATG 1
 RESULT 327
 AAV54266/C
 ID AAV54266 standard; cDNA; 15 BP.
 XX
 AC AAV54266;
 XX
 DT 29-DEC-1998 (first entry)
 XX
 DE Primer KCL155 used in the method of the invention.
 XX
 XX PCR; primer; amplification; single chain T-cell receptor; scTCR; Vbc;
 KW bacteriophage coat protein; BCP; V-alpha chain; Vac; V-beta chain;
 KW immune response; T-cell receptor; TCR; cancer; allergy; T lymphocyte; ss.
 XX
 OS Synthetic.
 XX
 PN WO9839482-A1.
 PD
 PD 11-SEP-1998.
 XX
 PF 05-MAR-1998; 98WO-US004274.
 PR

```
PR 07-MAR-1997; 97US-00813781.
XX (SUNO-) SUNOL MOLECULAR CORP.
XX Weidanz JA, Card KF, Wong HC;
XX WPI; 1998-506374/43.
XX
XX New soluble T cell receptor fusion proteins - comprise V-alpha chain,
XX peptide linker, V-beta chain and bacteriophage coat protein, used to,
XX e.g. develop products for modulating immune responses.
XX
XX Disclosure; Fig 21D; 150pp; English.
XX
XX The present primer was used to construct DNA vectors which were used in
XX the method of the invention. The invention provides single chain T-cell
XX receptor (scTCR) fusion proteins which comprise of a bacteriophage coat
XX protein (BCP; e.g. gene III or VIII product) covalently linked to a scTCR
XX comprising of a V-alpha chain (Vac) covalently linked to a V-beta chain
XX (Vbc) by a peptide linker sequence. The BCP increases solubility of the
XX scTCR fusion proteins, thereby enhancing yield and functionality. The
XX scTCR fusion proteins are fully soluble and functional, and can be
XX isolated in significant quantities without performing difficult
XX solubilisation, cleaving or re-folding steps. The scTCR fusion proteins
XX can be produced in a variety of formats including bacteriophage display
XX libraries to screen for binding molecules which specifically bind the
XX scTCR fusion proteins. The scTCRs are claimed to be useful for reducing
XX an immune response by competing with an antigen with T-cell receptors
XX (TCR) occurring on pathogenic T cells such as those accompanying cancer,
XX infectious disease, allergy, etc. The scTCRs are also claimed to be
XX useful for inducing an immune response for immunisation against TCR
XX structures to reduce or eliminate the pathogenic or undesirable effects
XX of T cells, and they can also be used for the production of antibodies
XX and in diagnostic applications
XX
XX Sequence 15 BP; 1 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1656 GCACCAGGCTCACAG 1670
Db | | | | | | | | | | | | | | |
15 GAACCAGACTCACAG 1

RESULT 328
AA55348/c
ID AAX55348 standard; DNA; 15 BP.
XX
XX AAX55348;
XX
XX 08-JUL-1999 (first entry)
XX
XX Soluble sc-TCR fusion protein constructing primer KC155.
XX
XX Fusion protein; soluble; immunoglobulin; Ig; sc-TCR; immune response;
XX single-chain T-cell receptor; T cell activation; therapy; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO9918129-A1.
XX
XX 15-APR-1999.
XX
XX 28-SEP-1998; 98WO-US020263.
XX
XX 02-OCT-1997; 97US-00943086.
XX
XX (SUNO-) SUNOL MOLECULAR CORP.
XX
XX Weidanz JA, Card KF, Wong HC;
XX
```

```
DR WPI; 1999-264000/22.
XX Soluble single-chain T cell receptor proteins.
XX
XX Example; Fig 6D; 145pp; English.
XX
XX The invention relates to a soluble fusion protein that comprises an
XX immunoglobulin (Ig) light chain constant region or fragment, covalently
XX linked to a single-chain T-cell receptor (sc-TCR) comprising a V-alpha
XX chain covalently linked to a V-beta chain by a peptide linker sequence.
XX The soluble fusion protein can induce an immune response in a mammal, so
XX that the mammal is immunized against pathogenic T cell receptor epitopes.
XX It can also be used to inhibit T-cell activation in a mammal. The sc-TCR
XX can be used to kill a cell containing a TCR specific ligand. The sc-TCR
XX proteins can be used in vitro to detect and analyse ligands such as
XX peptides and MHC/HLA molecular components of TCR ligands. They can also
XX be used to detect T-cells with pathogenic properties. Other uses include
XX functional, cellular and molecular assays and structural analysis. In
XX vivo the sc-TCRs can compete with pathogenic T cells or to raise
XX antibodies for use in therapy. Fusion of an Ig light chain constant
XX region to a sc-TCR facilitates soluble expression. The sc-TCR can be
XX isolated in significant quantities without performing difficult
XX solubilisation, cleaving or re-folding steps. The fusion also confers a
XX means of detecting and purifying the fusion proteins by conventional
XX immunological methods. Sequences AAX5301 to AAX5445 represent PCR
XX primers used for constructing the fusion proteins of the invention
XX
XX Sequence 15 BP; 1 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1656 GCACCAGGCTCACAG 1670
Db | | | | | | | | | | | | | | |
15 GAACCAGACTCACAG 1

RESULT 329
AA66971/c
ID AAA66971 standard; DNA; 15 BP.
XX
XX AAA66971;
XX
XX 19-OCT-2000 (first entry)
XX
XX Human leukocyte antigen A allele DNA probe A539T SEQ ID NO:29.
XX
XX Human leukocyte antigen; HLA; class I allele type; probe; PCR primer;
XX amplification; hybridisation; organ transplant; gene typing; diagnosis;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200031295-A1.
XX
XX 02-JUN-2000.
XX
XX 07-OCT-1999; 99WO-JPC05527.
XX
XX 26-NOV-1998; 98JP-00335151.
XX
XX (SHIO ) SHIONOGI & CO LTD.
XX
XX Moribe T, Kaneshige T;
XX
XX WPI; 2000-400097/34.
XX
XX Simple, rapid and accurate method for distinguishing HLA class I allele
XX type with possibility of mechanization and automation, applicable in
XX judging donor-recipient compatibility during organ transplant and disease
XX diagnosis.
XX
```


PS Claim 8; Page 56; 83pp; Japanese.

XX The present invention describes a method for distinguishing a human

CC leukocyte antigen (HLA) class I antigen or allele by a combination of

CC polymerase chain reaction (PCR) using a primer pair whereby all HLA-A, -B

CC or -C alleles can be amplified or using reverse hybridisation analysis

CC comprising a DNA probe covalently bonded to microtitre plate wells which

CC are hybridisable specifically with the base sequence of at least one

CC specific HLA-A, -B or -C allele. The method is applicable in gene typing,

CC judging donor-recipient compatibility during organ transplant and

CC correlation analysis for diagnosis of various diseases. The method is

CC simple, rapid and accurate, with possibility of mechanisation and

CC automation, without the problems encountered by using the prior-art

CC techniques. AAA66943 to AAA67072 represent oligonucleotide probes and PCR

CC primers for use in the method of the present invention

XX

SQ Sequence 15 BP; 4 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 GGCTCCGAACTCTC 1748

DB 15 GGCTCTCAACTGCTC 1

RESULT 330

AAF47176/c

ID AAF47176 standard; DNA; 15 BP.

XX

AC AAF47176;

XX

DT 30-MAR-2001 (first entry)

DE IGFBP3 oligonucleotide #596.

XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

PN WO200078341-A1.

XX

PD 28-DEC-2000.

XX

PF 21-JUN-2000; 2000WO-AU000693.

XX

PR 21-JUN-1999; 99US-0140345P.

XX

PA (MURD-) MURDOCH CHILDRENS RES INST.

XX

PI Wright CJ, Werther GA, Edmondson SR;

XX

DR WPI; 2001-041421/05.

XX

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX

PS Example 7; Page 48; 201pp; English.

XX

CC The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

XX

SQ Sequence 15 BP; 3 A; 9 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1696 GTGFTGGAGTTGGG 1710

DB 15 GGGGTGGAACTTGGG 1

RESULT 331

AAF52890

ID AAF52890 standard; DNA; 15 BP.

XX

AC AAF52890;

XX

DT 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #3850.

XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

PN WO200078341-A1.

XX

PD 28-DEC-2000.

XX

PF 21-JUN-2000; 2000WO-AU000693.

XX

PR 21-JUN-1999; 99US-0140345P.

XX

PA (MURD-) MURDOCH CHILDRENS RES INST.

XX

PI Wright CJ, Werther GA, Edmondson SR;

XX

DR WPI; 2001-041421/05.

XX

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX

PS Example 8; Page 86; 201pp; English.

XX

CC The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

XX Sequence 15 BP; 3 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

SQ

Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1722 GAGATGGAGATTGGC 1736
1 GAGATGGAGCTGGC 15

Db

RESULT 332
AAF47174/c
ID AAF47174 standard; DNA; 15 BP.
XX
AC AAF47174;
XX
DT 30-MAR-2001 (first entry)
DE
DE IGFBP3 oligonucleotide #594.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.
XX
PS Example 7; Page 48; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

XX Sequence 15 BP; 4 A; 7 C; 1 G; 3 T; 0 U; 0 Other;

SQ

Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1698 GGTGGAAGTTGGTT 1712
15 GGTGGAAGTTGGAT 1

Db

RESULT 333
AAF52891
ID AAF52891 standard; DNA; 15 BP.
XX
AC AAF52891;
XX
DT 30-MAR-2001 (first entry)
DE
DE IGF-I oligonucleotide #3851.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AUC00693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.
XX
PS Example 8; Page 86; 200pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

SQ	Sequence	15 BP; 3 A; 3 C; 6 G; 3 T; 0 U; 0 Other;	Matches	13; Conservative	0; Mismatches	2; Indels	0; Gaps	0;
	Query Match	8.5%; Score 11.8; DB 1; Length 15;						
	Best Local Similarity	86.7%; Pred. No. 3.3e+02;						
	Matches	13; Conservative	0; Mismatches	2; Indels	0; Gaps	0;		
QY	1723	AGATGGAGATTGGCT 1737						
DB	1	AGATGGAGCTGGCT 15						
RESULT 334								
AAF52889								
ID	AAF52889	standard; DNA; 15 BP.						
XX								
AC	AAF52889;							
XX								
DT	30-MAR-2001	(first entry)						
XX								
DE	IGF-I oligonucleotide #3849.							
XX								
KW	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;							
KW	cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;							
KW	skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;							
KW	IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;							
KW	growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;							
KW	keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;							
KW	hyperneovascular condition; hyperplasia; kidney disease;							
KW	neovascular condition of the retina; ss.							
XX								
OS	Homo sapiens.							
XX								
PN	WO2000078341-A1.							
XX								
PD	28-DEC-2000.							
XX								
PF	21-JUN-2000; 2000WO-AU000693.							
XX								
PR	21-JUN-1999; 99US-0140345P.							
XX								
PA	(MURD-) MURDOCH CHILDRENS RES INST.							
XX								
PI	Wraight CJ, Werther GA, Edmondson SR;							
XX								
DR	WPI; 2001-041421/05.							
XX								
PT	Ameliorating the effects of a disorder, e.g. psoriasis, by administering							
PT	UV (ultra-violet) treatment (optional) and an antisense nucleic acid that							
PT	inhibits or reduces growth factor mediated cell proliferation and/or							
PT	inflammation.							
XX								
PS	Example 8; Page 86; 201pp; English.							
XX								
CC	The present invention relates to a method for ameliorating the effects of							
CC	skin disorders. The method comprises contacting the skin with an							
CC	antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1							
CC	receptor, IGF binding protein [IGFBP]-2 or [IGFBP3], which is capable of							
CC	inhibiting or reducing growth factor mediated cell proliferation,							
CC	inflammation and/or other disorders. The present sequence is an							
CC	oligonucleotide which can be used to design the antisense							
CC	oligonucleotides of the present invention (see AAF45151 and AAF45153-							
CC	F45161). The method is useful for ameliorating the effects of psoriasis,							
CC	ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,							
CC	neoplasias, scleroderma, warts, benign growths, cancers of the skin, a							
CC	hyperneovascular condition such as a neovascular condition of the retina,							
CC	brain or skin, growth factor-mediated malignancies, other sclerotic							
CC	disease, kidney disease, hyperproliferation of the inside of blood							
CC	vessels or any other hyperplasia							
XX								
SQ	Sequence	15 BP; 3 A; 2 C; 8 G; 2 T; 0 U; 0 Other;						
	Query Match	8.5%; Score 11.8; DB 1; Length 15;						
	Best Local Similarity	86.7%; Pred. No. 3.3e+02;						
	Matches	13; Conservative	0; Mismatches	2; Indels	0; Gaps	0;		
QY	1677	CCCTGGTGTCTCTC 1691						
DB	1	CCCTGGTGTCTC 15						
RESULT 336								
AAS99376/C								
ID	AAS99376	standard; DNA; 15 BP.						
XX								
AC	AAS99376;							
XX								
DT	12-MAR-2002	(first entry)						
XX								

RESULT 338
 ACD56644
 ID ACD56644 standard; RNA; 15 BP.
 XX
 AC ACD56644;
 DT 24-SEP-2003 (first entry)
 XX
 DE HBV enzymatic nucleic acid substrate sequence #241.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN W0200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 PT
 PS Example 1; Page 224; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC enzymatic nucleic acid sequences disclosed in the present invention
 XX
 SQ Sequence 15 BP; 0 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 53.3%; Pred. No. 3.3e+02;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1677 CCTGGTGTCTCTC 1691
 DB 1 CCUUGUGUCUCCUC 15
 RESULT 339
 AAQ91451/c
 ID AAQ91451 standard; DNA; 16 BP.
 XX
 AC AAQ91451;
 DT 25-MAR-2003 (revised)
 DT 30-AUG-1995 (first entry)
 XX
 DE Dysprosium (III) texaphyrin (DyTx) DNA conjugate.
 XX
 KW Dysprosium (III) texaphyrin (DyTx) DNA conjugate; liver disease;
 KW targeted intracellular mRNA hydrolysis; gene expression inhibition;
 KW hormone regulation; hydrolysis reagents; alkyl phosphate esters;
 KW detoxification; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /mod_base= OTHER
 FT /note= "DyTx-NH(CH2)6-PO4-thymine"
 XX
 PN W09429316-A2.
 XX
 PD 22-DEC-1994.
 XX
 PF 09-JUN-1994; 94WO-US006284.
 XX
 PR 09-JUN-1993; 93US-00075123.
 PR 14-APR-1994; 94US-00227370.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (PHAR-) PHARMACYCLICS INC.
 XX
 PI Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;
 PI Kral VA, Iverson B, Mody T, Miller RA, Magda D;
 XX
 DR WPI; 1995-036382/05.
 XX
 PT Texaphyrin metal complex mediated ester hydrolysis - esp. useful for
 PT targeted intracellular hydrolysis of mRNA and for inhibiting gene
 PT expression.
 XX
 PS Disclosure; Fig 21; 125pp; English.
 XX
 CC AAQ91451-Q91457 are texaphyrin lanthanide metal DNA conjugates, which are
 CC esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting
 CC gene expression. They may also be used for the treatment of liver disease,
 CC as hormone regulation agents and as hydrolysis reagents for the
 CC detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 16 BP; 1 A; 2 C; 8 G; 5 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 16;
 Best Local Similarity 86.7%; Pred. No. 3.6e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1655 AGCACCAGGCTCACA 1669
 DB 15 AACACCCGGCTCACA 1

```

Query Match      8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCGGCTCACA 1669
DB 15 AACACCGGCTCACA 1

RESULT 340
AAV07300/c
ID AAV07300 standard; DNA; 16 BP.
XX
AC AAV07300;
XX
DT 08-JUL-1998 (first entry)
XX
DE Texaphyrin oligonucleotide conjugate.
XX
KW Texaphyrin oligonucleotide conjugate; dysprosium; metal complex;
KW hydrolytic cleavage activity; ribonucleic acid cleavage; RNA; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "A texaphyrin dysprosium metal complex, bound to
FT thymine via a linking phosphate group"
XX
PN WO9807733-A1.
XX
PD 26-FEB-1998.
XX
PF 20-AUG-1997; 9WO-US014682.
XX
PR 20-AUG-1996; 96US-00700277.
XX
PA (PHAR-) PHARMACYCLICS INC.
XX
PI Magda D, Crofts SP, Wright M;
XX WPI; 1998-179049/16.
XX
DR
XX
PT New conjugates which have hydrolytic cleavage activity for RNA - comprise
PT a texaphyrin metal complex bound to an internal linkage of an
PT oligonucleotide.
XX
PS Example 4; Page 53; 77fp; English.
XX
CC This sequence is shown in the specification. The invention relates to a
CC texaphyrin oligonucleotide conjugate, which has hydrolytic cleavage
CC activity for ribonucleic acid (RNA). It comprises a texaphyrin metal
CC complex bound to an internal linkage of an oligonucleotide or
CC oligonucleotide analogue. The conjugates may be used for the destruction
CC of retroviral RNA, messenger RNA, ribosomal RNA, RNA cofactors, transfer
CC RNA, small nuclear RNA and small cytoplasmic RNA. They may be used for
CC eliminating diseased or cancerous cells or tissues, in blood purification
CC protocols (in vivo or in vitro), in antiviral treatments, or as
CC diagnostic probes (e.g. in determination of the nucleotide sequence of
CC RNA or to detect polymorphisms in RNA). Administration of the conjugates
CC is, e.g., oral, topical or parenteral, especially topical or intravenous.
CC The conjugates are especially effective under conditions where the
CC concentration of RNA target exceeds that of available conjugate
XX
SQ Sequence 16 BP; 1 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match      8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCGGCTCACA 1669
DB 15 AACACCGGCTCACA 1

RESULT 340
AAV07300/c
ID AAV07300 standard; DNA; 16 BP.
XX
AC AAV07300;
XX
DT 14-AUG-1998 (first entry)
XX
DE Metallotexaphyrin-oligonucleotide conjugate #14.
XX
KW Metallotexaphyrin; dysprosium; europium; conjugate; RNase H;
KW antisense therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base
FT /note= "DyTXNH-(CH2)6-PO4-thymine, where DyTx is
FT dysprosium (III) texaphyrin"
XX
PN US5763172-A.
XX
PD 09-JUN-1998.
XX
PF 07-JUN-1995; 95US-00486962.
XX
PR 21-JAN-1992; 92US-00822964.
XX
PD 09-JUN-1993; 93US-00075123.
XX
PR 14-APR-1994; 94US-00227370.
XX
PR 09-JUN-1994; 94WO-US006284.
XX
PR 26-MAY-1995; 95US-00452261.
XX
PR 07-JUN-1995; 95US-00485581.
XX
PA (PHAR-) PHARMACYCLICS INC.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Sessler JL, Wright M, Miller RA, Dow WC, Magda D;
XX WPI; 1998-347306/30.
XX
DR
XX
PT Enhancing therapeutic activity of oligo-nucleotides in cells - using
PT conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester
PT bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.
XX
PS Example 6; Fig 5; 34pp; English.
XX
CC The invention relates to a method of enhancing the therapeutic activity
CC of oligonucleotides in cells. It comprises contacting a targeted
CC intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide
CC conjugate. The contact is carried out under physiological conditions for
CC a time sufficient to hydrolyse the phosphate ester bond of the targeted
CC RNA. The metallotexaphyrin of the conjugate has catalytic activity for
CC phosphate ester bond hydrolysis. The oligonucleotide of the conjugate has
CC complementary binding affinity to the targeted RNA. The conjugate may be
CC used in antisense therapies for treating, e.g. cancer, viral infections,
CC autoimmune diseases and restenosis. The conjugate may also be used as
CC hydrolysis reagents for the detoxification of di- and trialkyl phosphate
CC esters, which are used in solvents, insecticides and chemical nerve
CC gases. The metallotexaphyrin complex enhances the therapeutic activity of
CC the oligonucleotide, not only by facilitating cellular uptake of the
CC oligonucleotide but also by hydrolysing target RNA within the cell,
CC independent of RNase H. Attachment to the complex may also cause the
CC oligonucleotide to take on some of the pharmacodynamic and biodistribution
CC properties of the texaphyrin, such as selective localisation in tumours.
CC The present sequence represents a metallo- texaphyrin-oligonucleotide
XX
SQ Sequence 16 BP; 1 A; 2 C; 8 G; 5 T; 0 U; 0 Other;
```

Db 15 AACACCCGGCTCAC 1

RESULT 342
AAZ97664
ID AAZ97664 standard; DNA; 16 BP.
XX AC AAZ97664;
XX DT 15-SEP-2003 (revised)
XX DT 26-APR-2000 (first entry)
XX DE HIV-1 protease gene probe SEQ ID NO:154.
XX KW Human immunodeficiency virus; HIV; protease; probe; detection;
XX KW drug selected mutation; hybridisation; genotyping; infection;
XX KW drug resistance; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9967428-A2.
XX PD 29-DEC-1999.
XX PF 22-JUN-1999; 99WO-EP004317.
XX PR 24-JUN-1998; 98EP-00870143.
XX PA (INNO-) INNOGENETICS NV.
XX FI Stuyver L;
XX DR WPI; 2000-147219/13.
XX PT Detection of drug-selected mutations in the HIV protease gene used to
XX PT treat HIV infections.
XX PS Claim 3; Page 35; 76pp; English.
XX CC The present invention describes the detection of drug-selected mutations
XX CC in the HIV protease gene. The method of detection allows the simultaneous
XX CC characterisation of a range of codons involved in drug resistance using
XX CC sets of probes optimised to function together in a reverse-hybridisation
XX CC assay. AAZ97517 to AAZ97997 represent specifically claimed probes for use
XX CC in the assay, and AAZ97479 to AAZ97501 represent specifically claimed HIV
XX CC protease gene polymorphic nucleotide sequences. AAZ97502 to AAZ97515, and
XX CC AAZ98004 to AAZ98007, represent PCR primers for the HIV protease gene,
XX CC and AAZ97516 represents an HIV protease probe used in an example from the
XX CC present invention. The method, probes and primers can be used for the
XX CC detection of drug-selected mutations in the HIV protease gene. The method
XX CC allows the simultaneous characterisation of a range of codons involved in
XX CC drug resistance. The method may also be used for HIV protease genotyping
XX CC assays. The probes are able to discriminate between wild type and mutated
XX CC protease sequences. The method allows rapid and reliable detection of
XX CC drug-selected mutation in HIV. (Updated on 15-SEP-2003 to standardise OS
XX CC field)

XX SQ Sequence 16 BP; 2 A; 0 C; 10 G; 4 T; 0 U; 0 Other;
Query Match 8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1721 GGAGTGGAGATTGG 1735
Db 2 GGAGTGGAGATTGG 16
|||||

RESULT 343
AAZ88440/c
ID AAZ88440 standard; DNA; 16 BP.
XX AC AAZ88440;

XX DT 08-MAY-2000 (first entry)
XX DE Exemplary texaphyrin oligonucleotide conjugate SEQ ID NO:6.
XX KW Texaphyrin; metal complex; catalytic; RNA hydrolysis; virucide;
XX KW antibacterial; cytostatic; antiinflammatory; antitumour; antiviral; ss.
XX OS Synthetic.
XX PN US6022959-A.
XX PD 08-FEB-2000.
XX PF 20-NOV-1997; 97US-00975522.
XX PR 20-AUG-1996; 96US-0077185P.
XX PR 20-AUG-1997; 97WO-US014682.
XX PA (PHAR-) PHARMACYCLICS INC.
XX PI Wright M, Crofts SP, Magda D;
XX PI WPI; 2000-160391/14.
XX DR Texaphyrin metal complex derivatized ribonucleic acids possessing
XX PT hydrolytic cleavage activity against RNA are useful as e.g. antiviral,
XX PT antibacterial, antitumor and antiinflammatory agents.
XX PS Example 4; Col 33; 30pp; English.
XX CC The present invention describes a conjugate with hydrolytic cleavage
XX CC activity for ribonucleic acid (RNA), which comprises a texaphyrin metal
XX CC complex bound to an internal linkage of an oligonucleotide or
XX CC oligonucleotide analogue. AAZ88435 to AAZ88440 represent exemplary
XX CC texaphyrin oligonucleotide conjugates used in the exemplification of the
XX CC present invention. The novel conjugates have virucide, antibacterial,
XX CC cytostatic and antiinflammatory properties, and are involved in RNA
XX CC hydrolysis. The conjugates are useful for inhibiting the expression of a
XX CC gene by targeted intracellular mRNA (messenger ribonucleic acid) and
XX CC bacterial therapy as well as cancers and inflammatory responses caused by
XX CC overexpression of certain proteins

XX SQ Sequence 16 BP; 1 A; 2 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAC 1669
Db 15 AACACCCGGCTCAC 1
|||||

RESULT 344
ABX14989
ID ABX14989 standard; DNA; 16 BP.
XX AC ABX14989;
XX DT 14-MAR-2003 (first entry)
XX DE Human delta opioid receptor OPRD1-1 SNP genotyping PCR primer #1.
XX DE Human; delta opioid receptor; OPRD1-1; ss; PCR; primer; SNP;
XX KW single nucleotide polymorphism; eating disorder; anorexia nervosa;
XX KW energy homeostasis disorder; chromosome 1.
XX OS Homo sapiens.
XX OS WO200292838-A2.
XX PN

21-NOV-2002.

13-MAY-2002; 2002WO-US014940.

11-MAY-2001; 2001US-0290016P.

(BIOI-) BIOINVEST LTD.

Bergen AW;

WPI; 2003-129306/12.

New isolated nucleic acid molecule encoding a delta opioid receptor variant associated with an eating or energy homeostasis disorder, useful for diagnosing a genetic predisposition to such disorder, e.g. anorexia nervosa.

Example; Page 19; 39pp; English.

The invention relates to an isolated nucleic acid molecule encoding a delta opioid receptor variant associated with an eating or energy homeostasis disorder. Also included are a delta opioid receptor variant encoded by the nucleic acid, an isolated antibody that specifically recognises the delta opioid receptor variant, a vector comprising the nucleic acid, a host cell transformed to contain the vector, producing the polypeptide by culturing the host cell, identifying an agent which modulates the expression of the nucleic acid, diagnosing a genetic predisposition to an eating or energy homeostasis disorder by detecting the presence or absence of the variant nucleic acid in a patient sample, an allele specific primer that detects a polymorphism in the gene encoding a delta opioid receptor associated with an eating or energy homeostasis disorder and a non-human transgenic animal modified to contain the variant nucleic acids. The variants are named OPRD1-1 to OPRD1-8. The human opioid receptor gene is located on chromosome 1. The nucleic acid molecules and delta opioid receptor variant are useful for diagnosing a genetic predisposition to an eating or energy homeostasis disorder, such as anorexia nervosa. The allele specific primer is useful for detecting polymorphism in the gene encoding a delta opioid receptor associated with the disorder cited. The present sequence is a genotyping PCR primer for detecting the presence of a particular SNP (single nucleotide polymorphism) in a sample

Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGGAA 1676
|||||||
DB 2 GGCTCACCTGTAA 16

RESULT 345
ABT34281
ID ABT34281 standard; DNA; 16 BP.
AC ABT34281;
XX
XX
XX 12-JUN-2003 (first entry)
XX
XX Opioid receptor D1 PCR primer SEQ ID No 67.
XX
XX Eating disorder; polymorphism; dataset; allele; HGBASE identification;
KW serotonin receptor ID; delta-opioid receptor; dopamine receptor D2;
KW anorexia nervosa; bulimia nervosa; PCR; primer; ss.
XX
XX Unidentified.
XX
XX WO2003012143-A1.
XX
XX PD 13-FEB-2003.

XX WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 59; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 5 A; 7 C; 1 G; 0 T; 4 U; 0 Other;
 CC
 CC Query Match 8.5%; Score 11.8; DB 1; Length 17;
 CC Best Local Similarity 66.7%; Pred. No. 3.9e+02;
 CC Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 CC
 QY 1745 CCTCCTATCCTATAA 1759
 DB ||:||:|:||||
 2 CCUCUUUAUCCGAA 16
 CC
 RESULT 347
 AAX69126
 ID AAX69126 standard; RNA; 17 BP.
 XX
 AC AAX69126;
 XX
 XX 28-JUL-1999 (first entry)
 DT
 XX Human flt1 VEGF receptor hammerhead ribozyme substrate #421.
 DE
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9715662-A2.
 XX
 XX 01-MAY-1997.
 PD
 XX 25-OCT-1996; 96WO-US017480.
 PF
 XX 26-OCT-1995; 95US-0005974P.
 PR
 XX 11-JAN-1996; 96US-00584040.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX WPI; 1997-259017/23.
 DR
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 XX Claim 4; Page 59; 218pp; English.
 PS
 XX The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more

CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 5 A; 7 C; 1 G; 0 T; 4 U; 0 Other;
 CC
 CC Query Match 8.5%; Score 11.8; DB 1; Length 17;
 CC Best Local Similarity 66.7%; Pred. No. 3.9e+02;
 CC Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 CC
 QY 1745 CCTCCTATCCTATAA 1759
 DB ||:||:|:||||
 3 CCUCUUUAUCCGAA 17
 CC
 RESULT 348
 AAV97558
 ID AAV97558 standard; RNA; 17 BP.
 XX
 AC AAV97558;
 XX
 XX 17-MAR-1999 (first entry)
 DT
 XX Human EGF-R target sequence nucleotide position 2960.
 DE
 XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KW cancer; genetic drift; detection; mutation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9833893-A2.
 XX
 XX 06-AUG-1998.
 PD
 XX 14-JAN-1998; 98WO-US000730.
 PF
 XX 31-JAN-1997; 97US-0036476P.
 PR
 XX 04-DEC-1997; 97US-00985162.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (UVAS-) UNIV ASTON.
 XX
 XX Akhtar S, Fell P, Mcswiggen JA;
 XX WPI; 1998-437449/37.
 DR
 XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and for
 PT treating cancers.
 XX
 XX Claim 5; Page 75; 109pp; English.
 PS
 XX The present invention describes enzymatic nucleic acid molecules (NAMs)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMs can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell
 XX
 SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;
 CC
 CC Query Match 8.5%; Score 11.8; DB 1; Length 17;

```

XX DE Aryl hydrocarbon nuclear transport substrate sequence SEQ ID NO:645.
XX KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
XX KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX KW age related macular degeneration; inflammation; neovascular glaucoma;
XX KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX OS Homo sapiens.
XX PN WO9950403-A2.
XX PD 07-OCT-1999.
XX PF 24-MAR-1999; 99WO-US006507.
XX PR 27-MAR-1998; 98US-0079678P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX DR WPI; 1999-591315/50.
XX PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX PS Claim 53; Page 78; 305pp; English.
XX CC The present invention describes enzymatic nucleic acid molecules with RNA
XX CC cleaving activity, which specifically cleave RNA encoded by an aryl
XX CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX CC and AAA19155 to AAA19222 represent their corresponding target sequences;
XX CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX CC AAA21596 to AAA21688 represent their corresponding target sequences;
XX CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX CC AAA23422 represent their corresponding target sequences. The ribozymes of
XX CC the invention are used for modulating the synthesis, expression and/or
XX CC stability of an mRNA encoding angiogenic factor, especially ARNT,
XX CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX CC especially used to treat cancer, diabetic retinopathy, age related
XX CC macular degeneration (ARMD), inflammation, and arthritis, as well as
XX CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX CC integrin subunit alpha-6, or integrin subunit beta-3
XX SQ Sequence 17 BP; 4 A; 7 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTGTCCTCCCGCGT 1695
Db 2 GGCAUCCUCCUCCAGC 16

RESULT 351
AAA18520/c

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XX DE Best Local Similarity 60.0%; Pred. No. 3.9e+02;
XX KW Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX QY 1685 TCTCTCCAGCGTGG 1699
XX Db 3 UCUCUCCAUCCUGG 17
XX RESULT 349
XX AAX57626
XX ID AAX57626 standard; DNA; 17 BP.
XX AC AAX57626;
XX XX
XX DT 16-JUL-1999 (first entry)
XX DE HSV-1 thymidine kinase gene mutagenic primer #3.
XX KW HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme;
XX KW pathogen; tumour; hyperkeratosis; psoriasis; prostate hypertrophy;
XX KW hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis;
XX KW viral disease; AIDS; hepatitis; parasite; bacterial infection; ss.
XX OS Synthetic.
XX OS Herpes simplex virus unknown type.
XX PN WO9919466-A2.
XX PD 22-APR-1999.
XX PF 14-OCT-1998; 98WO-US021672.
XX PR 14-OCT-1997; 97US-0061812P.
XX PA (DARW-) DARWIN MOLECULAR CORP.
XX PI Black ME;
XX WPI; 1999-277631/23.
XX DR New Herpesviridae thymidine kinase mutants - useful for treating prostate
XX PT hypertrophy, allergies, cystic fibrosis and Alzheimer's disease.
XX XX
XX PS Example 1; Page 34; 126pp; English.
XX CC This sequence represents a primer used to construct a mutation in the
XX CC herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) gene
XX CC (AAX57623). The invention relates to the generation of novel HSV-1 TK
XX CC gene with a mutation upstream, within or downstream from a DRH nucleoside
XX CC binding site. The TK enzymes can be used for inhibiting pathogenic
XX CC agents, e.g. tumours, hyperkeratosis, psoriasis, prostate hypertrophy,
XX CC hyperthyroidism, endocrinopathies, autoimmune diseases, allergies,
XX CC restenosis, viral diseases such as AIDS, hepatitis, intracellular
XX CC parasitic diseases or bacterial infection
XX SQ Sequence 17 BP; 2 A; 9 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1686 CTCTCCAGCGTGGT 1700
Db 1 CCCTCCAGCGCGT 15

RESULT 350
AAA17419
XX ID AAA17419 standard; RNA; 17 BP.
XX AC AAA17419;
XX DT 19-JUN-2000 (first entry)

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ID AAA18520 standard; RNA; 17 BP.
 AC AAA18520;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Human TIE-2 substrate sequence SEQ ID NO:1746.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 XX 07-OCT-1999.
 PD
 XX 24-MAR-1999; 99WO-US006507.
 PF
 XX 27-MAR-1998; 98US-0079678P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mowswiggen JA;
 PI WPI; 1999-591315/50.
 XX
 DR Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 PS Claim 56; Page 100; 305pp; English.
 CC
 CC The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC sequences for integrin alpha 6 subunit, and AAA20361 to AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA19222 represent their corresponding target sequences;
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 17 GCAGTACAGAGATGG 3
 RESULT 352
 AAA22628
 ID AAA22628 standard; RNA; 17 BP.
 XX
 AC AAA22628;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5854.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 XX 07-OCT-1999.
 PD
 XX 24-MAR-1999; 99WO-US006507.
 PF
 XX 27-MAR-1998; 98US-0079678P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mowswiggen JA;
 PI WPI; 1999-591315/50.
 XX
 DR Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 PS Claim 54; Page 232; 305pp; English.
 CC
 CC The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC sequences for integrin alpha 6 subunit, and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20361 to AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA19222 represent their corresponding target sequences;
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 1 A; 8 C; 3 G; 0 T; 5 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 60.0%; Pred. No. 3.9e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1683 TGTCTCCCTCCAGCGT 1697
 Db 1 UGCCUCCUCCAGUGU 15

RESULT 353
 AAV93558/C
 ID AAV93558 standard; RNA; 17 BP.
 XX AC AAV93558;
 XX DT 18-FEB-1999 (first entry)
 XX DE Human B-raf substrate nucleotide position 1679.
 XX KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.
 XX OS Homo sapiens.
 XX PN WO9850530-A2.
 XX PD 12-NOV-1998.
 XX PF 05-MAY-1998; 98WO-US009249.
 XX PR 09-MAY-1997; 97US-0046059P.
 XX PR 09-JUN-1997; 97US-0049002P.
 XX PR 03-JUL-1997; 97US-0051718P.
 XX PR 22-AUG-1997; 97US-0056808P.
 XX PR 02-OCT-1997; 97US-0061321P.
 XX PR 02-OCT-1997; 97US-0061324P.
 XX PR 05-NOV-1997; 97US-0064866P.
 XX PR 19-DEC-1997; 97US-0068212P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswigen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX WPI; 1999-009494/01.
 XX DR Identifying new catalytic nucleic acid that modulates selected processes
 XX PT - especially ribozymes that cleave Raf RNA for treating cancer,
 XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 XX PT used as antiviral agents and synthons.
 XX PS Claim 177; Page 170; 259pp; English.
 XX CC A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and

CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for: modulating the expression of a Raf gene
 XX Sequence 17 BP; 5 A; 7 C; 0 G; 0 T; 5 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1718 TACGAGATGGAGAT 1732
 Db 15 TATGGAGATGGTGTAT 1

RESULT 354
 AAV91355/C
 ID AAV91355 standard; RNA; 17 BP.
 XX AC AAV91355;
 XX DT 18-FEB-1999 (first entry)
 XX DE Human C-raf target site nucleotide position 2701.
 XX KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.
 XX OS Homo sapiens.
 XX PN WO9850530-A2.
 XX PD 12-NOV-1998.
 XX PF 05-MAY-1998; 98WO-US009249.
 XX PR 09-MAY-1997; 97US-0046059P.
 XX PR 09-JUN-1997; 97US-0049002P.
 XX PR 03-JUL-1997; 97US-0051718P.
 XX PR 22-AUG-1997; 97US-0056808P.
 XX PR 02-OCT-1997; 97US-0061321P.
 XX PR 02-OCT-1997; 97US-0061324P.
 XX PR 05-NOV-1997; 97US-0064866P.
 XX PR 19-DEC-1997; 97US-0068212P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswigen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX WPI; 1999-009494/01.
 XX DR Identifying new catalytic nucleic acid that modulates selected processes
 XX PT - especially ribozymes that cleave Raf RNA for treating cancer,
 XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 XX PT used as antiviral agents and synthons.
 XX PS Claim 177; Page 153; 259pp; English.
 XX CC A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and

ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-rat RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-rat. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene

Sequence 17 BP; 3 A; 8 C; 3 G; 0 T; 3 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1722 GAGATGGGATTGGC 1736
 ||||| |||||
 Db 17 GAGATGGGATTGGC 3

RESULT 355

AAV92633
 ID AAV92633 standard; RNA; 17 BP.

XX AC AAV92633;
 XX

18-FEB-1999 (first entry)

Human A-Raf substrate position 2219.

Human; c-rat; A-rat; B-rat; hammerhead ribozyme; hairpin ribozyme;
 target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 screening; identification; synthesis; deprotection; purification; cancer;
 inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 restenosis; rheumatoid arthritis; ss.

OS Homo sapiens.

XX WO9850530-A2.

XX 12-NOV-1998.

XX 05-MAY-1998; 98WO-US009249.

XX 09-MAY-1997; 97US-0046059P.

XX 09-JUN-1997; 97US-0049002P.

XX 03-JUL-1997; 97US-0051718P.

XX 22-AUG-1997; 97US-0056808P.

XX 02-OCT-1997; 97US-0061321P.

XX 02-OCT-1997; 97US-0061324P.

XX 05-NOV-1997; 97US-0064866P.

XX 19-DEC-1997; 97US-0068212P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Meswigen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 DR WPI; 1998-009494/01.

Identifying new catalytic nucleic acid that modulates selected processes
 - especially ribozymes that cleave Raf RNA for treating cancer,
 restenosis, and also new ribozymes and modified nucleoside triphosphates
 used as antiviral agents and synthons.

Claim 177; Page 161; 259pp; English.

A method has been developed for the identification of a nucleic acid
 capable of modulating a process in a biological system. The method
 comprises: (a) introducing into the system a random library of nucleic
 acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 a random sequence, and a catalytic domain (CD); and (b) identifying NAC

in systems where modulation has occurred and/or determining the sequence
 of at least part of the SBDs in such systems. Nucleic acid molecules with
 endonuclease activity and catalytic activity, from the present invention,
 are used to modulate gene expression in plant and mammalian cells and to
 cleave target nucleic acid, particularly for treating systemic diseases
 caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 ascites and infection. They may also be used to detect genetic drift and
 mutations in diseased cells and to determine c-rat RNA. Specifically NACs
 with RNA-cleaving activity that modulate expression of the Raf gene, are
 used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 generally any condition associated with the level of c-rat. Introduction
 of sugar/phosphate modifications increases stability against nuclease and
 activity. AAV90922 to AAV93877 represent NACs that can be used in the
 method, specifically for modulating the expression of a Raf gene

Sequence 17 BP; 2 A; 6 C; 1 G; 0 T; 8 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 53.3%; Pred. No. 3.9e+02;

Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1683 TGTCTCTCCAGCGT 1697

Db 1 UGUUCCUCCAU 15

RESULT 356

AAAX15355

ID AAX15355 standard; DNA; 17 BP.

XX AC AAX15355;
 XX

22-JUN-1999 (first entry)

HSV-1 thymidine kinase gene mutagenic primer #3.

HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme;
 pathogen; tumour; hyperkeratosis; psoriasis; prostate hypertrophy;
 hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis;
 viral disease; AIDS; hepatitis; parasite; bacterial infection; ss.

OS Synthetic.

OS Herpes simplex virus unknown type.

XX US5877010-A.

XX 02-MAR-1999.

XX 02-MAY-1995; 95US-00432871.

XX 02-MAY-1994; 94US-00237592.

XX (UNIW) UNIV WASHINGTON.
 XX Black ME, Loeb LA;
 XX WPI; 1999-189650/16.

XX New Herpesviridae thymidine kinase mutant nucleic acids - used to
 develop products for treating e.g. tumours, autoimmune diseases,
 allergies, restenosis or viral, bacterial or parasitic diseases.

Example 1; Col 20; 72pp; English.

This sequence represents a primer used to construct a mutation in the
 herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) gene
 (AAX15352). The invention relates to the generation of novel HSV-1 TK
 gene with a mutation upstream, within or downstream from a DRH nucleoside
 binding site. The TK enzymes can be used for inhibiting pathogenic
 agents, e.g. tumours, hyperkeratosis, psoriasis, prostate hypertrophy,
 hyperthyroidism, endocrinopathies, autoimmune diseases, allergies,
 restenosis, viral diseases such as AIDS, hepatitis, intracellular
 parasitic diseases or bacterial infection

XX		Sequence 17 BP; 2 A; 9 C; 4 G; 2 T; 0 U; 0 Other;	
SQ		Query Match 8.5%; Score 11.8; DB 1; Length 17; Best Local Similarity 86.7%; Pred. No. 3.9e+02; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1686 CTCCTCCAGCGTGTG 1700 1 CCCCTCAGCGCGTT 15		
DB			
RESULT 357			
AAAF01906			
ID	AAA79845 standard; DNA; 17 BP.		
AC	AAA79845;		
DT	20-NOV-2000 (first entry)		
DE	Hepatitis B virus related oligonucleotide probe #108.		
XX			
KW	Hepatitis B virus; HBV; Hepatitis A virus; HAV; probe; detection;		
KW	muation; high-density gene chip; ss.		
OS	Hepatitis B virus.		
XX	CN1252452-A.		
PX	10-MAY-2000.		
PF	24-SEP-1999; 99CN-00114460.		
PR	24-SEP-1999; 99CN-00114460.		
PA	(UYDO-) UNIV DONGNAN.		
PI	Sun X, Lu Z, Wang Y;		
XX			
DR	WPI; 2000-443233/39.		
PT	High-density gene chip making process.		
PS	Example 1; Fig 15; 19pp; Chinese.		
XX	The present invention describes a method which comprises making a high-		
CC	density gene chip, specifically for making high-density micro-array of		
CC	oligonucleotide probes. An oligonucleotide probe selecting process to		
CC	seek preferentially length variable and coverage variable probes is		
CC	provided to ensure identical cross melting temperature of probes to the		
CC	maximum limit, and this can make the cross control of gene chip		
CC	relatively simple and raise the reliability of the gene chip detecting		
CC	results. The process proposes a specific probe selection method for		
CC	detecting target sequence directly, detecting mutation in both specific		
CC	and non-specific sites and a probe overall arrangement scheme. AAA7938		
CC	to AAA8201 represent oligonucleotide probe sequences which are used in		
CC	examples from the present invention		
XX			
SQ	Sequence 17 BP; 3 A; 1 C; 10 G; 3 T; 0 U; 0 Other;		
	Query Match 8.5%; Score 11.8; DB 1; Length 17; Best Local Similarity 86.7%; Pred. No. 3.9e+02; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	1714 GGACTACGGAGATGG 1728 1 GGAGGACGGAGTG 15		
DB			
RESULT 358			
AAAF01906			
ID	AAA79845 standard; DNA; 17 BP.		
XX			

PR 22-OCT-1999; 99US-0160901P.

PA (MITO-) MITOKOR.

PI Herrnstadt C, Davis RE;

XX WPI; 2000-672748/65.

DR Diagnosing a subject at the risk for or having Alzheimer's disease
PT comprises determining at least one single nucleotide polymorphism in
PT mitochondrial DNA associated with the disease in the sample from the
PT subject.

XX Example 4; Page 38; 89pp; English.

XX The present invention describes a novel method for determining the risk
CC of or diagnosing Alzheimer's disease using single nucleotide
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC (mtDNA). In addition, the SNPs identified can be used to identify agents
CC suitable for use in treating Alzheimer's disease. Sequences AAC67301-
CC C67610 are PCR primers used to demonstrate the method of the invention

XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1652 GCAAGCACGAGGCTC 1666

Db 1 GCTATCACGAGGCTC 15

RESULT 360

AAC67310

ID AAC67310 standard; DNA; 17 BP.

AC AAC67310;

DT 14-FEB-2001 (first entry)

XX Alzheimer's disease-linked mitochondrial SNP PCR primer #10.

XX Human; mitochondrial genome; single nucleotide polymorphism; SNP;
XX Alzheimer's disease; mtDNA; PCR primer; ss.

OS Homo sapiens.

XX W0200063441-A2.

PN 26-OCT-2000.

XX 19-APR-2000; 2000WO-US010906.

XX 20-APR-1999; 99US-0130447P.

PR 22-OCT-1999; 99US-0160901P.

XX (MITO-) MITOKOR.

PI Herrnstadt C, Davis RE;

XX WPI; 2000-672748/65.

XX Diagnosing a subject at the risk for or having Alzheimer's disease
PT comprises determining at least one single nucleotide polymorphism in
PT mitochondrial DNA associated with the disease in the sample from the
PT subject.

XX Example 2; Page 33; 89pp; English.

XX The present invention describes a novel method for determining the risk
CC of or diagnosing Alzheimer's disease using single nucleotide
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA

CC (mtDNA). In addition, the SNPs identified can be used to identify agents
CC suitable for use in treating Alzheimer's disease. Sequences AAC67301-
CC C67610 are PCR primers used to demonstrate the method of the invention

XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1652 GCAAGCACGAGGCTC 1666

Db 1 GCTATCACGAGGCTC 15

RESULT 361

ABA81112

ID ABA81112 standard; DNA; 17 BP.

XX ABA81112;

DT 24-JAN-2002 (first entry)

XX LDLR mutation correcting oligonucleotide SEQ ID NO: 3958.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
KW antileptic; ss.

XX Homo sapiens.

XX W0200173002-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US009761.

XX 27-MAR-2000; 2000US-0192176P.

PR 27-MAR-2000; 2000US-0192179P.

PR 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244989P.

XX (UYDE) UNIV DELAWARE.

XX Kmiec EB, Gamper HB, Rice MC;

XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.

XX Claim 7; Page 257; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,

CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention

XX
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1661 AGGCTCAGCTGGA 1675
||||| |||||||
DB 2 AGGCTTCCAGCTGGA 16

RESULT 362
ABA77557
ID ABA77557 standard; DNA; 17 BP.
XX
AC ABA77557;
XX
DT 24-JAN-2002 (first entry)
XX
DE Beta globin mutation correcting oligonucleotide SEQ ID NO: 403.
XX
KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytostatic; antislacking; antianaemic; haemostatic;
KW antilipemic; ss.
XX
OS Homo sapiens.
XX
PN WO200173002-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009761.
XX
PR 27-MAR-2000; 2000US-0192176P.
PR 27-MAR-2000; 2000US-0192179P.
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC;
XX
DR WPI; 2001-639230/73.
XX
PT Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.
XX
PS Claim 7; Page 67; 294pp; English.
XX
CC The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases

CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention

XX
SQ Sequence 17 BP; 3 A; 1 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1695 CGTGTGGAAGTTG 1709
||||| |||||||
DB 1 CGTGGATGAAGTTG 15

RESULT 363
ABA77558/c
ID ABA77558 standard; DNA; 17 BP.
XX
AC ABA77558;
XX
DT 24-JAN-2002 (first entry)
XX
DE Beta globin mutation correcting oligonucleotide SEQ ID NO: 404.
XX
KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytostatic; antislacking; antianaemic; haemostatic;
KW antilipemic; ss.
XX
OS Homo sapiens.
XX
PN WO200173002-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009761.
XX
PR 27-MAR-2000; 2000US-0192176P.
PR 27-MAR-2000; 2000US-0192179P.
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC;
XX
DR WPI; 2001-639230/73.
XX
PT Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.
XX
PS Claim 7; Page 67; 294pp; English.
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CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
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CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and

CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention
 XX
 SQ Sequence 17 BP; 5 A; 8 C; 1 G; 3 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1695 CGTGGTGAAGTTGG 1709
 ||||| |||||
 Db 17 CGTGGATGAAGTTGG 3
 RESULT 364
 ABA77561
 ID ABA77561 standard; DNA; 17 BP.
 XX
 AC ABA77561;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Beta globin mutation correcting oligonucleotide SEQ ID NO: 407.
 XX
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antiskickling; antianaemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 EN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US009761.
 XX
 PR 27-MAR-2000; 2000US-0192176P.
 PR 27-MAR-2000; 2000US-0192179P.
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 XX Kniec EB, Gamper HB, Rice MC;
 PI WPI; 2001-639230/73.
 XX
 DR Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification.
 XX
 PS Claim 7; Page 68; 294pp; English.
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 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase

CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention
 XX
 SQ Sequence 17 BP; 4 A; 1 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1695 CGTGGTGAAGTTGG 1709
 ||||| |||||
 Db 2 CGTGGATGAAGTTGG 16
 RESULT 365
 ABA81113/c
 ID ABA81113 standard; DNA; 17 BP.
 XX
 AC ABA81113;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3959.
 XX
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antiskickling; antianaemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 EN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US009761.
 XX
 PR 27-MAR-2000; 2000US-0192176P.
 PR 27-MAR-2000; 2000US-0192179P.
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 XX Kniec EB, Gamper HB, Rice MC;
 PI WPI; 2001-639230/73.
 XX
 DR Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
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 PS Claim 7; Page 257; 294pp; English.
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 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,

CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention
XX
SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1661 AGGCTCAGCTGGGA 1675
Db 16 AGGCTCAGCTGGGA 2
||||| |||||||

RESULT 366
ABA77562/c
ID ABA77562 standard; DNA; 17 BP.
XX
AC ABA77562;
XX
DT 24-JAN-2002 (first entry)
XX
DE Beta globin mutation correcting oligonucleotide SEQ ID NO: 408.
XX
KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytostatic; antislacking; antianaemic; haemostatic;
KW antileptic; ss.
XX
OS Homo sapiens.
XX
PN WO200173002-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009761.
XX
PR 27-MAR-2000; 2000US-0192176P.
PR 27-MAR-2000; 2000US-0192179P.
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
XX
PA (UYDE) UNIV DELAWARE.
XX
XX Kmlec EB, Gamper HB, Rice MC;
XX
XX WPI; 2001-639230/73.
XX
PT Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.
XX
PS Claim 7; Page 68; 294pp; English.
XX
CC The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus

CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1695 CGTGTGGAAGTTGG 1709
Db 16 CGTGTGGAAGTTGG 2
||||| |||||||

RESULT 367
AAH24589
ID AAH24589 standard; DNA; 17 BP.
XX
AC AAH24589;
XX
DT 07-AUG-2001 (first entry)
XX
DE Human endometrium cDNA clone 3-7-SP6 PCR primer #1.
XX
KW Human; endometrium; gynaecological; cytostatic; gene therapy;
KW peptide therapy; endometriosis; gene expression; drug screening;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200132920-A2.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-GB004228.
XX
PR 03-NOV-1999; 99GB-00026074.
PR 03-NOV-1999; 99GB-00026076.
PR 03-NOV-1999; 99GB-00026079.
PR 03-NOV-1999; 99GB-00026081.
XX
PA (METR-) METRIS THERAPEUTICS LTD.
XX
XX Pappa H, Lnenicek M;
XX
XX WPI; 2001-328804/34.
XX
PT Screening for a gene or gene product associated with endometriosis, for
PT diagnosing or treating endometriosis, comprises selecting a gene whose
PT level of expression differs between healthy and diseased endometrium
PT tissues.
XX
XX Example; Fig 3; 106pp; English.
XX
CC The invention relates to a method for screening for a gene or gene
CC product associated with endometriosis. The method comprises comparing the
CC pattern of gene expression in a diseased endometrium tissue from a
CC patient suffering from endometriosis to the pattern of gene expression in
CC healthy endometrium tissue from the same patient, and selecting a gene
CC whose level of expression differs between healthy and diseased tissues.
CC The gene, gene product and their antagonists and agonists are useful in
CC the manufacture of a medicament for diagnosing or treating endometriosis.
CC The method is useful for screening genes or gene products that are
CC implicated in endometriosis. It is particularly useful in diagnosing
CC endometriosis, as well as for screening for agents for treating
CC endometriosis. Prior methods of diagnosing endometriosis are more

CC difficult to perform and are more expensive, normally involving surgery.
 CC The present method allows the disease to be diagnosed and treated at
 CC earlier stage. The present sequence is a primer used in a reverse
 CC transcription polymerase chain reaction (RT-PCR) procedure to validate
 CC the results of differential gene expression studies. It was used to
 CC amplify human endometrium cDNA encoding ferritin L chain
 XX Sequence 17 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1648 GAAGGCAAGCACCAG 1662
 Db 3 GAAGGCTGSCACCAG 17
 RESULT 368
 ABN02361/c
 ID ABN02361 standard; DNA; 17 BP.
 XX AC ABN02361;
 XX DT 29-MAY-2002 (first entry)
 XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2353.
 XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 OS Homo sapiens.
 XX WO200192524-A2.
 XX PN 06-DEC-2001.
 XX PD 25-MAY-2001; 2001WO-US016981.
 XX PF 26-MAY-2000; 2000US-0207456P.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PR 30-JAN-2001; 2001WO-US000661.
 XX PR 30-JAN-2001; 2001WO-US000662.
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 05-FEB-2001; 2001WO-US000670.
 XX PA (AEOM-) AEOMICA INC.
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 XX or as specific biomolecule capture probes for surface-enhanced laser
 XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX Disclosure; SEQ ID NO 2353; 214pp; English.
 XX
 XX The present invention describes a human genome-derived myosin-like
 XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 XX nucleic acids can be used as probes to detect, characterise and quantify
 XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1632 GATGGGGCTTGTAGC 1646
 Db 15 GATGGGGCTTGTAGC 1
 RESULT 369
 ABN02360/c
 ID ABN02360 standard; DNA; 17 BP.
 XX AC ABN02360;
 XX DT 29-MAY-2002 (first entry)
 XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2352.
 XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 OS Homo sapiens.
 XX WO200192524-A2.
 XX PN 06-DEC-2001.
 XX PD 25-MAY-2001; 2001WO-US016981.
 XX PF 26-MAY-2000; 2000US-0207456P.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PR 30-JAN-2001; 2001WO-US000661.
 XX PR 30-JAN-2001; 2001WO-US000662.
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 05-FEB-2001; 2001WO-US000670.
 XX PA (AEOM-) AEOMICA INC.
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX

PT New polypeptide, for raising antibodies that recognize hGDMPL-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption/ionization comprises human mvosin-like protein hGDMPL-1.
PT

Disclosure: SEO ID NO 2352; 214pp; English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption/ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct sequence

Sequence 17 RP: 4 A: 7 C: 4 G: 2 T: 0 U: 0 Other: 0

Query Match	8.5%	Score 11.8;	DB 1;	Length 17;
Best Local Similarity	86.7%	Pred. No. 3.9e+02;		
Matches 13:	Conservative	0;	Mismatches 2;	Indels 0;
	Conservative			Gaps 0;

1632 GATGGGCTTGTAGC 1646
Ov

16 GATCGGGCCTGTAGC 2

RESULT 370
ABN00533
ID ABN00533 standard: DNA; 17 BP.

XX
AC
ARN00533:

28-MAY-2002 (first entry)

XX
DT 17-max cpmt s-1 17-max scanning seo td no-4 sequence seo id no:525;

XX Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; ampicillin; screening; ss.

xx Homo sapiens.

XX
PN
WO200192524-A2.

XX
PD
06-DEC-2007

XX
PF 25-MAY-2001: 2001WO-US016981.

XX
DD
36-MAY-2000.

PR 21-SEP-2000; 2000US-023468/P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US0006664.

PR 30-JAN-2001; 2001WO-US000666.

444

PR 30-JAN-2001; 2001WO-US000658.
PR 30-JAN-2001; 2001WO-US000659.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR

PA (AEOM-) AEOMICA INC.

XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX
DB WPT: 2002-179446/23

New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser

XX
NS
disclosure. SEO ID NO 525: 214pp: English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption/ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at www.int/pub/published/pct sequence

XX
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Sentence 17 BP. 7 A: 3 C: 5 G: 2 T: 0 U: 0 Other:

Query Match

Query Match	86.7%	Pred. No. 3.9e+02	0	Gaps	0
Best Local Similarity	86.7%	Pred. No. 3.9e+02	0	Mismatches	2
Matches	13	Conservative	0	Indels	0

1644 AGCAGAAGGCAAGCA 1658
Ov

3 AGCAGATGACCAAGCA 17

RESULT 371

RESOL 274
ABN00534

ID
YY
ABN00334

AA
AC ARN00534:XX
DT 29-MAY-2002 (first entry)XX
--- cover 1 17 max scanning seq ID NO:4 sequence seq ID NO:526.
--

XX Human; genome-derived myosin-like protein 1; GDMPL-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; ampicillin; screening; ss.
WV

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Homo sapiensXX
NW
W0000103524-22

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

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PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX (AEOM-) AEOMICA INC.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX Disclosure; SEQ ID NO 526; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX Sequence 17 BP; 7 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
 SQ Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1644 AGCAGAGGCAAGCA 1658
 ||||| |
 DB 2 AGCAGATGACAAGCA 16
 RESULT 372
 ABNO7838
 ID ABNO7838 standard; DNA; 17 BP.
 XX AC
 XX ABNO7838;
 XX 29-MAY-2002 (first entry)
 DT Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7830.
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
 XX KW

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 XX WO200192524-A2.
 XX 06-DEC-2001.
 XX 25-MAY-2001; 2001WO-US016981.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX (AEOM-) AEOMICA INC.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX Disclosure; SEQ ID NO 7830; 214pp; English.
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1661 AGGCTCACAGCTGGA 1675
 ||||| |
 DB 2 AGCTCACAGCTGAA 16

RESULT 373
ABN02359/C
ID ABN02359 standard; DNA; 17 BP.
XX
AC ABN02359;
XX
XX 29-MAY-2002 (first entry)
DT
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2351.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
XX WO200192524-A2.
PN
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
PR
XX 30-JAN-2001; 2001WO-US000661.
PR
XX 30-JAN-2001; 2001WO-US000662.
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XX 30-JAN-2001; 2001WO-US000663.
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XX 30-JAN-2001; 2001WO-US000664.
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XX 30-JAN-2001; 2001WO-US000665.
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XX 30-JAN-2001; 2001WO-US000666.
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XX 30-JAN-2001; 2001WO-US000667.
PR
XX 30-JAN-2001; 2001WO-US000668.
PR
XX 30-JAN-2001; 2001WO-US000669.
PR
XX 30-JAN-2001; 2001WO-US000670.
PR
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
PA
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
DR
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
PT
XX
XX Disclosure; SEQ ID NO 2351; 214pp; English.
PS
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed form
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX

SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. NO. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1632 GATGGGCTGTAGC 1646
Db ||||| ||||| ||||| |||||
17 GATGGGCTGTAGC 3
RESULT 374
ABN07837
ID ABN07837 standard; DNA; 17 BP.
XX
AC ABN07837;
XX
XX 29-MAY-2002 (first entry)
DT
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7829.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
XX WO200192524-A2.
PN
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
PR
XX 30-JAN-2001; 2001WO-US000661.
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XX 30-JAN-2001; 2001WO-US000662.
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XX 30-JAN-2001; 2001WO-US000663.
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XX 30-JAN-2001; 2001WO-US000664.
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XX 30-JAN-2001; 2001WO-US000665.
PR
XX 30-JAN-2001; 2001WO-US000666.
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XX 30-JAN-2001; 2001WO-US000667.
PR
XX 30-JAN-2001; 2001WO-US000668.
PR
XX 30-JAN-2001; 2001WO-US000669.
PR
XX 30-JAN-2001; 2001WO-US000670.
PR
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
PA
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PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
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XX WPI; 2002-179446/23.
DR
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
PT
XX
XX Disclosure; SEQ ID NO 7829; 214pp; English.
PS
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as

CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the patent application of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX SQ Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1661 AGGCTCAGCTGGA 1675

Db 3 AGCCTCAGCTGAA 17

RESULT 375

ABV79508

ID ABV79508 standard; DNA; 17 BP.

XX AC ABV79508;

XX DT 03-JAN-2003 (first entry)

XX DT Human HTPL scanning oligonucleotide SEQ ID 754.

XX DE Human; Gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 XX KW human testis expressed Patched like protein; testis; adrenal; liver;
 XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EPI229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US0000663.

XX PR 30-JAN-2001; 2001WO-US0000664.

XX PR 30-JAN-2001; 2001WO-US0000665.

XX PR 30-JAN-2001; 2001WO-US0000667.

XX PR 30-JAN-2001; 2001WO-US0000668.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX DR WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 XX PT for identifying agonist and antagonist and specific binding partners, and
 XX PT for treating subjects having defects in HTPL.

XX PS Example 2; Page 162; 718pp; English.

XX CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar

CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention

SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAACC 1678

Db 1 CTCACAGCTGGAACC 15

RESULT 376

ABV79507

ID ABV79507 standard; DNA; 17 BP.

XX AC ABV79507;

XX DT 03-JAN-2003 (first entry)

XX DT Human HTPL scanning oligonucleotide SEQ ID 753.

XX DE Human; Gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 XX KW human testis expressed Patched like protein; testis; adrenal; liver;
 XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EPI229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US0000663.

XX PR 30-JAN-2001; 2001WO-US0000664.

XX PR 30-JAN-2001; 2001WO-US0000665.

XX PR 30-JAN-2001; 2001WO-US0000667.

XX PR 30-JAN-2001; 2001WO-US0000668.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX DR WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 XX PT for identifying agonist and antagonist and specific binding partners, and
 XX PT for treating subjects having defects in HTPL.

XX PS Example 2; Page 162; 718pp; English.

XX CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar

CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1664 CTCACGCTGGAACC 1678
|||||
DB 2 CTCACGCTGGAACC 16

RESULT 377
ABV78965
ID ABV78965 standard; DNA; 17 BP.
AC ABV78965;
XX
XX 03-JAN-2003 (first entry)
DE Human HTPL scanning oligonucleotide SEQ ID 211.
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX Homo sapiens.
XX
XX EP1229046-A2.
XX
XX 07-AUG-2002.
XX
XX 28-JAN-2002; 2002EP-00001167.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 23-MAY-2001; 2001US-00864761.
XX 09-OCT-2001; 2001US-0327898P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
XX for identifying agonist and antagonist and specific binding partners, and
XX for treating subjects having defects in HTPL.
XX
XX Example 2; Page 91; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
XX protein (HTPL, see ABV78759 to ABV78762 and ABV78762 to ABV78762). HTPL
XX has two isoforms, with a few single base pair differences between the

CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAAGCAAGCACC 1660
|||||
DB 3 CGGAAGCAAGCAGC 17

RESULT 378
ABV78967
ID ABV78967 standard; DNA; 17 BP.
XX
XX ABV78967;
AC
XX 03-JAN-2003 (first entry)
DE Human HTPL scanning oligonucleotide SEQ ID 213.
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX Homo sapiens.
XX
XX EP1229046-A2.
XX
XX 07-AUG-2002.
XX
XX 28-JAN-2002; 2002EP-00001167.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 23-MAY-2001; 2001US-00864761.
XX 09-OCT-2001; 2001US-0327898P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
XX for identifying agonist and antagonist and specific binding partners, and
XX for treating subjects having defects in HTPL.
XX
XX Example 2; Page 91; 713pp; English.
XX
XX The present invention relates to human testis expressed Patched like

CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1646 CAGAAGGCAAGCACC 1660
 Db 1 CGGAAGGCAAGCAGC 15

RESULT 379
 ABV78966

ID ABV78966 standard; DNA; 17 BP.

AC ABV78966;

03-JAN-2003 (first entry)

Human HTPL scanning oligonucleotide SEQ ID 212.

Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 Human testis expressed patched like protein; testis; adrenal; liver;
 male germ cell development; bone marrow; brain; kidney; lung; placenta;
 prostate; skeletal muscle; colon; male infertility; cancer; ss.

Homo sapiens.

EP1229046-A2.

07-AUG-2002.

28-JAN-2002; 2002EP-00001167.

30-JAN-2001; 2001WO-US000663.

30-JAN-2001; 2001WO-US000664.

30-JAN-2001; 2001WO-US000665.

30-JAN-2001; 2001WO-US000667.

30-JAN-2001; 2001WO-US000668.

23-MAY-2001; 2001WO-US000669.

09-OCT-2001; 2001US-0327898P.

(AEOM-) AEOMICA INC.

Zhan J;

WPI; 2002-676582/73.

Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.
 XX Example 2; Page 91; 718pp; English.
 PS

XX

The present invention relates to human testis expressed patched like
 protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
 has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX

Sequence 17 BP; 5 A; 5 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1646 CAGAAGGCAAGCACC 1660

Db 2 CGGAAGGCAAGCAGC 16

RESULT 380
 ABK18405/C

ID ABK18405 standard; RNA; 17 BP.

AC ABK18405;

09-APR-2002 (first entry)

Human ERG hammerhead ribozyme target sequence, Seq ID No 1052.

Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 tumour angiogenesis; diabetic retinopathy; macular degeneration;
 neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNazyme; inozyme;
 amberzyme.

Homo sapiens.

WO200188124-A2.

22-NOV-2001.

16-MAY-2001; 2001WO-US015866.

16-MAY-2000; 2000US-00572021.

(RIBO-) RIBOZYME PHARM INC.

(GLAX) GLAXO GROUP LTD.

Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;

WPI; 2002-082995/11.

Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX

PS Claim 4; Page 78; 149pp; English.

XX The invention relates to a nucleic acid molecule (I) which down regulates

CC expression of an Ets-related gene (ERG). (I) is useful for treating

CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge

CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu

CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for

CC treating a patient having a condition associated with the level of ERG,

CC by contacting cells of the patient with (I) under conditions suitable for

CC the treatment. The method comprises the use of one or more therapies

CC under conditions suitable for the treatment. Leukaemia or tumour

CC angiogenesis is treated by administering (I) to the patient in

CC conjunction with one or more of other therapies such as radiation or

CC chemotherapy treatment. (I) is useful for reducing ERG activity in a

CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent

CC cation such as Mg2+. (I) is useful for diagnosis of conditions and

CC diseases related to the expression of ERG, and as diagnostic tool to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of ERG RNA in a cell. (I) is useful for specifically

CC targeting genes that share homology with ERG gene or ERG fusion genes.

CC ABK7354-ABK2719 represent nucleic acids, including antisense and

CC enzymatic nucleic acid molecules which regulate expression of ERG, and

CC related PCR primers of the invention

XX Sequence 17 BP; 4 A; 2 C; 7 G; 0 T; 4 U; 0 Other;

SQ Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 2;

QY 1675 AACCTCGGTGCTCC 1689

Db 17 AACCTCGGTGCTCC 3

RESULT 381

ABV90894

ID ABV90894 standard; DNA; 17 BP.

XX ABV90894;

AC ABV90894;

XX 23-DEC-2002 (first entry)

DT Human POSHL1 scanning oligonucleotide SEQ ID NO 1607.

XX Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;

KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;

KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EF1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 23-MAY-2001; 2001US-00864761.

PR 10-OCT-2001; 2001US-0328205P.

XX (ABOM-) AEOMICA INC.

PA

XX Shannon M;

PI WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide. POSHL

DR -1, useful for treating disorders associated with decreased expression or

PT activity of human POSHL1.

PT Example 2; SEQ ID NO 1607; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling

CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino

CC acids (S1, AB83999), a sequence having 65% sequence identity to (S1),

CC (S1) having 95% deviations, especially conservative substitutions or a

CC fragment of the sequences comprising at least 8 contiguous amino acids.

CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an

CC adaptor protein that interacts with Rho family small GTPases as well as

CC downstream components of the signal transduction pathway. (I) is useful

CC for identifying a specific binding partner. (I) and nucleic acids (II)

CC encoding (I) are useful for diagnosing, monitoring disease and treating

CC caused by altered expression of human POSHL1 including diagnosing and

CC treating cancer, they are useful in the development of vaccines and (II) is

CC useful in gene therapy. (II) is useful for constructing microarrays which

CC are useful for measuring and for surveying gene expression and creating

CC transgenic non-human animals capable of producing the proteins. The

CC present sequence is that of a scanning oligonucleotide useful in examples

CC of the invention. Note: The present sequence did not form part of the

CC printed specification, but is based on sequence information supplied to

CC Derwent by the European Patent Office

XX Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

SQ Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 2;

QY 1673 GGAACCCCTGGTGTCT 1687

Db 2 GGAGCCCTGGTGTCT 16

RESULT 382

ABV91048/c

ID ABV91048 standard; DNA; 17 BP.

XX ABV91048;

AC ABV91048;

XX 23-DEC-2002 (first entry)

DT Human POSHL1 scanning oligonucleotide SEQ ID NO 1761.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;

KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;

KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EF1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 23-MAY-2001; 2001US-00864761.

PR 23-MAY-2001; 2001US-00864761.

PR

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PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
XX -1, useful for treating disorders associated with decreased expression or
XX activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1761; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX (S1) having 95% deviations, especially conservative substitutions or a
XX fragment of the sequences comprising at least 8 contiguous amino acids.
XX Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX adaptor protein that interacts with Rho family small GTPases as well as
XX downstream components of the signal transduction pathway. (I) is useful
XX for identifying a specific binding partner. (I) and nucleic acids (II)
XX encoding (I) are useful for diagnosing, monitoring disease and treating
XX cancer, they are useful in the development of vaccines and (II) is
XX useful in gene therapy. (II) is useful for constructing microarrays which
XX are useful for measuring and for surveying gene expression and creating
XX transgenic non-human animals capable of producing the proteins. The
XX present sequence is that of a scanning oligonucleotide useful in examples
XX of the invention. Note: The present sequence did not form part of the
XX printed specification, but is based on sequence information supplied to
XX Derwent by the European Patent Office
XX
XX Sequence 17 BP; 5 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 8.5%; Score 11.8; DB 1; Length 17;
XX Best Local Similarity 86.7%; Pred. No. 3.9e+02;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1751 TATCCTAAAGGCCCA 1765
XX Db 16 TGTCTAAAGTCCCA 2
XX
XX RESULT 383
XX ABV91047/c
XX ID ABV91047 standard; DNA; 17 BP.
XX AC ABV91047;
XX
XX DT 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1760.
XX
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX
XX OS Homo sapiens.
XX
XX KW EPI239051-A2.
XX
XX PN 11-SEP-2002.
XX
XX PD 28-JAN-2002; 2002EP-00001165.
XX
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.

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PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
XX -1, useful for treating disorders associated with decreased expression or
XX activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1760; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX (S1) having 95% deviations, especially conservative substitutions or a
XX fragment of the sequences comprising at least 8 contiguous amino acids.
XX Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX adaptor protein that interacts with Rho family small GTPases as well as
XX downstream components of the signal transduction pathway. (I) is useful
XX for identifying a specific binding partner. (I) and nucleic acids (II)
XX encoding (I) are useful for diagnosing, monitoring disease and treating
XX cancer, they are useful in the development of vaccines and (II) is
XX useful in gene therapy. (II) is useful for constructing microarrays which
XX are useful for measuring and for surveying gene expression and creating
XX transgenic non-human animals capable of producing the proteins. The
XX present sequence is that of a scanning oligonucleotide useful in examples
XX of the invention. Note: The present sequence did not form part of the
XX printed specification, but is based on sequence information supplied to
XX Derwent by the European Patent Office
XX
XX Sequence 17 BP; 4 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 8.5%; Score 11.8; DB 1; Length 17;
XX Best Local Similarity 86.7%; Pred. No. 3.9e+02;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1751 TATCCTAAAGGCCCA 1765
XX Db 17 TGTCTAAAGTCCCA 3
XX
XX RESULT 384
XX ACCS2599
XX ID ACCS2599 standard; DNA; 17 BP.
XX AC ACCS2599;
XX
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #1366.
XX
XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX tumour regression; apoptosis; virus resistance; diagnosis;
XX cellular degeneration.
XX
XX OS Homo sapiens.
XX
XX PN FR2826373-A1.
XX
XX PD 27-DEC-2002.
XX
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX
XX (MOLE-) MOLECULAR ENGINES LAB SA.

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XX Tuijnder M, Telerman A, Amson R;
XX WPI; 2003-250498/25.
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX Claim 1; Page 356; 798pp; French.
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumor suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumor cells or cellular degeneration
XX
XX Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
SQ Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1735 GCTCCCAACTCTCTCC 1749
DB 1 GATCCCAACTGCTCC 15

RESULT 385
ABT40179
ID ABT40179 standard; DNA; 17 BP.
XX AC ABT40179;
XX DT 13-JUN-2003 (first entry)
XX Tumour suppression related human fukutin oligo SEQ ID No 5816.
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX Homo sapiens.
XX WO2003025175-A2.
PN 27-MAR-2003.
XX 17-SEP-2002; 2002WO-IB004208.
XX 17-SEP-2001; 2001FR-00011978.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX Disclosure; Page 713; 720pp; French.
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

XX acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
XX Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
SQ Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1735 GCTCCCAACTCTCTCC 1749
DB 1 GATCCCAACTGCTCC 15

RESULT 386
ABT40171
ID ABT40171 standard; DNA; 17 BP.
XX AC ABT40171;
XX DT 13-JUN-2003 (first entry)
XX Tumour suppression related human fukutin oligo SEQ ID No 5808.
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX Homo sapiens.
XX WO2003025175-A2.
PN 27-MAR-2003.
XX 17-SEP-2002; 2002WO-IB004208.
XX 17-SEP-2001; 2001FR-00011978.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX Disclosure; Page 713; 720pp; French.
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX

SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e-02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCTCTCC 1749

DB 1 GATCCCACTCTCTCC 15

RESULT 387

ABT36364/C

ID ABT36364 standard; DNA; 17 BP.

XX AC ABT36364;

XX DT 12-JUN-2003 (first entry)

XX DE Tumour suppression related human fukutin oligo SEQ ID No 2001.

XX KW Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; gene chip;

XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

XX KW schizophrenia; protein chip; gene therapy; tumour suppression;

XX KW human fukutin; ds.

XX OS Homo sapiens.

XX PN WO2003025175-A2.

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-IB004208.

XX PR 17-SEP-2001; 2001FR-00011978.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX DR WPI; 2003-313353/30.

XX PT New isolated nucleic acid, useful for treating viral diseases associated

XX PT with tumors and cell degeneration, also related polypeptides, antibodies

XX PT and transfected cells.

XX PS Disclosure; Page 267; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,

XX CC given in the specification, a sequence containing at least 15 consecutive

XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal

XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that

XX CC hybridizes to them under highly stringent conditions, or the complement

XX CC of any of them, or the corresponding RNA. The novel isolated nucleic

XX CC acids of the invention are useful as probes and primers for detecting,

XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

XX CC component of a gene chip, in vitro as (anti)sense reagents, and for

XX CC production of recombinant polypeptides. Any of the nucleic acids,

XX CC

CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX

SQ Sequence 17 BP; 2 A; 7 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e-02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1712 TAGGAGTACGGAGAT 1726

DB 16 TAGGAGGAGGAGAT 2

RESULT 388

ABT38111/C

ID ABT38111 standard; DNA; 17 BP.

XX AC ABT38111;

XX DT 12-JUN-2003 (first entry)

XX DE Tumour suppression related human fukutin oligo SEQ ID No 3748.

XX KW Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; gene chip;

XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

XX KW schizophrenia; protein chip; gene therapy; tumour suppression;

XX KW human fukutin; ds.

XX OS Homo sapiens.

XX PN WO2003025175-A2.

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-IB004208.

XX PR 17-SEP-2001; 2001FR-00011978.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX DR WPI; 2003-313353/30.

XX PT New isolated nucleic acid, useful for treating viral diseases associated

XX PT with tumors and cell degeneration, also related polypeptides, antibodies

XX PT and transfected cells.

XX PS Disclosure; Page 472; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,

XX CC given in the specification, a sequence containing at least 15 consecutive

XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal

XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that

XX CC hybridizes to them under highly stringent conditions, or the complement

XX CC of any of them, or the corresponding RNA. The novel isolated nucleic

XX CC acids of the invention are useful as probes and primers for detecting,

XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

XX CC component of a gene chip, in vitro as (anti)sense reagents, and for

XX CC production of recombinant polypeptides. Any of the nucleic acids,

XX CC polypeptides, vectors containing the nucleic acids, cells containing the

XX CC vector or antibodies directed against the polypeptides are useful for

```
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
XX Sequence 17 BP; 5 A; 6 C; 1 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 8.5%; Score 11.8; DB 1; Length 17;
XX Best Local Similarity 86.7%; Pred. No. 3.9e-02;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1702 GAAGTTGGGTAGGA 1716
XX ||||| ||||| |||||
XX Db 17 GAAGATGTGTAGGA 3
XX
XX RESULT 389
XX ACA07737
XX ID ACA07737 standard; RNA; 17 BP.
XX AC ACA07737;
XX XX
XX DT 03-JUN-2003 (first entry)
XX DE NFKB sub-unit modulating zinzyme substrate #136.
XX
XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
XX G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
XX lung cancer; prostate cancer; colorectal cancer; brain cancer;
XX oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
XX cervical cancer; head and neck cancer; ovarian cancer; melanoma;
XX lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
XX chemotheraphy; paclitaxel; docetaxel; cisplatin; methotrexate;
XX cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
XX gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
XX rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
XX gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
XX transplant/grat rejection; reperfusion injury; glomerulonephritis;
XX allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
XX Homo sapiens.
XX OS
XX US2002177568-A1.
XX
XX 28-NOV-2002.
XX
XX 23-MAY-2001; 2001US-00864785.
XX
XX 07-DEC-1992; 92US-00987132.
XX PR 18-MAY-1994; 94US-00245466.
XX PR 15-AUG-1994; 94US-00291932.
XX PR 23-DEC-1996; 96US-00777916.
XX
XX (STIN/) STINCHOMB D T.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (DRAP/) DRAPER K G.
XX
XX Stinchcomb DT, Mcswiggen J, Draper KG;
XX PI
XX WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
XX a sequence encoding a subunit of nuclear factor kappa B useful for
XX treating cancer, inflammatory disorders and autoimmune diseases.
XX
XX Claim 3; Page 39; 72pp; English.
XX
XX
```

```
CC The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg2+. The enzymatic and
CC antisenase nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotheraphy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisenase nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/grat
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel enzymatic
CC nucleic acid molecule
XX
XX Sequence 17 BP; 2 A; 6 C; 3 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 8.5%; Score 11.8; DB 1; Length 17;
XX Best Local Similarity 53.3%; Pred. No. 3.9e-02;
XX Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1676 ACCCTGGTGTCCT 1690
XX ||||| :||| :|||
XX Db 3 ACCAUGGUGUUCU 17
XX
XX RESULT 390
XX ADA99592/C
XX ID ADA99592 standard; DNA; 17 BP.
XX AC ADA99592;
XX XX
XX DT 20-NOV-2003 (first entry)
XX DE Human MDZ3 scanning oligonucleotide SEQ ID 581.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX OS
XX EP1281758-A2.
XX PN
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX PR
XX (AEOM-) AEOMICA INC.
XX PA
XX Shannon M, Gu Y, Nguyen C;
XX PI
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 581; 103pp; English.
XX
XX
```

CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 CC
 SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1668 CAGCTGGACCTGG 1682
 Db ||||| |||||
 16 CAGCTGGAGCCTGG 2
 RESULT 391
 ADA99303
 ID ADA99303 standard; DNA; 17 BP.
 AC ADA99303;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD23 scanning oligonucleotide SEQ ID 292.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 DR WPI; 2003-423107/40.
 XX
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 XX Example 8; SEQ ID NO 292; 103pp; English.
 PS
 PS The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 CC

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 CC
 SQ Sequence 17 BP; 5 A; 6 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1668 CAGCTGGACCTGG 1682
 Db ||||| |||||
 1 CAGCTGGACCCAGG 15
 RESULT 392
 ADA99591/c
 ID ADA99591 standard; DNA; 17 BP.
 XX
 AC ADA99591;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD23 scanning oligonucleotide SEQ ID 580.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 DR WPI; 2003-423107/40.
 XX
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 XX Example 8; SEQ ID NO 580; 103pp; English.
 PS
 PS The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 CC

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XX SQ Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTGG 1682
Db 17 CAGCTGGATGCTGG 3

RESULT 393
ADA99302
ID ADA99302 standard; DNA; 17 BP.
XX AC ADA99302;
XX 20-NOV-2003 (first entry)
XX Human MDZ3 scanning oligonucleotide SEQ ID 291.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MD24; MD27; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX Homo sapiens.
XX EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX Example 8; SEQ ID NO 291; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTGG 1682
Db 17 CAGCTGGATGCTGG 3

RESULT 394
ADA99301
ID ADA99301 standard; DNA; 17 BP.
XX AC ADA99301;
XX 20-NOV-2003 (first entry)
XX Human MDZ3 scanning oligonucleotide SEQ ID 290.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MD24; MD27; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX Homo sapiens.
XX EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX Example 8; SEQ ID NO 290; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX Sequence 17 BP; 3 A; 6 C; 7 G; 1 T; 0 U; 0 Other;

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTGG 1682
Db 3 CAGCTGGACCCCTGG 17

RESULT 395
ABZ64947/c
ID ABZ64947 standard; RNA; 17 BP.
XX

```



```
AC ABZ64947;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human HER2 DNzyme substrate #404.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 4; Page 140; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX
XX Sequence 17 BP; 2 A; 7 C; 6 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 8.5%; Score 11.8; DB 1; Length 17;
XX Best Local Similarity 86.7%; Pred. No. 3.9e+02;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1660 CAGGCTCACAGCTGG 1674
XX | ||| ||||| |||||
XX 15 CCGGCGCACAGCTGG 1
XX
XX Db
XX
XX RESULT 396
XX ABZ65447
XX ID ABZ65447 standard; RNA; 17 BP.
XX
XX AC ABZ65447;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human HER2 DNzyme substrate #904.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
```

```
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 4; Page 150; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX
XX Sequence 17 BP; 2 A; 6 C; 4 G; 0 T; 5 U; 0 Other;
XX
XX Query Match 8.5%; Score 11.8; DB 1; Length 17;
XX Best Local Similarity 53.3%; Pred. No. 3.9e+02;
XX Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1677 CCCTGGTGTCTCTCC 1691
XX ||||| :| :| :| :|
XX 2 CCCTGAUGUGUCCTC 16
XX
XX Db
XX
XX RESULT 397
XX ABZ64946/C
XX ID ABZ64946 standard; RNA; 17 BP.
XX
XX AC ABZ64946;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human HER2 DNzyme substrate #403.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.
XX
```

PA (RIBO-) RIBOZYME PHARM INC.
 PI Mcswiggen J;
 XX
 XX WPI; 2003-140484/13.
 DR
 XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX
 XX Claim 4; Page 140; 185pp; English.
 PS
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 XX Sequence 17 BP; 2 A; 8 C; 5 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1660 CAGGCTCACAGCTGG 1674
 DB 17 CGGGCGCACAGCTGG 3
 RESULT 398
 ABZ64792/c
 ID ABZ64792 standard; RNA; 17 BP.
 AC ABZ64792;
 XX
 XX 21-MAR-2003 (first entry)
 DT
 XX Human HER2 DNzyme substrate #249.
 DE
 XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200297114-A2.
 PN
 XX 05-DEC-2002.
 PD
 XX 29-MAY-2002; 2002WO-US016840.
 PF
 XX 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Mcswiggen J;
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 XX WPI; 2003-140484/13.
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 XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
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 XX Claim 4; Page 137; 185pp; English.
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 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
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 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
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 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 XX Sequence 17 BP; 2 A; 8 C; 5 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1660 CAGGCTCACAGCTGG 1674
 DB 17 CGGGCGCACAGCTGG 3
 RESULT 398
 ABZ64792/c
 ID ABZ64792 standard; RNA; 17 BP.
 AC ABZ64792;
 XX
 XX 21-MAR-2003 (first entry)
 DT
 XX Human HER2 DNzyme substrate #249.
 DE
 XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200297114-A2.
 PN
 XX 05-DEC-2002.
 PD
 XX 29-MAY-2002; 2002WO-US016840.
 PF
 XX 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
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 XX Mcswiggen J;
 PI
 XX WPI; 2003-140484/13.
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 XX Claim 4; Page 137; 185pp; English.
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 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
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 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
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 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 XX Sequence 17 BP; 2 A; 6 C; 5 G; 0 T; 4 U; 0 Other;
 SQ
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1660 CAGGCTCACAGCTGG 1674
 DB 15 CAGTCACACAGCTGG 1
 RESULT 399
 ABZ64791/c
 ID ABZ64791 standard; RNA; 17 BP.
 AC ABZ64791;
 XX
 XX 21-MAR-2003 (first entry)
 DT
 XX Human HER2 DNzyme substrate #248.
 DE
 XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200297114-A2.
 PN
 XX 05-DEC-2002.
 PD
 XX 29-MAY-2002; 2002WO-US016840.
 PF
 XX 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Mcswiggen J;
 PI
 XX WPI; 2003-140484/13.
 DR
 XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX
 XX Claim 4; Page 137; 185pp; English.
 PS
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention

CC AB266530 - AB266585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 6 G; 0 T; 4 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1660 CAGGCTCAGCTGG 1674
 |||||
 Db 17 CAGTCACACAGCTGG 3
 RESULT 400
 ACD62967/c
 ID ACD62967 standard; RNA; 17 BP.
 XX
 AC ACD62967;
 XX
 DT 24-SEP-2003 (first entry)
 XX
 DE HCV minus strand DNazyme substrate sequence #830.
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 DR
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Claim 1; Page 289; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention
 XX
 SQ Sequence 17 BP; 5 A; 8 C; 1 G; 0 T; 3 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1631 GCATGGGCGCTGTAG 1645
 |||||
 Db 15 GGAAGGTGCTGTAG 1
 RESULT 401
 ACD52213
 ID ACD52213 standard; RNA; 17 BP.
 XX
 AC ACD52213;
 XX
 DT 24-SEP-2003 (first entry)
 XX
 DE HBV inozyme substrate sequence #292.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 DR

PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.

XX Example 1; Page 155; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, ambarzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or ambarzyme sequences
 CC disclosed in the present invention

XX Sequence 17 BP; 2 A; 4 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 60.0%; Pred. No. 3.9e+02;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1672 TGGAAACCTCGTGTGTC 1686
 :|||||:|:|:
 Db 3 UGARACCUUGUGUC 17

RESULT 402

ACD59647

ID ACD59647 standard; RNA; 17 BP.

XX ACD59647;

DT 24-SEP-2003 (first entry)

DE HCV DNazyme substrate sequence #1449.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW ambarzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.

OS WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

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 (PAVC/) PAVCO P.
 (LEEP/) LEE P.
 (DRAP/) DRAPER K.
 (ROBE/) ROBERTS E.

Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 Draper K, Roberts E;
 WPI; 2003-229207/22.

Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.

Claim 1; Page 259; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, ambarzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
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 CC compounds and/or potential therapies directed against HBV, and compounds
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 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention

XX Sequence 17 BP; 4 A; 1 C; 8 G; 0 T; 4 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1631 GGATGGGCTGTGTAG 1645
 :|||:|:|:|:
 Db 2 GGNAGGUGUGUGAG 16

RESULT 403

ACD62966/C

ID ACD62966 standard; RNA; 17 BP.

XX ACD62966;

DT 24-SEP-2003 (first entry)

DE HCV minus strand DNazyme substrate sequence #829.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW ambarzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.

OS Hepatitis C virus.

PN WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
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 PA (PAVC/) PAVCO P.
 PA (LEPP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 XX Novel compound useful for treating cirrhosis, liver failure,
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 XX Claim 1; Page 289; 387pp; English.
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 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
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 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention
 XX
 XX Sequence 17 BP; 4 A; 7 C; 2 G; 0 T; 4 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1631 GGATGGGCTGTAG 1645
 Db ||||| |||||
 17 GGAAGTGCTGTAG 3
 RESULT 404
 ACC65896/C
 ID ACC65896 standard; DNA; 17 BP.
 XX ACC65896;
 AC
 AC
 DT 01-JUL-2003 (first entry)
 XX Murine oligonucleotide associated with tumour suppression, SEQ ID 3143.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 XX

OS Mus musculus.
 XX WO2003025176-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004210.
 XX 17-SEP-2001; 2001FR-00011979.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-333167/31.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumours and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 XX Disclosure; Page 398; 738pp; French.
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 XX Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1663 GCTCACAGCTGGAAC 1677
 Db ||||| |||||
 15 GCTCACAGTTGGATC 1
 RESULT 405
 ACC67445
 ID ACC67445 standard; DNA; 17 BP.
 XX ACC67445;
 AC
 XX 01-JUL-2003 (first entry)
 XX Murine oligonucleotide associated with tumour suppression, SEQ ID 4692.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 XX Mus musculus.
 XX WO2003025176-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004210.
 XX 17-SEP-2001; 2001FR-00011979.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-333167/31.

DR WPI; 2003-333167/31.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 XX Disclosure; Page 579; 738pp; French.
 PS
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 XX Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 1687 TCCTCCAGCGTGTG 1701
 Db 3 TCCTCTCGGTGTG 17
 XX
 RESULT 406
 ACC63689/c
 ID ACC63689 standard; DNA; 17 BP.
 XX
 AC ACC63689;
 XX
 XX 01-JUL-2003 (first entry)
 DT
 XX Murine oligonucleotide associated with tumour suppression, SEQ ID 936.
 DE
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 XX WO2003025176-A2.
 PN
 XX 27-MAR-2003.
 PD
 XX 17-SEP-2002; 2002WO-IB004210.
 XX
 XX 17-SEP-2001; 2001FR-00011979.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI
 XX WPI; 2003-333167/31.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 XX Disclosure; Page 140; 738pp; French.
 PS
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX

CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 XX Sequence 17 BP; 6 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 1724 GATGAGATTGCTC 1738
 Db 15 GATGACATTGATC 1
 XX
 RESULT 407
 ACC63888/c
 ID ACC63888 standard; DNA; 17 BP.
 XX
 AC ACC63888;
 XX
 XX 01-JUL-2003 (first entry)
 DT
 XX Murine oligonucleotide associated with tumour suppression, SEQ ID 1135.
 DE
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 XX WO2003025176-A2.
 PN
 XX 27-MAR-2003.
 PD
 XX 17-SEP-2002; 2002WO-IB004210.
 XX
 XX 17-SEP-2001; 2001FR-00011979.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI
 XX WPI; 2003-333167/31.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 XX Disclosure; Page 163; 738pp; French.
 PS
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 XX Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 9.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 1635 GGGGCTTGTCAGCA 1649
 Db 17 GGGGTTTGATCAGA 3

RESULT 408
 ID ABX04768
 XX ABX04768 standard; DNA; 17 BP.
 XX AC ABX04768;
 XX DT 15-JAN-2003 (first entry)
 XX Thymidine kinase (TK) mutant associated oligonucleotide #4.
 DE Herpesviridae; thymidine kinase; TK; DRH nucleoside binding region;
 KW viral inhibitor; bacterial inhibitor; parvovirus inhibitor; tumour;
 KW autoreactive immune cell; cancer; hyperkeratosis; psoriasis;
 KW prostate hypertrophy; hyperthyroidism; endocrinopathy; allergy;
 KW autoimmune disease; restenosis; AIDS; hepatitis; HCV; HBV;
 KW acquired immunodeficiency syndrome; intracellular parasitic disease;
 KW gene therapy; adenosine deaminase deficiency; Alzheimer's disease; ss.
 XX OS Synthetic.
 OS US6451571-B1.
 XX PN 17-SEP-2002.
 PD 17-SEP-2002.
 XX PF 17-MAR-1999; 99US-00270956.
 XX PR 02-MAY-1994; 94US-00237592.
 XX PR 02-MAY-1995; 95US-00432871.
 XX PR 02-NOV-1995; 95US-00552304.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PI Loeb LA, Black ME;
 XX WPI; 2003-045581/04.
 XX Novel Herpesviridae thymidine kinase mutant useful for inhibiting
 PT pathogens e.g. viruses, bacteria, tumor in animals, has one or more
 PT mutations encoding amino acid substitutions upstream from the DRH
 PT nucleoside binding site.
 XX Example 1; Col 21; 78pp; English.
 CC The invention describes an isolated Herpesviridae thymidine kinase (TK)
 CC comprising a 12 amino acid (aa) nucleoside binding region having a site 3
 CC made up of a DRH nucleoside binding site and a site 4 and mutation(s), at
 CC least one of the mutations being an aa substitution 2 or 3 aa upstream or
 CC 5 or more aa downstream from the DRH motif that increases a biological
 CC activity, preferably ability of TK to phosphorylate a nucleoside
 CC analogue, as compared to unmutated TK. TK mutants are useful for
 CC inhibiting a pathogenic agent such as viruses, bacteria, parasites,
 CC tumour cells or autoreactive immune cells in a warm-blooded animal. TK
 CC mutant is useful for inhibiting a tumour or cancer in a warm-blooded
 CC animal, for treating a variety of disease e.g., hyperkeratosis
 CC (psoriasis), prostate hypertrophy, hyperthyroidism, endocrinopathies,
 CC autoimmune diseases, allergies, restenosis, viral diseases such as
 CC acquired immunodeficiency syndrome (AIDS) hepatitis (HCV or HBV),
 CC intracellular parasitic diseases, and to correct aberrant expression of a
 CC gene within a cell, or to replace a specific gene which is defective in
 CC proper expression using gene therapy, e.g. including adenosine deaminase
 CC deficiency, and Alzheimer's diseases. The mutants are utilised as a
 CC conditionally lethal marker for homologous recombination. This sequence
 CC represents an oligonucleotide used in the creation of thymidine kinase
 CC mutants
 XX Sequence 17 BP; 2 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1686 CTCCTCAGCGTGGT 1700
 Db 1 CCCCTCAGCGCGGT 15
 RESULT 409
 ADC37712
 XX ID ADC37712 standard; DNA; 17 BP.
 XX AC ADC37712;
 XX DT 18-DEC-2003 (first entry)
 XX Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:61.
 DE human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1a; ss.
 KW Synthetic.
 OS Homo sapiens.
 XX WO2003037931-A2.
 XX PN 08-MAY-2003.
 PD 08-MAY-2003.
 XX PF 01-NOV-2002; 2002WO-US035129.
 XX PR 01-NOV-2001; 2001US-0334773P.
 XX PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX PI Shannon M, Phan T;
 XX WPI; 2003-430501/40.
 XX New isolated nucleic acid molecule encoding a human angiominotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX Example 2; SEQ ID NO 61; 172pp; English.
 CC The present invention describes the human angiominotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1a, which is used in an example from the
 CC present invention.
 XX Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 8.5%; Score 11.8; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1716 AGTACGAGATGGAG 1730
 Db 3 AATACGATGGAG 17
 RESULT 410
 AAQ20431
 ID AAQ20431 standard; DNA; 18 BP.
 XX AC AAQ20431;
 XX DT 07-APR-1992 (first entry)
 XX Debrisoquine polymorphism PCR primer.
 DE Debrisoquine polymorphism PCR primer.
 XX Polymerase chain reaction; ss.
 KW Polymerase chain reaction; ss.

PS Disclosure; Fig 7C-2; 1C4pp; English.

XX The method aims to provide a collection of highly reproducible

CC microsatellite marker sequences (MMS) at approx. 10-50 cm intervals

CC throughout the human genome which can be detectably labelled. The MSS are

CC polymorphic, simple sequence repeats and can be used in automated

CC genotyping, esp. fluorescence-based. The primers correspond to the unique

CC DNA sequence surrounding each marker, and PCR is used to detect each

CC polymorphism. When the MSS show considerable polymorphism (ie. a

CC difference in the number of repeats) between individuals, the markers can

CC be particularly informative. The MSS can be ideal for linkage studies.

CC Kits comprise at least 4 groups, of at least 3 sets, each comprising

CC labelled primers for PCR amplification of the DNA. Group 3 primer pairs

CC are shown in AA095417-454. The published size range of the DIS243 allele

CC is 142-170 bp, and the degree of heterozygosity in the population is

CC about 87%

XX Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

SQ

Query Match 8.5%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. NO. 4.2e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1689 CTCACGCTGGTGGGA 1703

Db ||||| ||||| |||||

2 CTCACGCTGGTGGGA 16

RESULT 412

AAV49520/c

ID AAV49520 standard; DNA; 18 BP.

XX

AC AAV49520;

XX

DT 20-OCT-1998 (first entry)

DE Mycobacterium sp. AlAdE oligonucleotide AlAdH-R2.

XX

KW Alanine dehydrogenase; AlAdH; ADH; diagnosis; tuberculosis; pathogen;

KW swimmers disease; vaccine; epidemic; infection; identification; ss.

XX

OS Synthetic.

OS Mycobacterium sp.

PN WO9832862-A2.

XX

PD 30-JUL-1998.

XX

PF 29-JAN-1998; 98WO-EP000484.

XX

PR 29-JAN-1997; 97EP-00101339.

XX

PA (FLOH/) FLOHE L.

XX

PI Flohe L, Singh M, Hunter B, Kolk A;

XX

WPI; 1998-427958/36.

XX

PT Nucleic acid encoding alanine dehydrogenase of Mycobacterium marinum -

PT used for diagnosis of tuberculosis and other mycobacterial diseases, also

PT for treatment and prevention, for drug screening and for bio-

PT transformation.

XX

PS Disclosure; Page 10; 57pp; German.

XX

CC AAV49512-V49526 are oligonucleotides used in a method to isolate an

CC alanine dehydrogenase (ADH) protein from a Mycobacterium sp. This protein

CC is used to diagnose tuberculosis and other mycobacterial infections

CC (including 'swimmers' disease', caused by M. marinum, a fish pathogen) in

CC humans or animals. The protein can also be used for control of epidemics

CC and for vaccination, to screen for agents with anti-mycobacterial

CC activity, and in bio-transformations that are specific for L-alanine.

CC Also mycobacteria can be identified by analysis of genomic ADH sequences.

OS Synthetic.

XX

PN EP463395-A.

XX

PD 02-JAN-1992.

XX

PF 29-MAY-1991; 91EP-00108867.

XX

PR 22-JUN-1990; 90EP-00810467.

XX

PA (HOFF) HOFFMANN-LA ROCHE AG.

XX

WPI; 1992-009068/02.

XX

PT New PCR primers for detecting poor metaboliser of drugs - useful to

PT highlight cases of debrisoquine, mephenytoin and acetylation-

PT polymorphism.

XX

PS Claim 11; Page 18; 31pp; English.

XX

CC The sequence is that of an oligonucleotide primer which is used in a

CC polymerase chain reaction (PCR) for the detection of normal and genes

CC coding for drug metabolising enzymes which allow the phenotyping of poor

CC metabolisers. Detection of debrisoquine polymorphism (CY2D6 gene -

CC encodes the P450IID6 enzyme) is possible using this primer. See also

CC AAQ20421-Q20436

XX

SQ Sequence 18 BP; 4 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. NO. 4.2e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGAAACC 1679

Db ||||| ||||| |||||

4 TCACAGCTGGAAATCC 18

RESULT 411

AAQ95428

ID AAQ95428 standard; DNA; 18 BP.

XX

AC AAQ95428;

XX

DT 08-FEB-1996 (first entry)

DE Primer B (Group 3, Set A) for marker DIS243, chromosome 1.

XX

KW primer; polymerase chain reaction; PCR; linkage study; locus;

KW microsatellite marker sequence; automated genotyping; allele;

KW polymorphism; detection; Homo sapiens; ss.

XX

OS Synthetic.

XX

PN WO9515400-A1.

XX

PD 08-JUN-1995.

XX

PF 05-DEC-1994; 94WO-US013945.

XX

PR 03-DEC-1993; 93US-00160837.

XX

PA (UVJO) UNIV JOHNS HOPKINS.

XX

PI Levitt RC;

XX

WPI; 1995-215278/28.

XX

PT Kit for automated genotyping contg. pairs of PCR primers - designed to

PT amplify polymorphic nucleotide repeat sequences, arranged in sets each

PT with a characteristic fluorescence label, useful e.g. in detection of

PT disease related genetic rearrangement.

XX

KW therapy; diagnosis; ss.
 -----; cancer; metastasis; angiogenesis;

```

PF 20-MAR-1998; 98WO-US0C5651.
XX
XX 21-MAR-1997; 97US-0041182P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Fett JW, Olson KA;
XX
XX WPI; 1998-531944/45.
XX
XX New oligo:nucleotide(s) that inhibit expression of angiogenin - for
XX treatment of tumours and metastases, or other conditions involving
XX abnormal angiogenesis.
XX
XX Example 4; Page 26; 71pp; English.
XX
XX Sense oligonucleotide JF1S encompasses the AUG initiation codon of the
XX human angiogenin gene (see AAV60918). Its sequence is complementary to
XX claimed antisense phosphorothioate oligonucleotide JF2S. JF2S, and other
XX claimed antisense oligonucleotides (see AAV60912-17) with base sequences
XX complementary to target regions of the angiogenin gene, are able to
XX inhibit expression of angiogenin. JF1S is used as a control
XX oligonucleotide in experiments with these antisense sequences. The
XX antisense oligonucleotides are used in claimed methods to decrease
XX production of angiogenin, particularly to reduce the size of tumours
XX associated with angiogenesis, to inhibit metastases, establishment of
XX tumour cells or growth of tumours and, when labelled, to detect
XX angiogenin for diagnosis of conditions associated with abnormal
XX angiogenesis
XX
XX Sequence 18 BP; 5 A; 1 C; 9 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 8.5%; Score 11.8; DB 1; Length 18;
XX Best Local Similarity 86.7%; Pred. No. 4.2e+02;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1722 GAGATGGAGATTGGC 1736
DB ||||| |||||
4 GAGATGGTGAATGGC 18
XX
RESULT 417
AXX86530
ID AAX86530 standard; DNA; 18 BP.
XX
XX AAX86530;
XX
XX 04-OCT-1999 (first entry)
XX
XX Primer rb21 used for amplification and sequencing of Rhd gene exons.
XX
XX Allele; Rhesus D antigen; RHD; weak D phenotype; blood transfusion;
XX PCR primer; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9937763-A2.
XX
XX 29-JUL-1999.
XX
XX 18-DEC-1998; 98WO-EF008319.
XX
XX 23-JAN-1998; 98EP-00101203.
XX
XX (DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG.
XX
XX Flegel WA, Wagner FF;
XX
XX WPI; 1999-469127/39.
XX
XX Nucleic acid sequences correlated with Rhesus weak D phenotype, useful
XX for screening blood from donors and recipients for transfusion methods.

```

XX
XX
XX Example; Page 33; 64pp; English.

CC PCR primers AAX86523-62 were used for amplification and sequencing of
CC exons of the Rhesus D (RhD) antigen gene. The specification and sequencing of
CC RhD contributing to or indicative of the weak D phenotype, where the RhD
CC polynucleotide carries at least one missense mutation as compared to the
CC wild-type RhD, in its transmembrane and/or intracellular regions,
CC especially in amino acid positions 2-16, 114-149, 179-225 or/and 267-397,
CC with the proviso that the D antigen does not carry a single missense
CC mutation leading to a F223V or T283I substitution. The probes and
CC antibodies are useful in the methods for detection of weak D phenotypes.
CC Red blood cells, from probands, are useful for the assessment of the
CC affinity, avidity and/or reactivity of monoclonal anti-D antibodies.
CC Polyclonal anti-D antisera or of anti-globulin or anti-human-globulin
CC antisera. Detecting the presence of the RhD associated with weak D
CC phenotype is useful for determining that a patient in need of a blood
CC transfusion is to be transfused with RhD negative blood from a donor.
CC Alternatively, testing for weak D phenotype RhD in the blood of a donor
CC is useful for determining whether the donor blood should be excluded for
CC transfusion to patients having wild type RhD or weak D types, other than
CC that of the donor weak D type

XX
XX
XX SQ Sequence 18 BP; 3 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTGTCCTCTCCAGC 1695
||| |||||
DB 2 GGTCCCTCTCCAGC 16

RESULT 418
AAA74957/c
ID AAA74957 standard; DNA; 18 BP.
AC AAA74957;
XX
XX
XX 02-JAN-2001 (first entry)
XX
XX PCR primer used to amplify a 316 bp fragment of murine VEGF-B gene.
XX VEGF-B; vascular endothelial growth factor-B; heart abnormality;
XX ischemia; atrioventricular conduction defect; myocardium; heart disease;
XX PCR primer; ss.
XX Mus sp.
XX
XX WO200052462-A1.
XX
XX 08-SEP-2000.
XX
XX 03-MAR-2000; 2000WO-US005465.
XX
XX 03-MAR-1999; 99US-0160083P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Aase K, Thoren P, Eriksson U;
XX WPI; 2000-638114/61.
XX
XX Use of vascular endothelial growth factor B deficient animals for
XX screening atrioventricular conduction or ischemia modulating compounds,
XX and characterization of the biological roles of the growth factor.
XX
XX Example 4; Page 31; 58pp; English.

XX
XX
XX PCR primers AAA74956-57 were used to amplify a 316 bp fragment from exons
CC 3 and 4 of the VEGF (vascular endothelial growth factor)-B. The primers
CC were used to analyse VEGF-B deficient transgenic mice. VEGF-B deficient

CC animals show heart abnormalities that appear to be caused by
CC atrioventricular conduction defects and ischemia of the myocardium. The
CC specification describes methods for screening a compound for
CC atrioventricular conduction or ischemia modulating activity. The method
CC comprises introducing the compound into a VEGF-B deficient non-human
CC animal, and assaying the effect on atrioventricular conduction or
CC ischemia. The methods are used for screening atrioventricular conduction
CC or ischemia modulating compounds, treatment or alleviation of these
CC conditions, diagnosis of heart disease characterized by loss of VEGF-B
CC expression, and detecting or diagnosing VEGF-B deficiency in heart of a
CC test subject

XX
XX SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1660 CAGGCTCACAGCTGG 1674
||| |||||
DB 17 CAGTCACACAGCTGG 3

RESULT 419
AAZ65415
ID AAZ65415 standard; DNA; 18 BP.
AC AAZ65415;
XX
XX 10-APR-2000 (first entry)
XX
XX Human CD71 phosphorothioate antisense oligonucleotide SEQ ID NO:66.
XX Human; CD71; transferrin receptor; antisense; phosphorothioate;
XX antiproliferative; anticancer; anti-inflammatory; gene therapy; ss.
XX Homo sapiens.
XX
XX US6004814-A.
XX
XX 21-DEC-1999.
XX
XX 25-SEP-1998; 98US-00161244.
XX
XX 25-SEP-1998; 98US-00161244.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowsert LM;
XX WPI; 2000-105082/09.
XX
XX Antisense oligonucleotides targeted to genes encoding CD71, useful for
XX preventing, diagnosing and treating inflammatory disorders and tumors.
XX
XX Claim 1; Col 27; 34pp; English.

XX
XX Sequences AAZ65357-Z65440 represent novel phosphorothioate antisense
XX oligonucleotides targetted against the human CD71 gene, which encodes the
XX CD71 transferrin receptor. Upon uptake in the small intestine, iron
XX immediately combines with the ubiquitous serum protein transferrin, the
XX primary vehicle by which iron is transported around the body. The uptake
XX of circulating iron-transferrin complexes is mediated by the transferrin
XX receptor, CD71. The requirement of both iron-transferrin complexes and
XX CD71 for cell proliferation suggests that inhibition of iron utilisation
XX could represent a strategy for the treatment of cancer. The
XX oligonucleotides may be used in the treatment of an animal suspected of
XX having a disease or disorder which can be treated by inhibition of CD71
XX expression. Use of the antisense compounds and methods of the invention
XX may also be useful prophylactically to prevent or delay infection,
XX inflammation or tumour formation. The antisense compounds may
XX additionally be useful for research and as diagnostic tools. The
XX antisense oligonucleotides provide a tool for effectively downregulating

DE Probe and primer for plant pathogen resistance proteins.
 XX DNA-binding domain; pathogen resistance protein; RRS1-S; RRS1-R;
 KW Ralstonia solanacearum; probe; primer; ss.
 XX

OS Arabidopsis thaliana.
 XX

XX FR279204-A1.
 XX

XX 06-APR-2001.
 XX

XX 01-OCT-1999; 99FR-00012315.
 XX

XX 01-OCT-1999; 99FR-00012315.
 XX

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX

XX Olivier J, Deslandes L, Marco Y;
 XX

XX WPI; 2001-275284/29.
 XX

XX New nucleic acid encoding pathogen-resistance protein from plants, useful
 PT for producing transgenic plants resistant particularly to Ralstonia
 PT solanacearum.
 XX

XX Claim 13; Page 67; 142pp; French.
 XX

XX AAF84555-AAF84605 represent probes and primers for DNA encoding plant
 CC pathogen resistance proteins, designated RRS1-S and RRS1-R. The pathogen
 CC resistance proteins contain a N-terminal region containing at least one
 CC Leu-rich sequence and at least one nucleotide-binding site, and a C-
 CC terminal region with a DNA-binding domain containing the present
 CC sequence. RRS1 polynucleotides are used for in vivo or in vitro
 CC expression of the RRS1-S or RRS1-R proteins (or their fragments),
 CC especially in transgenic plants, or as antisense sequences, for blocking
 CC or inhibiting expression of these genes. Fragments of these
 CC polynucleotides are useful as probes and primers for detection/
 CC amplification of these genes. The RRS1-R protein confers resistance to
 CC pathogens, specifically the bacterium Ralstonia solanacearum. The 3'- and
 CC 5'-regulatory regions from these genes may be used to control expression
 CC of other genes, e.g. those encoding toxic peptides that induce death of
 CC plant cells, thus blocking spread of pathogens. RRS1 proteins are used to
 CC raise antibodies, and to screen for agents that bind to RRS1-R or RRS1-S
 CC proteins
 XX

XX Sequence 18 BP; 3 A; 8 C; 2 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 8.5%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1741 AACTCTCTCCCTATCC 1755
 Db 1 AACTCTCTCCATGCC 15

RESULT 423
 AAS03672
 ID AAS03672 standard; DNA; 18 BP.
 XX
 XX AAS03672;
 XX

XX 29-AUG-2001 (first entry)
 XX
 XX PCR primer rb21, used to detect RHD positive haplotypes.
 XX
 XX Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; SMP1;
 KW RHCE; RHD negative; blood group typing; blood transfusion; antigen C;
 KW haemolytic disease of the newborn; chromosome 1 p34.1-p36; primer; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200132702-A2.
 PN

XX 10-MAY-2001.
 XX
 XX 31-OCT-2000; 2000WO-EP010745.
 XX
 XX 02-NOV-1999; 99EP-00121686.
 XX
 XX 31-MAY-2000; 2000EP-00111696.
 XX
 XX (DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG.
 XX

XX Flegel WA, Wagner FF;
 XX

XX WPI; 2001-291052/30.
 XX

XX New nucleic acid molecular structure, useful for detection of common RHD
 PT positive haplotypes in D-negative individuals, comprises RHD, SMP1 and
 PT RHCE genes.
 XX

XX Example 12; Page 66; 135pp; English.
 XX

XX The sequence represents PCR primer rb21, used to detect RHD positive
 CC haplotypes in RHD negative individuals. The primer was used in DNA typing
 CC using PCR-sequence length polymorphism (SSP) of the Rhesus genes locus
 CC comprising the RHD, SMP1 and RHCE (all undefined) genes and/or the Rhesus
 CC box(es), preferably the hybrid Rhesus box, the upstream Rhesus box and/or
 CC the downstream Rhesus box. The RHD and RHCE genes are located at
 CC chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the
 CC RHD deletion in the common RHD negative haplotypes. The primers of the
 CC invention are useful for: (1) the specific detection of the common RHD
 CC positive haplotypes in D-negative individuals; (2) blood group typing;
 CC (3) determining whether a patient can be transfused with RHD negative
 CC blood and whether blood is suitable for transfusion to patients who
 CC should not be exposed to antigen C; (4) assessing the risk of a RHD
 CC negative mother of conceiving or carrying an RHD positive foetus. Anti-D
 CC antibodies are useful for treating pregnant women who are Rhesus D
 CC negative, where the foetus is not homozygous for the RHD gene to treat or
 CC prevent haemolytic disease of the newborn
 XX

XX Sequence 18 BP; 3 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 8.5%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTGTCTCTCTCCAGC 1695
 Db 2 GGTCTCTCTCTCCAGC 16

RESULT 424
 ABZ72191/c
 ID ABZ72191 standard; DNA; 18 BP.
 XX
 XX ABZ72191;
 XX

XX 03-APR-2003 (first entry)
 XX
 XX Gene 216 SSCP sequencing primer SEQ ID NO 163.
 DE
 DE Human: Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;
 KW antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;
 KW obesity; inflammatory bowel disease; primer; ss.
 XX
 XX Synthetic.
 XX
 XX WO200178894-A2.
 PN

XX 25-OCT-2001.
 XX

XX 13-APR-2001; 2001WO-US012245.
 XX

XX 13-APR-2000; 2000US-00548797.
 XX

XX	20-JUL-2000; 2000EP-00202611.
XX	(AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX	PA Loukachov VV, Van Gemen B, Goudsmit J;
XX	PI WPI; 2001-639428/73.
XX	DR WPI; 2002-156696/21.
XX	Collection of binding groups for determining or typing samples,
XX	especially clinical samples, has groups capable to identify essentially
XX	all members of the family of nucleic acids of relatively high
XX	significance.
XX	Disclosure; Page 10; 165pp; English.
XX	The present invention describes a collection of binding groups for a
XX	family of nucleic acids comprising members of relative high and relative
XX	low significance, where the binding groups are selected to be capable to
XX	identify, alone or in combination, essentially all members of the family
XX	of nucleic acids of relatively high significance. The collection of
XX	binding groups is useful for typing of nucleic acid in a clinical sample,
XX	by contacting the nucleic acid with the collection and determining
XX	whether one or more binding groups bound to the nucleic acid of the
XX	sample. This method is useful for determining whether the sample
XX	comprises at least a part of a member of relatively high significance of
XX	a family of nucleic acids. The collection of binding groups is useful for
XX	diagnosing the severity of a disease caused by a pathogen containing a
XX	member of a family of nucleic acids. ABL88779 to ABL89321 represent
XX	oligonucleotide sequences used in the exemplification of the present
XX	invention
XX	Sequence 18 BP; 8 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
XX	Query Match 8.5%; Score 11.8; DB 1; Length 18;
XX	Best Local Similarity 86.7%; Pred. No. 4.2e+02;
XX	Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1717 GTACGGAGATGGAGA 1731
DB	1 GTACAGAAATGGAGA 15
RESULT 426	
ABL88789	
ID	ABL88789 standard; DNA; 18 BP.
XX	AC ABL88789;
XX	22-MAY-2002 (first entry)
XX	HIV-1 related binding molecule oligonucleotide sequence SEQ ID NO:11.
XX	Binding molecule; HIV-1; human immunodeficiency virus type 1;
XX	reverse transcriptase; binding group; ss.
XX	Human immunodeficiency virus 1.
XX	Synthetic.
XX	EP1174518-A1.
XX	23-JAN-2002.
XX	20-JUL-2000; 2000EP-00202611.
XX	20-JUL-2000; 2000EP-00202611.
XX	(AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX	Loukachov VV, Van Gemen B, Goudsmit J;
XX	WPI; 2002-156696/21.

XX	20-JUL-2000; 2000EP-00202611.
XX	(AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX	PA Loukachov VV, Van Gemen B, Goudsmit J;
XX	PI WPI; 2001-639428/73.
XX	DR WPI; 2002-156696/21.
XX	Collection of binding groups for determining or typing samples,
XX	especially clinical samples, has groups capable to identify essentially
XX	all members of the family of nucleic acids of relatively high
XX	significance.
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XX	family of nucleic acids comprising members of relative high and relative
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XX	identify, alone or in combination, essentially all members of the family
XX	of nucleic acids of relatively high significance. The collection of
XX	binding groups is useful for typing of nucleic acid in a clinical sample,
XX	by contacting the nucleic acid with the collection and determining
XX	whether one or more binding groups bound to the nucleic acid of the
XX	sample. This method is useful for determining whether the sample
XX	comprises at least a part of a member of relatively high significance of
XX	a family of nucleic acids. The collection of binding groups is useful for
XX	diagnosing the severity of a disease caused by a pathogen containing a
XX	member of a family of nucleic acids. ABL88779 to ABL89321 represent
XX	oligonucleotide sequences used in the exemplification of the present
XX	invention
XX	Sequence 18 BP; 8 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
XX	Query Match 8.5%; Score 11.8; DB 1; Length 18;
XX	Best Local Similarity 86.7%; Pred. No. 4.2e+02;
XX	Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1717 GTACGGAGATGGAGA 1731
DB	1 GTACAGAAATGGAGA 15
RESULT 426	
ABL88789	
ID	ABL88789 standard; DNA; 18 BP.
XX	AC ABL88789;
XX	22-MAY-2002 (first entry)
XX	HIV-1 related binding molecule oligonucleotide sequence SEQ ID NO:11.
XX	Binding molecule; HIV-1; human immunodeficiency virus type 1;
XX	reverse transcriptase; binding group; ss.
XX	Human immunodeficiency virus 1.
XX	Synthetic.
XX	EP1174518-A1.
XX	23-JAN-2002.
XX	20-JUL-2000; 2000EP-00202611.
XX	20-JUL-2000; 2000EP-00202611.
XX	(AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX	Loukachov VV, Van Gemen B, Goudsmit J;
XX	WPI; 2002-156696/21.

PT Collection of binding groups for determining or typing samples,
 PT especially clinical samples, has groups capable to identify essentially
 PT all members of the family of nucleic acids of relatively high
 XX significance.
 XX
 PS Disclosure; Page 9; 166pp; English.
 XX
 CC The present invention describes a collection of binding groups for a
 CC family of nucleic acids comprising members of relative high and relative
 CC low significance, where the binding groups are selected to be capable to
 CC identify, alone or in combination, essentially all members of the family
 CC of nucleic acids of relatively high significance. The collection of
 CC binding groups is useful for typing of nucleic acid in a clinical sample,
 CC by contacting the nucleic acid with the collection and determining
 CC whether one or more binding groups bound to the nucleic acid of the
 CC sample. This method is useful for determining whether the sample
 CC comprises at least a part of a member of relatively high significance of
 CC a family of nucleic acids. The collection of binding groups is useful for
 CC diagnosing the severity of a disease caused by a pathogen containing a
 CC member of a family of nucleic acids. ABL8779 to ABL8921 represent
 CC oligonucleotide sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 18 BP; 8 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1717 GTACGAGATGGAGA 1731
 ||||| |||||
 Db 1 GTACAGAGATGGAAA 15
 RESULT 427
 ABA97088/C
 ID ABA97088 standard; DNA; 18 BP.
 XX AC ABA97088;
 XX
 XX ABA97088;
 XX
 XX 17-APR-2002 (first entry)
 XX
 XX Human cathepsin B PCR primer #2.
 XX Human; PCR; primer; detection; cathepsin; leucocystatin; metastasis;
 XX tumour; asparaginyl endopeptidase; cathepsin B; ss.
 XX Homo sapiens.
 XX WO200198475-A2.
 XX
 XX 27-DEC-2001.
 XX
 XX 15-JUN-2001; 2001WO-EP006791.
 XX
 XX 23-JUN-2000; 2000DR-01030827.
 XX
 XX (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.
 XX
 XX Melms A, Wienhold W, Tolosa E;
 XX WPI; 2002-122278/16.
 XX
 XX Detecting nucleic acid that encodes cathepsins and related proteins, for
 XX diagnosis of tumors, comprises amplification with specific primers.
 XX
 XX Claim 4; Page 35; 39pp; German.
 XX
 CC This invention describes a novel method for the selective detection of
 CC nucleic acids that are specific for cathepsins, asparaginyl endopeptidase
 CC or leucocystatin. The method is used for diagnosis and/or early detection
 CC of tumors and/or their metastases, associated with overexpression of
 CC cathepsins, and also for evaluating treatment. The method is reliable,

CC simple and reproducible, since the PCR primers of the invention have very
 CC high specificity and sensitivity for their targets, including ability to
 CC differentiate between closely similar cathepsins. Only a small amount of
 CC sample, obtained by minimally invasive methods, is required. The PCR
 CC primers of the invention are designed to generate amplicons of 100-150bp,
 CC ensuring practically 100 % amplification efficiency, without non-specific
 CC amplification that could lead to false positives. This sequence
 CC represents a PCR primer used in the amplification of the human cathepsin
 CC B and is used to illustrate the method of the invention
 XX
 SQ Sequence 18 BP; 5 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1733 TGGCTCCCAACTCCT 1747
 ||||| |||||
 Db 17 TGGTTGCCCAACTCCT 3
 RESULT 428
 ABL44660
 ID ABL44660 standard; DNA; 18 BP.
 XX AC ABL44660;
 XX
 XX 11-APR-2002 (first entry)
 XX
 XX Human chromosome lp36-35 PCR primer SEQ ID NO:1704.
 XX Human; chromosome lp36-35; chromosome 21q22.1; genetic analysis; genome;
 XX PCR primer; ss.
 XX Homo sapiens.
 XX JP2001321190-A.
 XX
 XX 20-NOV-2001.
 XX
 XX 12-MAR-2001; 2001JP-00068285.
 XX
 XX 10-MAR-2000; 2000JP-00066716.
 XX (RIKA) RIKAGAKU KENKYUSHO.
 XX (GENO-) GENOTEX YG.
 XX WPI; 2002-144136/19.
 XX
 XX Arraying genome clones.
 XX
 XX Claim 4; Page 38; 528pp; Japanese.
 XX
 CC The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each wells of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome lp36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are

CC specifically claimed for use in the present invention

XX Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

SQ Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1689 CTCGAGCTGGTGGGA 1703
Db 2 CTCGAGCTGGTGGGA 16

RESULT 429

ABK94528

ID ABK94528 standard; DNA; 18 BP.

XX

AC ABK94528;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human BRCA1 gene reverse PCR primer for exon 21.

XX

KW hMLH1; DNA mismatch repair; BRCA1; ss; PCR; primer; BRCA1;

KW breast and ovarian cancer susceptibility gene; TGDS; human;

KW two-dimensional DNA electrophoresis; tumour suppressor gene;

KW breast cancer; ovarian cancer; tumour.

XX

OS Homo sapiens.

XX

PN WO200236819-A1.

XX

PD 10-MAY-2002.

XX

PF 06-NOV-2000; 2000WO-IB001607.

XX

PR 06-NOV-2000; 2000WO-IB001607.

XX

PA (SCSC-) ACAD APPLIED SCI.

XX

PI Vijg J;

XX

DR WPI; 2002-471507/50.

XX

PT Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting

PT amplification products to 2-dimensional gel electrophoresis to produce a

PT characteristic spot pattern for a specific mutation in either the BRCA1

PT or the hMLH1 gene.

XX

PS Claim 1; Page 52; 57pp; English.

XX

CC The invention relates to detecting mutations in the BRCA1 and hMLH1 gene

CC comprising subjecting a set of amplification products to two-dimensional

CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a

CC specific mutation in either the BRCA1 or the hMLH1 gene. Also included

CC are test kits for enabling BRCA1 or hMLH1 gene testing comprising short

CC PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM

CC KCl, 25 mM of dNTP, and 5 % formamide. The method is useful for

CC detecting mutations in the BRCA1 (breast and ovarian cancer

CC susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA

CC mismatch repair gene). The present sequence is a PCR primer specific to

CC BRCA1 used in the method of the invention

XX

SQ Sequence 18 BP; 2 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. No. 4.2e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1671 CTGGAACCTGGTGT 1685
Db 1 CTGGAACCTGGGT 15

RESULT 430

ABS97999

ID ABS97999 standard; DNA; 18 BP.

XX

AC ABS97999;

XX

DT 23-DEC-2002 (first entry)

XX

DE Human urokinase gene (uPA) PCR primer #14.

XX

KW Human; ss; primer; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1; PCR;

KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;

KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;

KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;

KW NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase 2B7;

KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;

KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;

KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;

KW multidrug resistance associated protein 3; cancer; prostate;

KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;

KW altered drug metabolism; cardiovascular function; colorectal tumour;

KW central nervous system; pulmonary; immunological.

XX

OS Homo sapiens.

XX

PN WO200257410-A2.

XX

PD 25-JUL-2002.

XX

PF 28-NOV-2001; 2001WO-US044838.

XX

PR 28-NOV-2000; 2000US-00724389.

XX

PA (DNAS-) DNA SCI LAB INC.

XX

PI Guida M, Hall J;

XX

DR WPI; 2002-698522/75.

XX

PT Isolated nucleic acid molecules having polymorphisms in known human genes

PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers

PT for locating, identifying and characterizing the genes responsible for

PT disorder-related traits.

XX

PS Example 21; Page 139; 714pp; English.

XX

CC This invention relates to the sequence of an isolated nucleic acid

CC molecule comprising at least one base variation from that of a known

CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),

CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),

CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator

CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding

CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating

CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl

CC transferase (HNMT), kallikrein 2 (KLK2), nicotinamide -N-methyl

CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),

CC sulfoxidoreductase 2B7 (UGT2B7), UDP-glucuronosyl

CC transferase (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl

CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1

CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3

CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic

CC receptor 1, 2, 3, 4, cr 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.

CC The polymorphisms in the human genes cited in the invention are useful as

CC genetic linkage markers for locating and characterising the genes that

CC are responsible for specific traits within the genome and eventually

CC identifying the genes responsible for a variety of disorder-related

CC traits as a result of their e.g., overexpression, constitutive

CC expression, mutation or underexpression, which may be used in diagnosing

CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC nervous system function, in FLAP and NNMT for altered pulmonary,
 CC immunological or haematological function, in KIK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central
 CC peripheral nervous system function. The present sequence represents a PCR
 CC primer used to amplify the sequences of the invention
 XX
 SQ Sequence 18 BP; 4 A; 9 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1739 CCAACTCTCTCCCTAT 1753
 Db 4 CCAACTCTCTCCCAT 18
 RESULT 431
 ABS98011
 ID ABS98011 standard; DNA; 18 BP.
 AC ABS98011;
 XX
 DT 23-DEC-2002 (first entry)
 DE Human urokinase gene (uPA) sequencing primer #12.
 XX
 KW Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
 KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRE3; NR1I2;
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KW NNMT; kallikrein 2; KIK2; nicotinamide-N-methyl transferase; NNMT;
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase; STM;
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KW multidrug resistance associated protein 3; cancer; prostate;
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KW altered drug metabolism; cardiovascular function; colorectal tumour;
 KW central nervous system; pulmonary; immunological; sequencing.
 XX
 OS Homo sapiens.
 XX
 PN WO200257410-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 28-NOV-2001; 2001WO-US044838.
 XX
 PR 28-NOV-2000; 2000US-00724389.
 XX
 XX (DNAS-) DNA SCI LAB INC.
 PA
 XX Guida M, Hall J;
 PI
 XX WPI; 2002-698522/75.
 DR
 XX Isolated nucleic acid molecules having polymorphisms in known human genes
 PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for

PT disorder-related traits.
 XX
 PS Example 21; Page 139; 714pp; English.
 XX
 CC This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoxyltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and NNMT for altered pulmonary,
 CC immunological or haematological function, in KIK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC sequencing primer used to sequence the polymorphic genes of the invention
 XX
 SQ Sequence 18 BP; 4 A; 9 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1739 CCAACTCTCTCCCTAT 1753
 Db 4 CCAACTCTCTCCCAT 18
 RESULT 432
 ABL30541/C
 ID ABL30541 standard; DNA; 18 BP.
 XX
 AC ABL30541;
 XX
 DT 21-MAR-2002 (first entry)
 XX
 DE Human HLA genotyping oligonucleotide SEQ ID NO 30.
 XX
 KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
 KW immunogenetic; transplantation; genetic disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192572-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 01-JUN-2001; 2001WO-JF004662.

Mon Aug 30 09:26:45 2004

polymorphic bovine acyl CoA-diacylglycerol transferase gene useful for testing a mammal for its predisposition for fat content of milk and for meat marbling.

Example 1; Page 36; 91pp; English.

The present invention describes a nucleic acid molecule (NA) (I) encoding a bovine acyl CoA-diacylglycerol transferase (DGAT) contributing to or indicative for low fat content of milk and to low meat marbling (intramuscular fat content). Human DGAT is located to chromosome 8, and bovine DGAT is located to chromosome 14. (I) is useful for testing a mammal for its predisposition for fat content of milk and/or its predisposition for meat marbling. The method comprises analysing the gene encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide polymorphisms (SNPs)) which are connected with the predisposition. The nucleotide polymorphisms are located in the coding region of the DGAT gene and result in substitution, deletion and/or addition of an amino acid sequence of the polypeptide which is encoded by the gene. The nucleic acid molecule has at the position 10433 and 10434 of the DGAT gene a guanine and a cytosine residue, at position 3343 a cytosine or guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a thymine, which correlate with a predisposition for low fat content of milk and low meat marbling. The nucleic acid molecule has at the position corresponding to position 10433 and 10434 of the DGAT gene two adenine residues which correlate with a predisposition for high content of milk and high meat marbling. The nucleotide polymorphisms are located in a region which is responsible for the regulation of the expression of the product of the gene encoding DGAT. ABZ76924 to ABZ77045 and ABP96035 to ABP96046 represent sequences used in the exemplification of the present invention

Sequence 18 BP; 3 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAAACCT 1680
DB 1 CACAGCTGGCTCCT 15

RESULT 434
ABZ75044/c
ID ABZ75044 standard; DNA: 18 BP.

AC ABZ75044;

DT 25-MAR-2003 (first entry)

DE Human gene 216 polymorphism detection PCR primer #101.

XX Human; mouse; ss; primer; gene 216; antiasthmatic; antiinflammatory;
KW anorectic; chromosome 20p13-p12; single nucleotide polymorphism; SNP;
KW gene therapy; respiratory disease; asthma; obesity; PCR;
KW bronchial hyper-responsiveness; chronic obstructive pulmonary disease;
KW adult respiratory distress syndrome; inflammatory bowel syndrome.

OS Homo sapiens.

PN WO200283077-A2.

PD 24-OCT-2002.

XX 15-APR-2002; 2002WO-US012063.

PF 06-JUL-2001; 2001EP-00116412.

PR 13-MAY-2002; 2002US-0379412P.

XX (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.

PA (SCHE) SCHERING CORP.

PA (GENO-) GENOME THERAPEUTICS CORP.

XX Keith T, Little RD, Van Eerdewegh P, Dupuis J, Del Mastro RG;

PT New nucleic acid molecule comprising a sequence of an allele of a

XX 01-JUN-2000; 2000JP-00164798.
PR (NISN) NISSHINEO IND INC.
XX (SYST-) SYSTEM RES INC.
PA Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX WPI; 2002-122074/16.
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of individuals e.g. by determining immunogenetic differences when transplanting between them.
PT Claim 10; Page 99; 345pp; Japanese.

XX The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucleotides (AB130512-AB131809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them, providing genetic information to decide compatibility of organ and tissue for transplantation e.g. of bone marrow, kidney, liver, pancreas, Langerhans islet in pancreas and cornea, susceptibility diagnosis of genetic diseases and identifying individuals

XX Sequence 18 BP; 1 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1650 AGGCAAGCACCAGGC 1664
DB 18 AGGCAACACACAGAC 4

RESULT 433
ABZ76994
ID ABZ76994 standard; DNA: 18 BP.

AC ABZ76994;

DT 07-MAY-2003 (first entry)

DE Bovine DGAT PCR primer #30.

XX Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;
KW milk; meat marbling; low fat; polymorphic; SNP;
KW single nucleotide polymorphism; PCR primer; ss.

OS Bos taurus.

OS Synthetic.

PN WO2003004630-A2.

PD 16-JAN-2003.

XX 05-JUL-2002; 2002WO-EP007520.

PR 06-JUL-2001; 2001EP-00116412.

XX 13-MAY-2002; 2002US-0379412P.

XX (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.

XX Fries H, Winter A;

XX WPI; 2003-239205/33.

XX New nucleic acid molecule comprising a sequence of an allele of a

PI Simon J, Allen K, Pandit S;
 XX WPI; 2003-092960/08.
 XX
 PT New isolated gene 216 nucleic acids, useful for diagnosing, preventing or
 PT treating a disorder, such as asthma, bronchial hyper-responsiveness,
 PT chronic obstructive pulmonary disease, obesity or inflammatory bowel
 PT syndrome.
 XX
 PS Example 10; Page 156; 650pp; English.
 XX
 CC This invention relates to a novel isolated nucleic acid, gene 216,
 CC identified from human chromosome 20p13-p12. The invention also discloses
 CC regions of the 216 gene that contain single nucleotide polymorphisms
 CC (SNP's) which may be used as markers for disease susceptibility or
 CC severity. The nucleotides of the invention may have antiasthmatic,
 CC antiinflammatory or anorectic activities and may be used in gene therapy.
 CC The nucleic acids, antibodies or its fragments are useful for diagnosing,
 CC preventing or treating a disorder, such as respiratory diseases (e.g.
 CC asthma, bronchial hyper-responsiveness, chronic obstructive pulmonary
 CC disease or adult respiratory distress syndrome), obesity, or inflammatory
 CC bowel syndrome. The nucleic acids are also useful for identifying
 CC increased susceptibility of a subject to the disorders mentioned. The
 CC nucleic acids can also be used as primers and templates for the
 CC recombinant production of disorder-associated peptides or polypeptides,
 CC for chromosome and gene mapping, or for tissue distribution studies. The
 CC present sequence represents a gene 216 specific PCR primer used in the
 CC scope of the invention
 XX
 SQ Sequence 18 BP; 2 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1649 AAGGCAAGCACCAGG 1663
 Db | ||| ||||| |||||
 17 ATGGGAAGCACCAGG 3
 RESULT 435
 ABZ58715
 ID ABZ58715 standard; DNA; 18 BP.
 XX
 AC ABZ58715;
 DT 14-APR-2003 (first entry)
 DE Human HAM cDNA fragment A sequencing sense primer.
 XX
 KW HAM; homologue of attractin/mahogany; immunosuppressive; cytostatic;
 KW antiinflammatory; cardiant; osteopathic; gene therapy; human; PCR;
 KW primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200297120-Al.
 XX
 PD 05-DEC-2002.
 XX
 XX 23-MAY-2002; 2002WO-US016391.
 XX
 XX 25-MAY-2001; 2001US-0293608P.
 PR 24-SEP-2001; 2001US-0324626P.
 XX
 XX (IMMUNEX CORP.
 PA
 XX
 PI Anderson DM;
 XX
 XX WPI; 2003-140486/13.
 DR
 XX New Homologue of Attractin/Mahogany (HAM) polypeptide, useful for
 PT treating HAM-associated disorder consisting of inflammatory, autoimmune,

PT cell proliferative or cardiovascular disorders.
 XX
 PS Example 1; Page 35; 89pp; English.
 XX
 CC The invention relates to Homologue of Attractin/Mahogany (HAM)
 CC polypeptides and encoding polynucleotides. The HAM polypeptides can be
 CC expressed by standard recombinant methodology. The HAM polypeptides are
 CC useful for treating HAM-associated disorder consisting of inflammatory,
 CC autoimmune, graft-versus-host, neurological, myelination, cell
 CC proliferative, cardiovascular, haematologic, liver, metabolic, weight or
 CC bone disorder. Sequences ABZ58715-26 represent PCR primers used for
 CC sequencing the human HAM cDNA
 XX
 SQ Sequence 18 BP; 5 A; 1 C; 10 G; 2 T; 0 U; 0 Other;
 Query Match 8.5%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1721 GGAGATGGAGATTGG 1735
 Db | ||||| ||||| |||||
 4 GAAGATGGAGACTGG 18
 RESULT 436
 ADC59461/c
 ID ADC59461 standard; DNA; 18 BP.
 XX
 AC ADC59461;
 DT 18-DEC-2003 (first entry)
 XX
 DE Human precutin PCR primer, SEQ ID NO:14, used in expression analysis.
 XX
 KW Human; epiplakin; epidermal autoantigen; autoimmune disease;
 KW skin disease; transgenic animals; diagnosis; drug screening; pemphigoid;
 KW pemphigus; dermatological; immunosuppressive; expression analysis;
 KW precutin; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2003047469-A.
 XX
 PD 18-FEB-2003.
 XX
 PF 16-JUL-2001; 2001JP-00216025.
 XX
 PR 16-JUL-2001; 2001JP-00216025.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 XX WPI; 2003-508702/48.
 XX
 XX Novel protein having epiplakin activity, useful for screening agents
 XX which inhibit and activate epiplakin activity, and for treating
 XX autoimmune skin disease such as pemphigoid or pemphigus.
 PS
 XX Example 4; SEQ ID NO 15; 55pp; Japanese.
 XX
 CC The invention relates to a 450 kD human epidermal autoantigen, epiplakin
 CC (ADC59448), and nucleic acids encoding it (ADC59447). The invention also
 CC encompasses an epiplakin antigenic epitope (ADC59449) which is reactive
 CC with serum from patients with autoimmune disease, fusion polypeptides
 CC containing epiplakin or its epitope, an antibody against epiplakin, host
 CC cells comprising human epiplakin nucleic acids, transgenic animals, which
 CC under- or over-express epiplakin, epiplakin nucleic acid probes for
 CC diagnosis of autoimmune disease, and methods of screening for agents
 CC which modulate epiplakin activity. Epiplakin polypeptides and
 CC polynucleotides are useful in drug screening for agents which promote or
 CC inhibit the activity of epiplakin which can be used in the treatment of
 CC autoimmune disease, particularly those of the skin such as pemphigoid or
 CC pemphigus. Epiplakin antibodies and nucleic acid probes are useful for
 CC diagnosis of these diseases. Sequences ADC59461-ADC59462 represent human

Mon Aug 30 09:26:45 2004

CC precut PCR primers used to generate a probe used in expression analysis
 CC in an example of the invention.

XX Sequence 18 BP; 5 A; 7 C; 5 G; 1 T; 0 U; 0 Other;
 SQ Query Match 8.5%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1687 TCCTCCAGCGGTG 1701
 Db 18 TCGTCCACCGTGTG 4

RESULT 437
 ADE13404
 ID ADE13404 standard; DNA; 18 BP.
 XX AC ADE13404;
 XX 29-JAN-2004 (first entry)
 DE HLA class I allele specific primer #20.
 XX ss; primer; PCR; human; Human Leukocyte Antigen; HLA; genotype.
 KW Homo sapiens.
 OS Homo sapiens.
 XX US2003165884-A1.
 PN 04-SEP-2003.
 PD 25-APR-2002; 2002US-00133779.
 PF 20-DEC-1999; 99US-0172768P.
 PR 20-DEC-2000; 2000US-00747391.
 XX (STEM-) STEM-CYTE INC.
 PA Chow R, Tonai R;
 PI WPI; 2003-874916/81.
 DR Identifying class I or II Human Leukocyte Antigen genotypes using
 PT hybridization and amplification assays.
 XX Claim 7; SEQ ID NO 20; 66pp; English.

XX The invention relates to a method of identifying a class I or II Human
 CC Leukocyte Antigen (HLA) genotype of a subject using hybridisation and
 CC amplification assay. The method is used for determining the HLA genotype
 CC of a subject. The present sequence represents a HLA class I allele
 CC specific primer.

XX Query Match 8.5%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1653 CAAGCACCAGGCTCA 1667
 Db 2 CAAGCGCCAGGCACA 16

RESULT 438
 AAH78641/c
 ID AAH78641 standard; DNA; 20 BP.
 XX AC AAH78641;
 XX 10-DEC-2001 (first entry)
 DT

XX Homo sapiens.

Probe for mechanically sensitive potassium channel gene fragment.

Human; mechanically sensitive potassium channel; riluzole; TWICK;
 polyunsaturated fatty acid; arachidonic acid; hTRAAC; chromosome 11q13;
 neuronal excitation; muscle excitation; cardiac rhythm; anoxia;
 hormone secretion; cardiac disease; vascular disease; ischemia;
 nervous system disorder; endocrinal disease; muscle disease;
 retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration; probe;
 ss.

Homo sapiens.
 WO200168670-A2.
 20-SEP-2001.

14-MAR-2001; 2001WO-FR000758.
 14-MAR-2000; 2000FR-00003264.

(CNRS) CNRS CENT NAT RECH SCI.
 Lazdunski M, Lesage F, Maingret F;
 WPI; 2001-590037/66.

New mechanically sensitive potassium channel, useful for treating
 cardiovascular diseases and in drug screening, is activated by
 polyunsaturated fatty acids.
 Disclosure; Page 15; 37pp; French.

The present probe was used to detect a gene fragment of the human
 mechanically sensitive potassium channel gene. The channel is activated
 by polyunsaturated fatty acids (particularly arachidonic acid (AA)) and
 by riluzole. The polypeptide is designated human TWICK-related AA-
 activated potassium channel (hTRAAC). The hTRAAC gene is located on
 chromosome 11q13. hTRAAC is involved in regulation of neuronal and muscle
 excitation, cardiac rhythm and secretion of hormones. Cells that express
 hTRAAC, designated to screen for modulators of hTRAAC activity. Such
 modulators are potentially useful for prevention or treatment, in humans
 and animals, of: cardiac and/or vascular disease; nervous system
 disorders associated with ischemia and anoxia; endocrinal diseases
 associated with anomalous hormone secretion or muscle diseases; and
 retinal diseases. Typical examples are epilepsy, cardiac arrhythmia and
 neurodegeneration

Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 20;
 Best Local Similarity 86.7%; Pred. No. 4.8e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1668 CAGCTGGACCTCG 1682
 Db 15 CAGCTGGACCTCG 1

RESULT 439
 ABH66153/c
 ID ABH66153 standard; DNA; 13 BP.

AC ABH66153;
 XX 22-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 266130 for detecting SNP TSC0064482.

SNP; single nucleotide polymorphism; human; diagnosis; PNB; cancer; CNS;
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX PN WO200177384-A2..
 XX XX 18-OCT-2001.
 XX PD 06-APR-2001; 2001WO-IB000713.
 XX PF 07-APR-2000; 2000DE-01019173.
 XX PR (EPIG-) EPIGENOMICS AG.
 XX PA Olek A, Piepenbrock C, Berlin K;
 XX PI WPI; 2001-657177/75.
 XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX PT designed to detect single-nucleotide polymorphisms and cytosine
 XX PT methylation status.
 XX XX Claim 1; SEQ ID NO 266130; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;
 CC Query Match 8.3%; Score 11.6; DB 1; Length 13;
 CC Best Local Similarity 91.7%; Pred. No. 3e+02;
 CC Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1722 GAGATGGAGATT 1733
 Db 12 GAGATGGAGATT 1
 RESULT 440
 ABH66152
 ID ABH66152 standard; DNA; 13 BP.
 XX AC ABH66152;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 266129 for detecting SNP TSC0064482.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX XX WO200177384-A2.
 XX XX 18-OCT-2001.
 XX XX 06-APR-2001; 2001WO-IB000713.
 XX XX 07-APR-2000; 2000DE-01019173.
 XX XX (EPIG-) EPIGENOMICS AG.
 XX XX Olek A, Piepenbrock C, Berlin K;
 XX XX WPI; 2001-657177/75.
 XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX PT designed to detect single-nucleotide polymorphisms and cytosine
 XX PT methylation status.
 XX XX Claim 1; SEQ ID NO 266130; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;
 CC Query Match 8.3%; Score 11.6; DB 1; Length 13;
 CC Best Local Similarity 91.7%; Pred. No. 3e+02;
 CC Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 266129; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 1 Other;
 CC Query Match 8.3%; Score 11.6; DB 1; Length 13;
 CC Best Local Similarity 91.7%; Pred. No. 3e+02;
 CC Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1722 GAGATGGAGATT 1733
 Db 2 GAGATGGAGATT 13
 RESULT 441
 AAZ44834
 ID AAZ44834 standard; DNA; 15 BP.
 XX AC AAZ44834;
 XX DT 27-APR-2000 (first entry)
 XX DE H. annuus sld1 homologue primer BN1.
 XX KW Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material; primer; ss.
 XX OS Helianthus annuus.
 XX XX DE19828850-A1.
 XX PN 30-DEC-1999.
 XX PD 27-JUN-1998; 98DE-01028850.
 XX PF 27-JUN-1998; 98DE-01028850.
 XX PR (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 XX PA Heinz E, Zaehrer U, Schmidt H, Sperling P;
 XX PI WPI; 2000-127549/12.
 XX DR New sphingolipid desaturase that selectively introduces double bond into
 XX PT sphingolipids and capnoids.
 XX PS Example 1; Page 24; 62pp; German.
 XX CC This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to

CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered delta
 CC -8-unsaturated long-chain base cis/trans ratio, especially to compensate
 CC for a delta-8-unsaturated long-chain base deficiency, to exclude
 CC production of delta-8-unsaturated bases, to increase tolerance or
 CC resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents a primer used in the isolation of a
 CC sphingolipid desaturase protein sidi homologue fragment isolated from
 CC *Halanthus annuus* which is used in the method of the invention
 XX
 XX Sequence 15 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 3 Other;

Query Match 8.3%; Score 11.6; DB 1; Length 15;
 Best Local Similarity 73.3%; Pred. No. 3.7e+02; Gaps 0;
 Matches 11; Conservative 2; Mismatches 2; Indels 0;

QY 1694 GCGTGGTGAAGTTG 1708
 | : ||||| : |
 DB 1 GSGTGGTGAARTGG 15

RESULT 442
 ABN81456/c
 ID ABN81456 standard; DNA; 15 BP.
 XX
 AC ABN81456;
 DT 16-AUG-2002 (first entry)
 XX
 DE Human HTATIP allele specific PCR primer SEQ ID NO 57.
 XX Human, HIV-1 Tat interactive protein; HTATIP; haplotyping; genotyping;
 KW transgenic; PCR; primer; ss.
 XX Homo sapiens.
 OS
 XX WO200229089-A2.
 XX 11-APR-2002.
 XX 05-OCT-2001; 2001WO-US031593.
 XX 06-OCT-2000; 2000US-0238655P.
 PR (GENA-) GENAISAANCE PHARM INC.
 PA Armstrong B, Bentivegna SC, Choi JY, Gilson CR, Parks KE;
 PI Sausker EA;
 XX WPI; 2002-330173/36.

XX New HIV-1 tat interactive protein, 60 kDa (HTATIP) gene polymorphic
 PT variants, for studying the expression and function of HTATIP and
 PT screening candidate drugs for treating familial glucocorticoid deficiency
 PT and cancer.
 XX
 PS Claim 14; Page 14; 89pp; English.

CC The invention relates to novel genetic variants of the HIV-1 Tat
 CC interactive protein, 60 kDa (HTATIP) gene. The polymorphic variants are
 CC useful in studying the expression and function of HTATIP, in expressing
 CC HTATIP protein for use in screening for candidate drugs to treat diseases
 CC related to HTATIP activity, in studying the effect of the variation on
 CC the biological activity of HTATIP and the binding affinity of candidate
 CC drugs targeting HTATIP for the treatment of disorders. Haplotyping
 CC methods are useful in validating HTATIP as a candidate target for
 CC treating a specific condition or disease predicted to be associated with
 CC HTATIP activity or in the design of clinical trials of candidate drugs

CC for treating a specific condition or disease associated with HTATIP
 CC activity. Transgenic animals are useful for studying expression of the
 CC HTATIP isogenes in vivo for in vivo screening and testing of drugs
 CC targeted against HTATIP protein and for testing the efficacy of
 CC therapeutic agents and compounds for disorders. The present sequence is
 CC that of a HTATIP allele specific PCR primer of the invention
 XX
 XX Sequence 15 BP; 3 A; 3 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 8.3%; Score 11.6; DB 1; Length 15;
 Best Local Similarity 91.7%; Pred. No. 3.7e+02; Gaps 0;
 Matches 11; Conservative 1; Mismatches 0; Indels 0;

QY 1657 CACCAAGGCTCAC 1668
 | : ||||| : |
 DB 15 CACCAGGCTCAC 4

RESULT 443
 ABL36320
 ID ABL36320 standard; DNA; 15 BP.
 XX
 AC ABL36320;
 DT 22-APR-2002 (first entry)
 XX
 DE Human lysosomal acid phosphatase 2 (ACP2) allele-specific probe 21.
 XX Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11;
 KW lysosome-specific enzyme; orthophosphoric monoester hydrolysis;
 KW Hodgkin's disease; HD; acid phosphatase deficiency;
 KW novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism;
 KW transgenic animal; primer; probe; primer-extension oligonucleotide; SNP;
 KW single nucleotide polymorphism.

XX Homo sapiens.
 OS
 XX WO200194362-A2.
 XX 13-DEC-2001.
 XX 07-JUN-2001; 2001WO-US018457.
 XX 07-JUN-2000; 2000US-0210047P.
 PR (GENA-) GENAISAANCE PHARM INC.
 PA Kiem SE, Messer C, Tanguay DA;
 XX WPI; 2002-154563/20.
 XX Novel genetic variants of acid phosphatase 2, lysosomal polypeptide gene
 PT useful in studying expression and function of the protein, and for
 PT screening drugs to treat diseases e.g. Hodgkin's disease.

Claim 17; Page 14; 109pp; English.

CC The invention comprises the human lysosomal acid phosphatase 2 (ACP2)
 CC nucleic acid and protein sequences. Specifically, the invention relates
 CC to the discovery of 22 novel polymorphic sites within the ACP2 gene. The
 CC invention also comprises methods for haplotyping and genotyping the ACP2
 CC gene in an individual. The ACP2 gene (located on chromosome 11) encodes a
 CC lysosomal-specific enzyme that catalyses the hydrolysis of
 CC orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and
 CC protein are pharmaceutically important in the treatment of Hodgkin's
 CC disease (HD) and acid phosphatase deficiency. The novel ACP2 gene
 CC polymorphisms of the invention are useful in haplotyping the ACP2 gene.
 CC ACP2 haplotyping is useful in validating ACP2 as a target (and designing
 CC drugs) for treating an ACP2-related disease or condition (e.g. Hodgkin's
 CC disease and acid phosphatase deficiency). The ACP2 gene polymorphisms are
 CC useful for ACP2 genotyping, which can also be used to develop diagnostic
 CC tests and therapeutic treatments. The ACP2 protein and nucleic acids of
 CC the invention are useful in the production of a transgenic animal which

The present invention describes an array of nucleic acid probes immobilised on a solid support, which comprises: (1) a first probe set, comprising probes with a segment of at least 6 nucleotides complementary to the CFTR (cystic fibrosis transmembrane conductance regulator) gene, where the segment includes at least 1 interrogation position complementary to a nucleotide in the CFTR gene sequence; and (2) second, third and fourth probe sets, each comprising probes identical to those in (1) except that the interrogation position is occupied by a different nucleotide. AAA05991 to AAA06240 represent CFTR gene analysis oligonucleotide probes for use in the exemplification of the present invention. The present invention also describes a method of comparing a target nucleic acid with a reference sequence consisting of a predetermined sequence of nucleotides, comprising: (a) hybridising a sample comprising the target nucleic acid to an array of nucleic acid probes immobilised on a solid support; (b) comparing the relative

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1745 CCTCCTATCCTA 1757
 |||||
 Db 1 CCTCCTAACCTA 13

RESULT 446
 ABC26848/c
 ID ABC26848 standard; DNA; 13 BP.
 XX
 AC ABC26848;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 26865 for detecting SNP TSC0007227.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 26865; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 4 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1739 CCAACTCCTCCT 1751
 |||||
 Db 13 CCAATCCTCCT 1

RESULT 447
 ABF15453
 ID ABF15453 standard; DNA; 13 BP.
 XX
 AC ABF15453;
 XX

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1739 CCAACTCCTCCT 1751
 |||||
 Db 13 CCAATCCTCCT 1

RESULT 448
 ABC93112/c
 ID ABC93112 standard; DNA; 13 BP.
 XX
 AC ABC93112;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 93129 for detecting SNP TSC0023277.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 115450; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 9 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1739 CCAACTCCTCCT 1751
 |||||
 Db 1 CCCACTCCTCCT 13

RESULT 448
 ABC93112/c
 ID ABC93112 standard; DNA; 13 BP.
 XX
 AC ABC93112;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 93129 for detecting SNP TSC0023277.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 115450; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 9 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1739 CCAACTCCTCCT 1751
 |||||
 Db 1 CCCACTCCTCCT 13

RESULT 448
 ABC93112/c
 ID ABC93112 standard; DNA; 13 BP.
 XX
 AC ABC93112;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 93129 for detecting SNP TSC0023277.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 115450; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 9 C; 0 G; 3 T; 0 U; 0 Other;


```

XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 93129; 29pp + Sequence Listing; German.
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 1 A; 0 C; 10 G; 2 T; 0 U; 0 Other;
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1738 CCCAACTCCTCC 1750
Db 13 CCCAACCCCTCC 1
RESULT 449
ABC93117
ID ABC93117 standard; DNA; 13 BP.
AC ABC93117;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 93134 for detecting SNP TSC0023277.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 93129; 29pp + Sequence Listing; German.
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 1 A; 0 C; 10 G; 2 T; 0 U; 0 Other;
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1738 CCCAACTCCTCC 1750
Db 13 CCCAACCCCTCC 1
RESULT 450
ABC70351
ID ABC70351 standard; DNA; 13 BP.
AC ABC70351;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 70368 for detecting SNP TSC0018290.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 70368; 29pp + Sequence Listing; German.
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 2 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1738 CCCAACTCCTCC 1750
Db 1 CCCAACCCCTCC 13

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CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1739 CCAACTCCTCCCT 1751
DB 1 CCAACTCCTCCCT 13

RESULT 451
ABC84787
ID ABC84787 standard; DNA; 13 BP.
XX
AC ABC84787;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 84804 for detecting SNP TSC0021342.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 84804; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1746 CTCCTACCTAA 1758
DB 1 CTCCTACCTAA 13

RESULT 452
ABC47949
ID ABC47949 standard; DNA; 13 BP.
XX
AC ABC47949;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 47966 for detecting SNP TSC0013727.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 47966; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
 CC Query Match 8.2%; Score 11.4; DB 1; Length 13;
 CC Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 CC Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1707 TGGCTTAGGAGTA 1719
 DB 13 TGGCTTAGGAGTA 1
 RESULT 454
 ABC49590/c
 ID ABC49590 standard; DNA; 13 BP.
 XX AC ABC49590;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 49607 for detecting SNP TSC0014014.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 110342; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 49607; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
 CC Query Match 8.2%; Score 11.4; DB 1; Length 13;
 CC Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 CC Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1745 CTCCTCTATCCTCA 1757
 DB 13 CTCCTCTATCCTCA 1
 RESULT 455
 ABF10345/c
 ID ABF10345 standard; DNA; 13 BP.
 XX AC ABF10345;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 110342 for detecting SNP TSC0027562.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 110342; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1701 GGAAGTGGGTTA 1713
 DB 13 GGAAGTGGGTTA 1

RESULT 456
 ABC16692
 ID ABC16692 standard; DNA; 13 BP.
 XX
 AC ABC16692;
 XX
 XX 20-FEB-2002 (first entry)
 DT
 DE Oligonucleotide SEQ ID NO 16699 for detecting SNP TSC0003627.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 16699; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 2 A; 1 C; 6 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1709 GGTTAGGAGTACG 1721
 DB 1 GGTTAGGAGTTCG 13

RESULT 457
 ABF16653
 ID ABF16653 standard; DNA; 13 BP.
 XX
 AC ABF16653;
 XX
 XX 21-FEB-2002 (first entry)
 DT
 DE Oligonucleotide SEQ ID NO 116650 for detecting SNP TSC0029189.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 116650; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 8.2%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1739 CCAACTCTCCCT 1751
 DB 1 CCAACTACTCCCT 13

RESULT 458
 ABC47948
 ID ABC47948 standard; DNA; 13 BP.

```

XX AC ABC47948;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 47965 for detecting SNP TSC0013727.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2000; 2000DE-01019173.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 47965; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
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XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1707 TGGGTTAGGAGTA 1719
XX Db ||||| |||||
XX 1 TGGGTTGGGAGTA 13
XX RESULT 459
XX ABC23225/C
XX ID ABC23225 standard; DNA; 13 BP.
XX AC ABC23225;
XX XX 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 23242 for detecting SNP TSC0004727.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
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XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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XX SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1707 TGGGTTAGGAGTA 1719
XX Db ||||| |||||
XX 1 TGGGTTGGGAGTA 13
XX RESULT 460
XX ABC62761
XX ID ABC62761 standard; DNA; 13 BP.
XX AC ABC62761;
XX XX 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 62778 for detecting SNP TSC0016623.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
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CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from Wipo at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 8 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1745 CCTCCTATCCTA 1757
XX
XX Db 1 CCCCCCTATCCTA 13
XX
XX RESULT 461
XX ABC65198
XX ID ABC65198 standard; DNA; 13 BP.
XX
XX AC ABC65198;
XX
XX XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 65215 for detecting SNP TSC0017166.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX OS
XX WO200177384-A2.
XX PN
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
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XX PR 07-APR-2000; 2000DE-01019173.
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